Collaboration for Environmental Evidence

Systematic Review CEE 11-001

What are the environmental impacts of the global cultivation of GM crops?

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Summary

1. Background & Objectives

Globally there continues to be a steady increase in the land area commercially cultivated to genetically modified (GM) crops (James 2007). Accompanying this increase in cultivation is an increase in publications assessing the environmental pros and cons from the uptake and use of the GM technology. With all of this information coming into existence it is important that government advisors and policy makers are presented with impartial, robust and accurate appraisal of this information to assist them with their advice to government.

The objective was to answer the question “What are the environmental impacts of the global cultivation of GM crops?”

This systematic review forms a partner to a sister review of the economic implications to GM adoption.

2. Methods

A systematic search for relevant articles was conducted in four databases and one search engine using search statements designed to identify any study in any country measuring environment parameters at the farm scale, or above, where there was cropping of a commercial GM trait. All retrieved articles were scanned at title, then abstract and finally full text level using the criteria set out below in order to select those most relevant.

- Relevant subject: an environmental indicator recorded at the farm level or above
- Types of intervention: the cultivation of any commercial GM modification in the last 5 years (i.e. 2006 onwards) later modified to any publication in the last 5 years
- Types of outcome: seasonal or environmental impacts where there was comparison with a conventional (non-GM) cropping system

3. Main Results

The use of a search statement particular to this review generated over 2 million hits in the search engine, databases and grey literature searches. From these hits 5737 titles were recovered from which 43 relevant papers were finally distilled. The information within these 43 papers was assessed using a narrative table and indicated that 84.6% found no adverse effects on the environment from the cultivation of GM, 10.3% reported a beneficial effect and 5.1% a deleterious impact.

The environmental data suitable for extraction in 28 of these 43 papers was compiled into a data set for subsequent meta-analysis. Initial investigation of the data set revealed that adoption of GM did not maintain the environmental conditions observed within conventional field sites, but significantly increased it from a background level of 1, indicating no difference, to a mean value of 1.31.

Subsequent regression analysis indicated that there was no standard model to explain variation in the extracted environmental outcomes. However, in models for both cotton and maize, variables relating to the design of the study had a significant effect on outcome.

4. Conclusions

The evidence presented in this study does not indicate a significant reduction in environmental indicators as a result of GM adoption. The undertaken analysis suggests that there may be an overall increase in the examined ratio of environmental change under GM over conventional systems. However, with the difficulties in interpreting environmental changes with regard to relevance in the ecosystem and the lack of universal environmental indicators, the wider field and landscape implications from GM adoption cannot be ascertained.

Main Text

1. Background

There is continued debate regarding the environmental consequences of introducing genetically modified (GM) crops and this underlies much of the global disparity in the uptake of the technology. Despite these differences in how various countries and their public have responded to the availability of a range of herbicide and insect tolerant crops the global cultivated area continues to increase (James 2010). Much of the public's uncertainty in the environmental safety of the GM technology arises out of divergence in personal belief and levels of trust in companies that hold the rights to the technology and in the scientific institutes that have conducted the risk assessments (Andow et al. 2006). With regard to the scientific risk assessments and associated experimentation there are many criticisms, particularly from Non Government Organisations, that these have often been insufficient. According to several research groups, many experiments used to test the environmental safety of GM crops are not field relevant, lack replication in design, cover single or limited timescales, are limited in what they record or have been incomplete due to their destruction by members of society opposed to the cultivation of GM (Marvier et al. 2007; Andow et al. 2006; Balog et al. 2010). Despite the potential flaws in some of the experiments conducted there is an abundance of literature covering a range of crops, traits, countries and environmental impact data (Ricroch et al. 2010).

Traditionally the interpretation of existing scientific data is undertaken by single authors or small scientific groups conducting reviews of the published literature relevant to a particular subject area as part of a new or existing project. Similar exercises have been undertaken for GM crops and their associated technology often presenting very clear and concise interpretation of the major findings (Beckie et al. 2006; Fitt 2008; Kleter et al. 2007; Lang and Otto 2010; Widmer 2007; Brookes and Barfoot 2011). However, the review process does little to address the discrepancies in personal concerns over GM or provide systematic evaluation of the covered literature, methodologies and measurement tools. In order to attempt to address this, a more novel approach is required that improves transparency, reproducibility, objectivity and provides confidence in the outcomes. One such novel approach is through systematic review (Stewart et al. 2005).

The process of systematic review differs to traditional literature reviewing in that the process is transparent, rigorous and replicable. In adhering to the process the systematic review achieves the removal of reviewer personal views, provides comprehensive summary of the relevant literature and through the use of meta-analysis can provide improved statistical interpretation of the findings and reasons for variation in the existing data and results. The aim of the review reported here is to address the question 'What have been the environmental impacts of the global cultivation of GM crops?'.

2. Objectives

2.1 Primary objective

The primary objective was to answer the question: 'What have been the environmental impacts of the global cultivation of GM crops?' Execution of a systematic review requires that a specific question be posed containing three key elements (Khan et al. 2001). The question for this review contains the following components:

(1) a *subject*: an environmental indicator recorded at the farm level or above

(2) an *intervention:* the cultivation of any commercial GM modification in the last 5 years (i.e. 2006 onwards) - later modified to any publication in the last 5 years

(3) the *desired outcome*: seasonal or environmental impacts where there was comparison with a conventional (non-GM) cropping system

The use of a comparator in the outcomes of the question is often included as a forth element of the question and is typical of many systematic reviews. In the study reported here the comparator was central to the review process.

3. Methods

3.1 Question formulation

Defra tendered a systematic review of peer reviewed and grey literature published since 2006 on GM crop technology. The aim was to assess the impacts that GM adoption may have on both the crop and wider environment, whether deleterious or beneficial. In order to achieve this SAC compiled a team of experts from a number of disciplines and external companies to undertake a systematic review. The review question was formulated following discussion between the SAC review panel and Defra, with subsequent modification following peer review conducted via the CEE.

3.1.1 Search terms

In order to address the question posed a web based search statement was established from three lists of keywords that were agreed by the expert panel conducting the review with the funders, Defra, based on the components of the question that had been identified (Table 1). The statement was further refined with numerous scoping studies and a peer review of the protocol. The use of the wildcards * and $ as well as SAME or quotation marks, as keyword linkers, had to be altered for the syntax preferences of some search engines (see appendix

1). Keywords were linked with the OR command and the three resultant search statements linked with AND.

Table 1 Components of the primary question and the descriptions of them that were used to populate a table of keywords subsequently integrated into the search statements used in this systematic review.

Subject	Intervention	Outcomes	Comparators	Design
Environmental impacts as recorded at the sacle of the farm level and above.	Genetically Modified (GM) crop cultivation in the past 5 years. Any commercial genetically modification (GM trait). Any GM crop.	Long term environmental impacts. Seasonal environmental impacts.	Conventional (non-GM) cropping system.	Any study comparing before or after GM crop cultivation OR comparing changes during GM crop cultivation with a conventional crop

3.1.2 Databases/websites

Alternative methods for searching some databases (e.g. advanced search instead of expert) also resulted in some truncation of the search term and similarly in some search engines the order of the AND command made a difference to the outcome of the Boolean search. These changes were noted when the search was run and the results recorded

The following databases were searched;

Web of Knowledge
Science Direct
CAB Direct
COPAC.
SCIRUS

3.1.3 Specialist sources

The words present in the search statement were also used in a manual search of the listings for publications from BCPC and Agbioview since 2006.

The review team contacted 14 individuals working in the area of the review.

3.2 Study inclusion criteria

Criteria for including studies were based on;

- Relevant subjects included any study conducted in any country considering the environment at the farm scale or above where there was cropping of a commercial GM trait.
- The intervention was focused on studies in which GM crop cultivation had occurred.

- Comparators of either the situation prior to cultivation of GM crop with the situation post GM crop cultivation or changes within the season/s when GM and conventional (non-GM) crops are cultivated together were presented.

The outcomes of these studies were likely to be changes in environmental parameters (e.g. changes in species presence [weeds, predators, non-target organisms], changes in soil diversity and function, impact on landscape) since cultivation of a GM crop.

In addition to this the review was limited to studies published since January 2006 (as established by the client). Reported field trials could include environmental impact at a range of scales (e.g. field, farm, valley, regional, countries, continental and global) across cropping types (e.g. plant species) and GM traits.

Exclusion of studies was made on the basis of the use of non-commercial GM traits, the use of only laboratory, glasshouse or modelled data and data acquired under experimental conditions that lacked sufficient detail to be reproducible.

To pass each stage of the SR the study had to meet these criteria.

3.2.1 Title review

The reviewers independently reviewed 157 of the 5737 recovered titles and established 95% similarity in title selection approach (Kappa 0.85). Review of the titles using the study criteria given above initially resulted in 283 titles being identified as suitable for continuation to abstract screening. 14 were found to have duplicates in the database that once removed resulted in 269 novel titled articles that were selected for screening at abstract.

3.2.2 Abstract screening

In the protocol (section 2.1) the intervention for the study was one of crop cultivation within the last 5 years. Imposing this intervention would have restricted the review to 10 papers. To increase the potential number of included papers and valid data sets, it was decided to change the intervention to simply include all papers published since January 2006, as had been the basis of the search strategy. Following all abstract screening and agreement between the reviewers a total of 102 papers was selected for full review, including 21 papers not captured by the web searches, but identified in the bibliographies of papers selected for full review that matched the selection criteria.
Analysis by both reviewers of a sub set of 24 of the abstracts indicated a 92% similarity (Kappa 0.62) of selection decisions.

3.2.3 Full review

Full review was conducted by two members of the review team who sought agreement on the list of papers suitable for final inclusion. The final list of papers for inclusion contained 43 papers and included 5 papers not identified in the web searches.

3.3 Study Quality Assessment

The scientific quality of the papers was ranked by the review authors who considered the content of the papers in accordance with CEE guidelines (section 3.3). This was achieved by assessment of the papers for:

- methods of assessment used
- trial design
- level of analysis (plot size, replication and number of years of trials)
- existence of comparable intervention between treatments
- inclusion of baselines methods of analysis
- level of detail of site descriptions
- management and the apparent quality and quantity of potential data within the paper.

On the basis of these criteria the reviewers assigned scores between 1 and 4 to represent; (1) valueless, (2) poor, (3) good and (4) high quality. This screening provided a final check on manuscript suitability and allowed for an initial narrative and qualitative analysis to be undertaken.

3.4 Data extraction

Environmental data for a range of functional, diversity and abundance measures pertaining to changes due to GM cultivation was extracted. Papers were initially pooled into whether they dealt with environmental impacts on microbiology (13 papers), non-target arthropods (22), earthworms (4), weeds (4) and pollen flow (4). Some papers contained information on several of the desired environmental comparators, which resulted in 47 environmental indicator studies being identified from the 43 papers. The papers were then screened for relevant and comparable sub-sets of data and comparator information as listed in the protocol. The overall findings of the papers were recorded according to whether the authors reported deleterious, no adverse or beneficial impacts of GM cultivation. In cases where the authors had not indicated an outcome, consultation followed by agreement on the status of the findings was made by the review authors.

Data extraction was taken directly from text, tables and figures within the reported work where it pertained to measures of environmental indicators that had similar comparators elsewhere within the extracted literature. Due to the decision to utilise a ratio approach for analysis data also had to have an identified paired comparator and that data with zero values within a possible pair was also excluded. Within the arthropod data, only that which pertained non-target organisms (i.e. not lepidopteran data) was extracted so that only unintended environmental perturbations were included. Where papers reported data from the same series of field experiments the data was pooled under the pertinent study to reduce bias from author publication prowess.
Data was extracted into Microsoft Excel where the study characteristics from the eligible papers were; author, title, year of publication, country of study, crop, trait, inserted genes, plot size, number of plots, seasonality of data, management characteristics, management modifications, environmental indicator and indicator specifics.

Four papers covering experimentation on seed movement or pollen flow were segregated at this point as they predominantly did not contain GM to non-GM comparisons, but the data is of relevance to environmental or landscape level of assessment of GM. Due to this the papers relating to pollen flow were extracted and analysed separately.

Not all papers contained data that was suitable for extraction and analysis because either;

- the data had no obvious GM to non-GM comparators;
- was graphed in such a way that values could not be accurately obtained or;
- was simply absent from either text, figures or tables within the manuscripts.

This further restricted the subsequent recovery of data from the 39 selected manuscripts, after removal of the pollen flow papers, to 28.

Reviewing the data for extraction quickly indicated that few of the papers contained sufficient detail or uniformity of information to undertake Hedge's *d* weighted mean effect analysis, as has been recently utilised elsewhere in GM systematic reviews (Marvier et al. 2007; Wolfenbarger et al. 2008), and time constraints for fulfilment of the project meant that contacting authors for additional information was impractical.

R, the ratio of the geometric mean of the GM treatment divided by the non-GM or in some cases the non-GM and modifier treatment was the adopted method for statistical analysis.

The basic premise was to determine if there was an environmental change under GM and would therefore be indicated by a R value significantly different to 1 being returned. A value of 1 would indicate no difference in effect between comparators. A value significantly different from 1 would indicate a change in the environmental indicator being assessed.

For each line of data extracted the calculated R value, the standard deviation, the standard error of the mean and the number of data pairs that were used to establish R were recorded.

3.5 Data Synthesis

Initial assessment of the R values was conducted with Chi square and T test with the assumption that if GM adoption had no impact on the environmental indicator then the expected values would be 1. The data was then grouped by various comparators to generate forest diagrams (Lewis and Clarke 2001) (Figures 2 to 6) and the independent data within these sets analysed with unbalanced ANOVA of natural logarithm transformed data. The meta-data set analysis of environmental outcomes from GM cultivation was conducted with ordinary least squares (OLS) models, estimated (using SPSS19.0) to determine the effects of the variables collected for the meta-analysis on the observed variation in environmental outcomes as represented by the R values.

The purpose of this analysis was to identify whether the variation in outcome can be explained by variables related to GM traits (e.g. trait type, genes); modifiers in the conventional comparator (e.g. no modifier, tillage, pesticide application); environmental indicators (e.g. arthropods, earthworms, microbiology, weeds); geographic location (e.g. country, continent); or variables specific to the study (e.g. publication year, single or multi-year data).

A number of dummy variables (1,0) were coded to account for the qualitative variables extracted from the studies, in addition the publication year was rebased so that the earliest year (2006) was given a value of 0 and subsequent years coded in increments of 1 (i.e. 2007=1, 2008=2 etc.).

4. Results

4.1 Studies found

The author reported findings of the papers indicated that 84.6% found no adverse effects on the environment from the cultivation of GM, 10.3% reported a beneficial effect and 5.1% a deleterious impact. This was equivalent to 89 trial years of no adverse effects, 9 years of beneficial effects and 6 trial years of deleterious impacts.

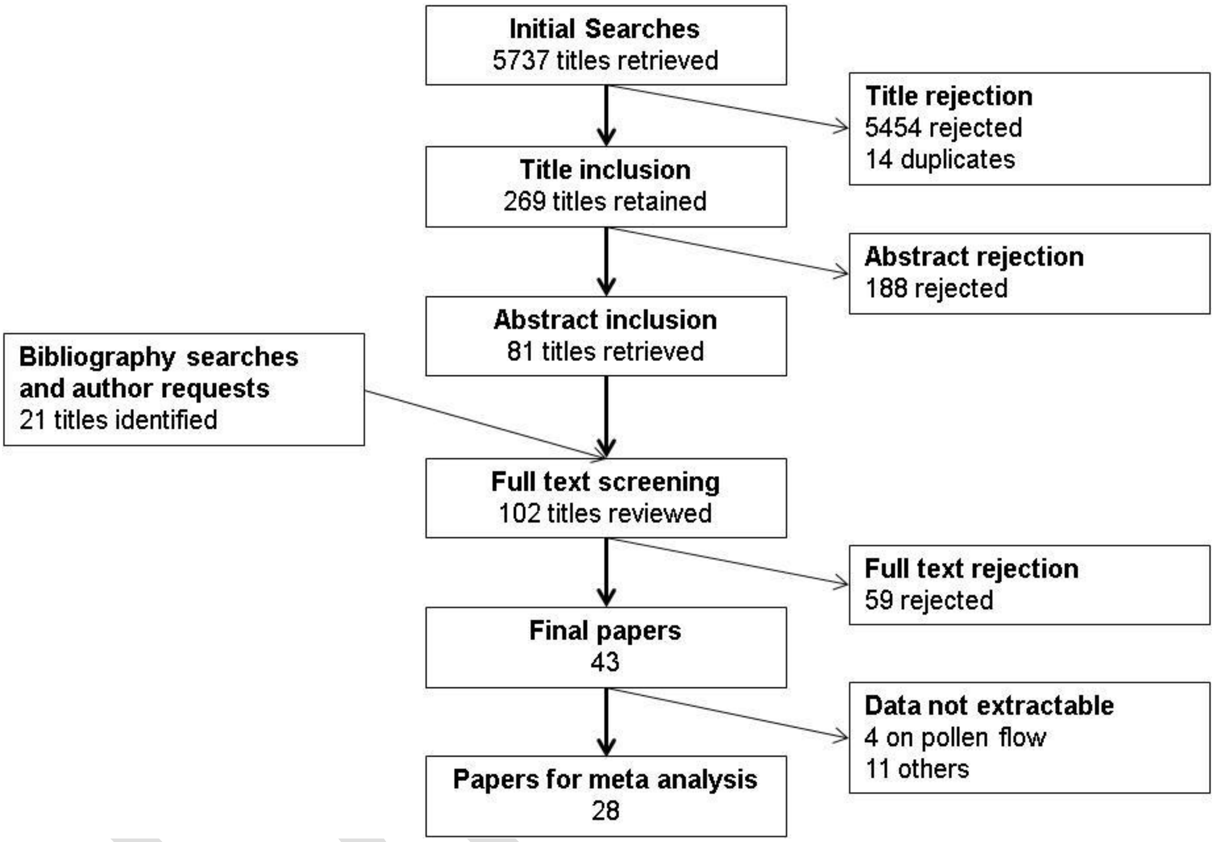

Figure 1. Flowchart illustrating the processes and sequential reduction at the various stages of the review to identify the papers and studies that contributed to the systematic review.

2340237 titles hits were recorded using the search statement in the indicated databases and search engines of which 5737 titles were retrieved (Figure 1). The number of retrieved titles was restricted from all hits due to exportation restrictions on some of the search engines and databases (Table 2). Initial review of the 43 papers that remained at the end of the search and criteria assessment indicated that there were 35 individual experimentation platforms present in the assembled data, covering 119 years of field trials from 15 countries (Australia (1), Canada (5), China (1), Czech Republic (1), Denmark (5), France (6), Germany (5), Hungary (3), India (3), Netherlands (1), Portugal (1), South Africa (1), Spain (1), UK (4) and the USA (9)).

The crops covered in the 43 papers included maize, cotton, oilseed rape (OSR), soy and sugar beet with 31, 9, 4, 1 and 1 papers on each of these crops, respectively. Ten of the papers dealt with herbicide tolerant traits, 29 investigated insect resistance and 4 dealt with both herbicide and insecticide traits (Table 3).

Table 2 Results of the internet hits for the searches conducted for the environmental systematic review and the offered additional papers. The number of titles retrieved is indicated as some of the search databases limited the number of retrievals possible. The number of titles taken through to abstract search as listed as Extracted titles and the totals are presented.

Search database	Statement modification	Hits	Retrieval	Extracted titles
Web of Knowledge	none	158	158	93
Science Direct	none	3954	1000	30
Science Direct	Six modifications to syntax and terms to use advanced search options	28, 32, 105, 15, 6 and 42	228 (160 novel)	17
CAB direct	none	9324	1000	72
CAB direct	Statement 2 AND 3	544	544	0
COPAC	none	9804	2500	1
COPAC	title word limit	180	180	0
Agbioview	Hand search	3374	62	57
BCPC	Hand search	1415	13	13
Search Engine				
Scirus	none	2311256	120	0
Bibliographies				21
Expert offered papers				12
	Total	**2340237**	**5737**	**316**

4.2 Study quality assessment

Data presented in the final papers was assessed against the described criteria (section 3.3) and is summarised in Table 3. The quality assessment had reviewer assigned quality mean and standard error (in parentheses) scores for no adverse, beneficial and deleterious findings of 3.42 (0.10), 2.75 (0.25) and 3 (0.71), respectively, on the1 – 4 scale where 1 related to valueless and 4 was high quality. The data was not significantly different.

Table 3 List of the 43 titles selected from the search for inclusion in the review. The initial data assessment of the papers is presented along with the indication of information potentially extractable for meta analysis. *NI in the genes column represents that the information was 'not indicated' and could not be discerned from other papers relating to the reported trial.

First Author	Year	linked sites	data quality	study dates	Country	Crop	Modification	Genes			Potential data
Balog, A	2010	3	4	2001-2003	Hungary	Maize	insect	Cry1Ab			abundance (table 2, table 3) and aphid (table 5)
Balog, A	2011	3	3	2008	Hungary	Maize	insect	Cry1F	Cry34Ab1	Cry35Ab1	abundance in table 1
Bourassa, S	2010		4	2004-2005	Canada	Maize	Herb	EPSPS			density (table 1 first 2 columns) activity density by rotation (table 3)
Carriere, Y	2009		3	2002-2003	USA	cotton	insect	Cry1Ac			none - no clear Bt to Conventional parameters expressed elsewhere
Cattaneo, N	2006		3	2002-2003	USA	Cotton	Both	Cry1Ac	EPSPS		density and species richness
Cortet, J	2007	1	3	2002-2003	France, Denmark	Maize	insect	Cry1Ab			none
Cortet, J	2006	1	4	2002-2003	France, Denmark	Maize	insect	Cry1Ab			abundance data (table 3)
Darmency, H	2007		4	1995-2000	France	Beet	Herb	*NI			gene movement %
Debeljak, M	2007	1	3	2002-2003	Denmark	Maize	insect	Cry1Ab			Earthworm biomass (table 1). Abundance of collembolla (table 1)
Demaneche, M	2008		3	2007	France	Maize	insect	Cry1Ab			none - antibiotic resistance levels
Deavare, M	2007		4	2001-2003	USA	Maize	insect	Cry3Bb1			biomass, mineralisation, nitrification
Farinos, G	2008		4	2000-2002	Spain	Maize	insect	Cry1Ab			richness data in tabel 2 and rations in table 3
Firbank, L	2006	2	4	2000-2002	UK	Maize, OSR, Beet	Herb	NI			R values, seedbank numbers
Floate, K	2007		3	2000-2003	USA	Maize	insect	Cry1Ab			means of abundance where differences detected (tabe 3)
Frouz, J	2008		3	2002-2004	Czech Republic	Maize	insect	Cry1Ab			biomass, decomposition and abundance (table 1)
Gathman,	2006		3	2001-2003	Germany	Maize	insect	Cry1Ab			ratio of insects between treatments (table 3)
Gibbins, D	2006	2	2	2000-2002	UK	Maize, OSR, Beet	Herb	NI			none - weed data of FSE fitted to proposed bird diets.
Griffiths, B	2007	1	4	2002-2005	France, Denmark	Maize	Both	Cry1Ab	bar		Bacteria to fungi ratios, nematode
Gulden, R	2009		4	2000-2006	Canada	Maize, soy bean	Herb	EPSPS			ground cover and weed desnsity
Heard, M	2006	2	4	2000-2002	UK	Maize	Herb	NI			R values, weeds, invertebrates for fields and margins
Hofs, J	2008		4	2003-2003	South Africa	Cotton	insect	Cry1Ac			diversity and abundance (table 1,2 and 3)

Hu, H	2009		2	2006	China	Cotton	insect	Cry1A				none - paper in Chinese
Icoz, I	2008		3	2003-2006	USA	Maize	insect	Cry3Bb1				log 10 CFU and enzyme activity
Krogh, P	2007	1	4	2003-2005	France, Denmark	Maize	Both	Cry1Ab	bar			abundance, biomass
Kumar, K	2007		2	2002	India	Cotton	insect	Cry1Ac	CryIIA			abundance (tables 1 and 2)
Lang, A	2007		3	2000-2003	Germany	Maize	insect	Cry1Ab				abundance, biomass,
Llewellyn, D	2007		4	2002-2005	Australia	Cotton	Both	Cry1Ac	Cry2Ab	EPSPS	bar	gene movement % into conventional buffers
Lupwayi, N	2007		3	2000-2005	Canada	OSR	Herb	EPSPS				biomass, diversity
Mann, R	2010		4	204-2005	India	cotton	insect	Cry1Ac	Cry2Ab			insect (pest and predator) numbers per plant
Miethling-Graff, R	2010		3	2005-2007	Germany	Maize	insect	Cry3Bb1				none
Oliveira, A	2008		4	2003-2004	Portugal	Maize	insect	Cry1Ab				cfu/g, dehydrogenase, ATP, nitrogenase
Powell, J	2009		3	2003-2006	Canada	Maize	herb	EPSPS				fungal to bacterial biomass, degradation
Prasad, N	2008		3	2005-2006	India	Cotton	insect	Cry1Ac				non-target in table 1
Priestley, A	2009		4	2003-2004	USA	Maize	insect	Cry1Ab				abundance data (tables 1, 3, 5, 6) species data (table 2)
Rauschen, S	2008		4	2002-2003	Germany	Maize	insect	Cry1Ab				ration estimates (table 4), abundance (table 2)
Rose, R	2007		3	2000-2001	USA	Maize	insect	Cry1Ab				none - data presentation limits use
Schier, A	2006		3	2002-2005	Germany	Maize	Herb	EPSPS				none - only RR maize planted
Simpson, E	2006		3	1998	UK	OSR	Herb	EPSPS	bar			percentage in crops at distance, data in text.
Szekeres, D	2006	3	3	2001-2003	Hungary	Maize	insect	Cry1Ab				abundance (table 1) species (table 2)
Torres, J	2007		4	2002-204	USA	Cotton	insect	Cry1Ac				abundance, diversity indices between bt and non-bt
Van De Wiel, C	2009		4	2006-2007	Netherlands	Maize	insect	Cry1Ac				pollen mediated gene flow percentages
Yanni, S	2011		3	2008-2009	Canada	maize	insect	NI				crop data, lignin, C\N
Zeilinger, A	2010		3	2005-2006	USA	Maize	insect	Cry1Ab	Cry3Bb1			ash free dry mass of earthworms

4.3 Qualitative synthesis

Herbicide tolerant traits

In the 16 papers dealing with herbicide traits, glufosinate ammonia (*bar* gene) and glyphosate resistance (EPSPS gene) were represented in 4 and 8 of the 43 final papers, respectively. In the remaining 4 papers pertaining to herbicide tolerant traits the gene or herbicide involved could not be determined. Insecticide resistance genes were not identifiable in 1(3% of papers dealing with insect resistance) of the papers dealing with these traits. The gene Cry1Ab reported on in 18 (46%) of the papers, Cry1Ac was found in 9 papers (23%), Cry3Bb1 in 4 papers (10%) and Cry2Ac in 2 papers (5%). The genes Cry1A, CryIIA, Cry1F, Cry34Ab1 and Cry35AB1 were identified in 1 paper each.
The 119 years of field data present in the papers covered trials from 1995 to 2009 and was normally distributed (Shapiro-Wilk p=0.1) from 1998 to 2009 with a range from 1 to 25 trials in 2003 and a mean of 9.67. The average number of years covered by the trials reported within the papers was 2.77 years with a standard deviation of 1.32, a minimum of 1, maximum of 7 and a median of 3.

Effect modifiers

It had been expected that several potential effect modifiers may have been recorded or examined as part of the reported work. During the initial review of the papers it was noted that effect modifiers pertaining to tillage, pesticide regimes, rotational changes and climatic data were reported in 33% of the 43 papers. The split of these effect modifiers was; conventional to reduced tillage 5 papers (12% of total), conventional to conventional without pesticides 5 papers (12%), pesticide and tillage effects 1 paper (2%, but no extractable data), rotations 2 papers (5%) and climate 1 paper (2%).

Pollen flow

Four papers from the search and selection process dealt with transgene escapes through out-crossing and pollen flow. These papers represented work on cotton (Llewellyn et al. 2007), sugar beet (Darmency et al. 2007), maize (Van De Wiel et al. 2009) and OSR (Simpson et al. 2006). There was no similarity in experimental design or in the nature of the presented data reducing the potential methods of data comparison to a narrative summary of the findings. Three of these four papers did not present a GM to non-GM comparison the exception being Simpson et al. (2006) who used a conventional imidazolinone tolerant variety to compare against glufosinate ammonia and glyphosate tolerant GM varieties. Whilst the imidazolinone out-crossing was lower than the GM varieties, numerous explanations for this observation are given (Simpson et al. 2006), which lead to the conclusion that more work is required.

4.4 Meta data analysis

For meta-data analysis the 43 papers were re-read and data extracted according to the presented criteria (section 3.5). The result of this was that information from 28 of the papers was extracted resulting in 209 lines of R value data derived from 1339 paired data points. The overall impression from the forest plots was that there was a general increase in the environmental indicators recovered from the data sets in so far as the mean R values were largely >1.

Country

Exceptions to this were observed for trial data from South Africa and Spain (R = 0.76 and 0.86, respectively, Figure 2), cotton with insecticide and herbicide trial effects (R= 0.89), sugar beet (R=0.88, Figure 3), studies involving Cry1Ab and Cry2Ac (as found in BollgardII cotton, R= 0.94) and trials with Cry1F and Cry35Ab1 (R= 0.98,Figure 4) and cultivation modifications where location (limited to South Africa) and rotation were included in the trial (R= 0.74,Figure 5). Despite these apparent differences, unbalanced ANOVA analysis of the natural log transformed data did not detect any significant differences (p>0.12 in all comparisons) between the indicated comparators. These unbalanced ANOVA assessments of the various comparators also served as a sensitivity analysis of the data set.

To attempt to determine if the meta-data set was similar to a R value of 1, which would have indicated no change from the adoption of GM, the data was run against a dummy set of R values equal to 1. Chi squared analysis showed that there was a significant difference between the two set (χ^2 = 622, df = 208, p<0.001). A two tailed T test of the data also indicated a significant difference (p<0.01) with the meta-data having a mean R value of 1.31. Within the data set there was significant heterogeneity (Q=1134, df = 208, p<0.001), which was explored further using regression analysis in SPSS with the recorded environmental factors as independent variables.

Initial model specifications including all crop types were estimated, but no significant explanatory variables were found for the R values. The next step was to explore models for individual crop types; models for beet (n=3), maize and soy (n=8) and oilseed rape (n=3) were not estimated due to low numbers of observations.

Cotton

The results of the regression analysis for the cotton studies (n=32) are presented in Table 4. The variables are all significant (p<0.01) as was the regression as a whole (p value of the F value), the adjusted R^2 value indicated that the variables explained 77% of the observed variation. The negative coefficient for the year variable indicated that more recently published studies report lower R values (less environmental benefit of GM), however, the extent to which this reflects more recently conducted studies is not clear. Studies reporting R values over multiple years (as opposed to single years) also show reduced R values. The positive value of the Asia dummy indicated that studies undertaken in India showed a more favourable environmental outcome for GM versus the conventional comparator. The reduced pesticide dummy was given a value of 1 where the conventional comparator was modified through reduced use of pesticides; the negative sign of that coefficient was as expected and reflected the higher environmental outcome (all based on arthropod data) under the conventional comparator, thus reducing any relative advantage of GM.

Comparison of the standardised coefficients indicated that publication year has the greatest influence in R value followed by multi-year data, country of study and modifier had opposite effects of similar magnitude. These results indicated that study related factors explain more of the variation in environmental outcome than both study location and what GM is compared to.

Table 4. Regression results for cotton studies (dependent variable = R value)

	Coefficients		**Standardised coefficients**	**t-stat**	**p-value**
	B	**Std. error**	**Beta**		
Constant	3.614	0.346		10.452	0.000
Year (2006=0)	-0.847	0.083	-1.940	-10.236	0.000
Asia dummy (India)	0.712	0.218	0.565	3.270	0.003
Multi-year data dummy	-1.445	0.251	-1.229	-5.767	0.000
Reduced pesticide dummy	-1.747	0.314	-0.558	-5.567	0.000
Number of observation	32				
Adjusted R^2	0.767				
F value	26.482				0.000

Maize

The results of the regression analysis for maize are presented in Table 5. Despite the higher number of observations (n=163) in this dataset we were unable to estimate a model that performed as well as that for cotton. The overall model had a low goodness of fit (R^2 = 2.7%), however, the model was significant (p<0.10). This suggests that there remain unreported but important variables explaining R. It should be noted that the dependent variable used for the maize model was the natural logarithm of the R value, this transformation was used to reduce the effect of a skewed distribution of R values that resulted from a small number of outliers.

Table 5. Regression results for maize studies using country variable (dependent variable = ln R value)

	Coefficients		**Standardised coefficients**	**t-stat**	**p-value**
	B	**Std. error**	**Beta**		
Constant	0.067	0.065		1.036	0.302
Insect modification dummy	0.240	0.093	0.244	2.582	0.011
France dummy	-0.169	0.104	-0.148	-1.625	0.106
Portugal dummy	-0.268	0.143	-0.158	-1.875	0.063
USA dummy	-0.218	0.102	-0.195	-2.130	0.035
Number of observations	163				
Adjusted R^2	0.027				
F value	2.142				0.078

Insect resistance

The insect modification dummy variable had a positive coefficient indicating this modification, rather than herbicide tolerance, resulted in more positive environmental outcomes (i.e. higher R values). This was also the most influential variable as demonstrated by the standardised coefficient. Alternate analysis that considered specific genes, rather than the broader trait, did not produce significant results. The remaining significant variables all related to country specific effects, with the negative coefficients in each case indicating lower

R values in each of these countries. The coefficient for the France dummy was marginally insignificant at p=0.10, but removal of this variable from the model reduced overall model performance and significance. These results might be interpreted as country level effects as the studies for each of these countries involved the same trait (insecticide), but showed an opposite effect to that trait and the same gene (Cry1Ab), which in itself was not significant. However, the studies in each of these countries primarily used microbiological environmental indicators. A simpler model for maize, where environmental indicator was used in place of country variables (Table 6) performs better in terms of overall significance (0.057 vs. 0.078) and suggests that what might have been interpreted as a country level effect was in fact due to the choice of the environmental indicator used to determine R. In this case the negative coefficient showed that studies using microbiological indicators will produce a reduced value of R. The standardised coefficient indicates that this effect is stronger than that due to trait. The results of the regression analysis indicate that there is no standard model to explain variation in environmental outcome. However, in both the cotton and maize models, variables relating to the design of the study have a significant effect on outcome.

Table 6. Regression results for maize using environmental indicator variable (dependent variable = ln R value)

	Coefficients		**Standardised coefficients**	**t-stat**	**p-value**
	B	**Std. error**	**Beta**		
Constant	0.106	0.068		1.563	0.120
Insect modification dummy	0.145	0.078	0.147	1.843	0.067
Microbiology dummy	-0.138	0.071	-0.155	-1.948	0.053
Number of observations	163				
Adjusted R^2	0.023				
F value	2.923				0.057

5. Discussion

Narrative analysis of all 43 of the extracted papers indicated most clearly stated either no adverse effects or positive environmental benefits from GM adoption, but it is perhaps worth considering this point from those that reported deleterious impacts. In total, 5.1% of the 43 papers reported deleterious environmental impacts of GM adoption. Five % is often taken as the point at which observations become significant and so, from the narrative analysis, there was evidence that deleterious environmental impacts from GM cultivation were occurring by mechanisms other than chance. However, this represents a crude interpretation of author opinions and hence the need for more rigorous analysis.

5.1 Evidence of environmental impact

The targeted approach to peer reviewed and grey literature recovery was deemed to have been successful in that none of the final material was found to be worthless during the qualitative assessment. Despite the effort exerted in the grey literature searches, none of the final 43 papers were a result of this undertaking. Theories for this were discussed and the general consensus was that because the target audience for this material is more diverse the content is generally less specific or in-depth.

The number of papers finally selected may seem small given the subject area and the content of the papers and the cropping areas covered is also limited in the number of crops identified and the countries covered. There are currently 29 countries growing 12 commercial GM crops (James 2010) and yet we identified papers covering only 15 countries and 5 crops. Differences in the crops detected may be partially due to the geographical restrictions on the commercialisation of crops like poplar, tomato, sweet pepper, squash and papaya. Another potential reason for this discrepancy is that we restricted our analysis to papers published in the past 5 years, which may have excluded some of the crops on the grounds of when the work on them was published. The country difference is harder to reconcile, but may be due to the rapid adoption of GM in developing countries that is being observed (James 2010) and that these countries may be looking elsewhere for scientific guidance (Bodulovic 2005).

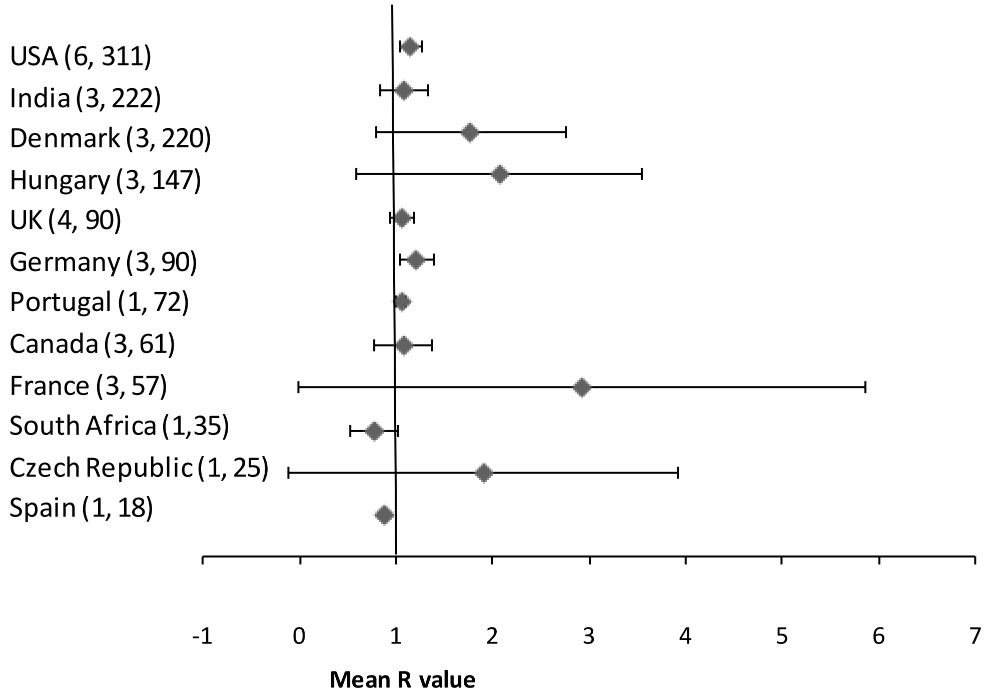

Figure 2. Forest plot of the mean R values by country resulting from the division of GM environmental indicator measurements by conventional paired data. Error bars represent 95% confidence intervals derived from the meta data set generated for this study. Numbers in brackets represent the corresponding number of papers and the number of paired data sets that went into the calculated value.

Papers on pollen transfer between genetically modified crops and either wild or cropped compatible recipients made it through the search and review process, but were dealt with independently of the other papers and data because they did not present a GM to non-GM comparison with the exception of Simpson et al. (2006). The aspect of isolation distances was tackled in the cotton and maize work, which is significant from an EU standpoint as thresholds dictate the requirement for labelling. Both papers indicate that the tested buffer or isolation distances of 20 m for cotton (Llewellyn et al. 2007) and 25 m for maize (Van De Wiel et al. 2009) would prevent pollen mediated gene flow from exceeding the 0.9% labelling

threshold. However, the authors note that changes in field sizes, extreme weather conditions, increased pollinator presence, areas of open ground and legislative threshold changes all require consideration. Pollen flow from sugar beet was reported as accounting for 0.4% of the resistant seeds that developed over the course of the work undertaken by Darmency et al. (2007). Pollen movement was recorded over 277 m, which was greater than that observed in the cotton and maize work, but the greatest issue with transgene escape came from sugar beet bolters appearing in the following crop, which implies that suitable management would be a required to restrict gene flow (Darmency et al. 2007).
A number of issues were identified within the papers that can have a further impact on the extent of pollen movement in the environment and 75% of theses papers identified the need for further study either before or when GM cropping status changes. The general findings were that pollen mediated gene flow occurred, but that it was within levels that would be acceptable under the EU labelling threshold of 0.9% in 50% of the identified studies, whilst not considered in this context in the remaining 50%.The limited number of studies relating to GM pollen flow issues, identified with the methodology used in this review, meant that more critical appraisal of the issue of pollen transfer was not possible and would be better achieved through a more targeted systematic review of pollen flow from specific crops with out time bound restrictions.

The systematic review of environmental indicators was undertaken using a ratio approach to data extraction and analysis, similar to those undertaken in previous medical systematic reviews (Crombie and Davies 2009). Given the wide range of potential environmental indicators available within the selected papers this approach was also seen as one that would allow for direct comparison across all possible data sets providing reported data could be paired according to one of the prescribed environmental comparators and that neither number in the pair was zero. Excluding pairs with 0 values meant that by not relying on total, summed or average data assessments from paper we could extract data down to lower levels of comparators and increase the number of data points in the meta-data set.
Additionally, comparison of data within five of the arthropod papers, in which there were several 0 values for either GM or conventional observations, produced a mean R value of 1.08 for the extracted paired data whilst the mean R value, based on the totals from the same paper had a mean of 1.02. Whilst omitting values for which there was not a non-zero corresponding data point may have slightly elevated the reported R values, this observation was not significant (p=0.68 in a two tailed T test) and indicated that the exclusion of pairs with 0 values had little consequence on the sensitivity of the subsequent analysis. Extracting the data in the way described meant that any positive response in an environmental indicator under GM cultivation would result in a value of more than 1, whilst a reduction would produce a value of less than 1 and no change a value of 1.
Standardising the data in this way meant that there was no direct GM and conventional data sets to compare in subsequent analysis.

In order to determine if the effect of GM adoption had no impact upon the environmental indicators a dummy set of values of 1 was constructed, the theory being that if the GM over conventional ratios were statistically similar to 1 then there was no environmental change in GM adoption. Results of the analysis clearly indicated that there was a significant difference (p<0.01) between the GM to conventional ratio data and a potential value of 1 and that the ratio data was higher with a mean of 1.31. However, this significant increase in the effect of GM on the environment does have to be treated with caution firstly due to the method by which it was derived, but also because at present it is not possible to necessarily associated an increase in most, if not all, environmental parameters with an improvement in fitness or health of the ecosystem. In order to attempt to resolve which of the reported and recorded comparators could potentially be causing a shift in measured environmental parameters forest plots were produced and a univariate meta-analysis undertaken.

5.2 Reasons for variation in impact

The results of the regression analysis indicated that there is no standard model to explain variation in environmental outcome. However, in both the cotton and maize models, variables relating to the design of the study had a significant effect on outcome, although the significance of trait or gene were often absent from these.

Analysis of the data, represented in the forest plots (figures 2 to 6), did not detect any significant differences between comparators.

The univariate meta-analysis when modelled for cotton produced an adjusted R^2 value that indicated that variables explained 77% of the observed variation. Comparison of the standardised coefficients indicated that publication year had the greatest influence in R value followed by multi-year data collection, with location and modifier comparators having opposite effects of similar magnitude (Table 4). These results indicate that study related factors explained more of the variation in environmental outcome than both study location and what GM is compared to. The effect of year is potentially due to improvements in data generation and handling techniques over the reported years. Multi-seasonal trials are likely to offer improved accuracy and more robust data than single season experiments as they capture the effects of seasonal environmental perturbations between trials and experiments. Whilst the observation that modification of the cropping system had only a slight effect on the variation it is worth mentioning that there was no explanation from the trait or gene insertion and as such management is therefore likely to be more important in terms of environmental impact that the presence of the GM as has been previously reported (Naranjo 2009).

This exercise was repeated for maize, but the R^2 value was 2.7 thus explaining less than 3% of the variation in the data despite making up the biggest number of data points (n=163). Insect modification had a positive coefficient, which indicated that insect resistance modification rather than herbicide tolerance resulted in more positive environmental outcomes. The remaining significant variables all related to country specific effects that generally lowered the R value. Why the maize data behaved in this way is largely unclear, but could be a result of the use of hybrids specific for the various regions of cultivation or due to differences in cultivation practices and differences in growing season lengths and climate around the world.

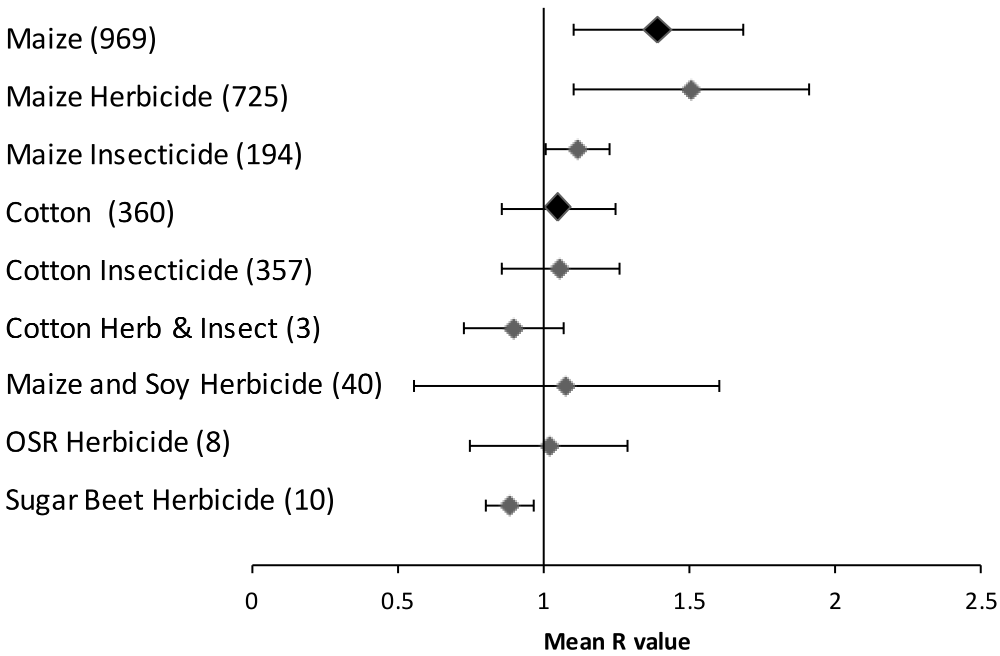

Figure 3. Forest plot of the mean R value for the crops and expressed GM trait represented in the meta data. Error bars represent 95% confidence intervals. Numbers in brackets are the paired data points used to generate the values. The values for overall maize and cotton (larger black diamonds) are presented, but are not independent of the subsequent crop data.

The results presented in this review are in keeping with earlier systematic reviews of GM. Marvier et al. (2007) reported that non-target invertebrates were generally more abundant in Bt cotton and maize fields than in their non-transgenic counterparts, but that removal of insecticides reversed this observation. Wolfenbarger et al. (2007) extended the data set to incorporate potato as well. They reported that there were no uniform effects of Bt on the functional guilds of non-target arthropods, but highlighted the use of these techniques in examining replacement of existing agricultural practices. The data for these systematic analysis does not overlap with that discussed here, whilst the review by Ricroch et al. (2010) does share some of the extracted literature. Ricrcoh et al. (2010) concluded that in 39 of the 41 papers they reviewed there was no impact from Cry1Ab adoption in maize and that in the 2 papers that reported minor effects these were either due to indirect responses or varied over the season.

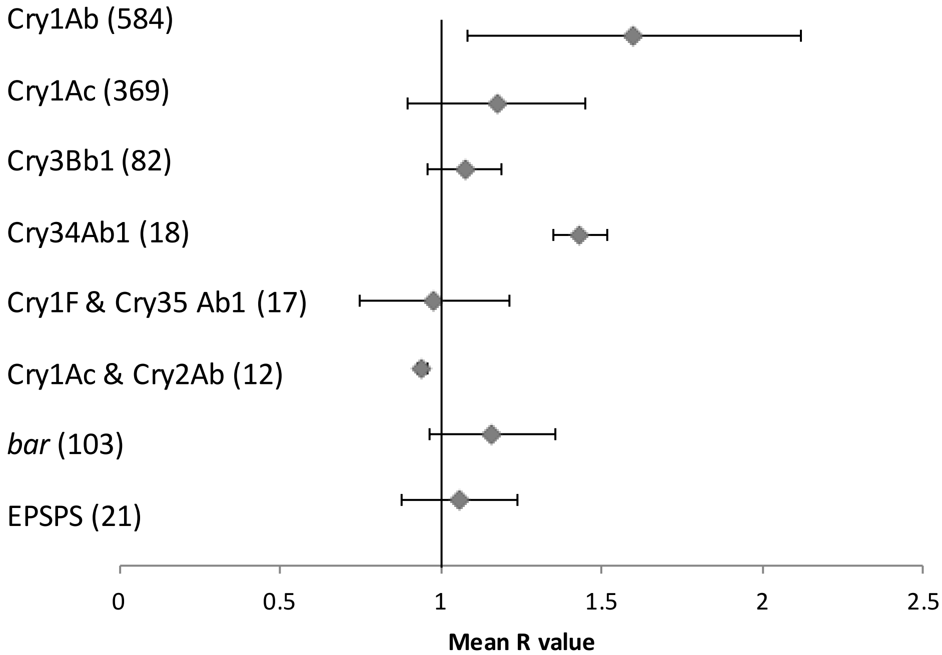

Figure 4. Forest plot of the effect of different genes present in the meta data on the ratio of GM to conventional environmental indicators. Error bars represent 95% confidence intervals. All data is independent and the numbers in brackets represent the unique data pairs that comprised the analysis.

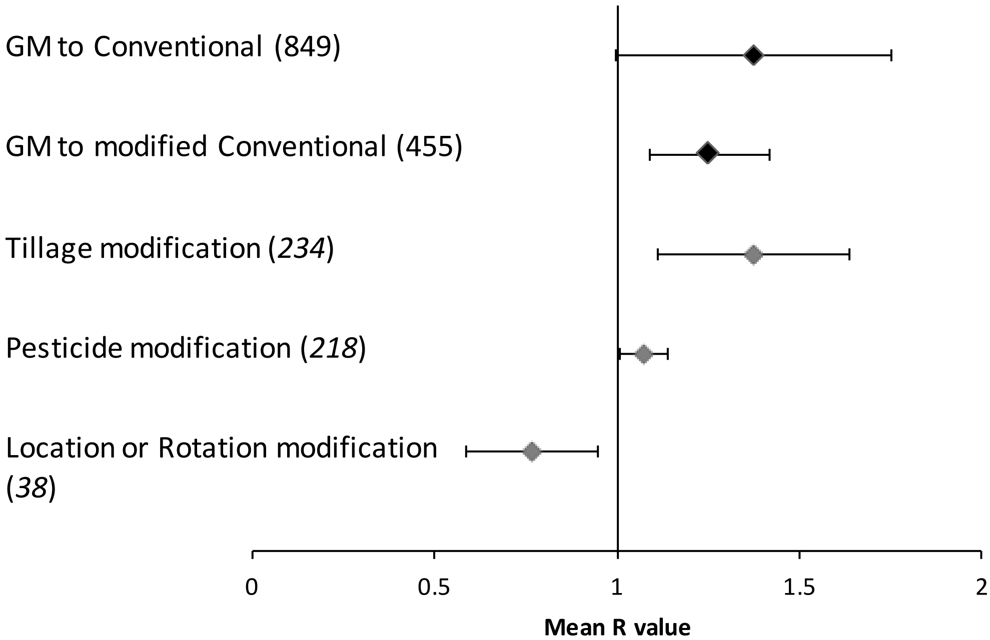

Figure 5. Comparison of the mean ratios for GM to conventional data for management conditions identified in the study. The tillage, pesticide and location or rotation data is not independent of the GM to modified conventional data. Error bars indicate 95% confidence intervals and numbers in brackets the paired data sets used to generate the result.

Differences among comparators were not significant based on unbalanced ANOVA assessment of transformed data.

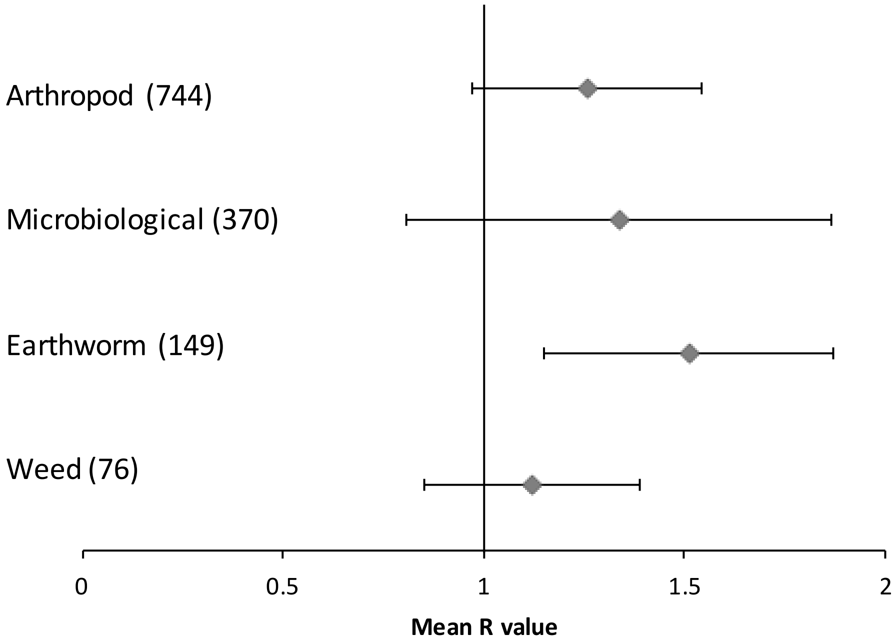

Figure 6. Forest plot of the mean ratio of GM to conventional data for the upper level of environmental indicator categories identified across the extracted data. Error bars represent 95% confidence intervals. Numbers in bracket indicate the number of independent paired data sets that comprised the result.

5.3 Review limitations

The posed question was too broad. Addressing the question to a specific crop, in less restrictive field conditions and focusing on a specific environmental indicator would better address whether the changes in GM adoption were beneficial or deleterious, rather than just a significant change. This has been the approach of other recent systematic reviews of GM impact that have been more focused in their approach, limiting themselves to specific traits in a certain crop or crops (Marvier et al. 2007; Wolfenbarger et al. 2008; Ricroch et al. 2010). Another alternative would have been to have used what is still seen as many as being the best environmental indicator, yield. However, yield was rarely reported in the examined papers. Whilst yield is a major component of the economics of crop production it was not directly included in the sister review to this that focused on the economics of GM adoption.

Searches had been limited to the English language, which was justified in a scoping study for relevant papers. Despite establishing English in the search criteria there were two papers found after the abstract screening process, which reduced the papers to 118, subsequently found to have the main text only available in Chinese or German. Two out of 118 or two out of the 43 final full texts represents relatively small proportions, so the exclusion of non-English papers is unlikely to have had a major effect on the findings of this review, however, one possible improvement may be to include other languages if this process was to be repeated.

We attempted here to provide an overview of all commercial traits and crops limited only by the caveats of field data and publication since 2006. Whilst this restricted the papers to 43, those that may have been missed or omitted might have been crucial in strengthening some aspects of the review. It was noted that there was a lack of multiple gene insertion events and stacked trait data in the extracted papers. According to James (2010) stacked traits are on the increase and accounted for 41% of all commercial GM plantings in the USA in 2010. Explanation for this may well be in the fact that the field trial data presented in the extracted literature peaked in 2003, the year Cry2Ab was added to Cry1Ac in commercial cotton (Monsanto Australia Limited 2003) and when herbicide resistance was still entering the market. Whatever the reasons for these unexpected observations the process used to derive the final 43 papers provided confidence in the selection.

Improvement in the analysis of the impact and the direction of the impact of the environmental data considered in this review would only be possible if the data extracted was comparable, probably through limitation to a specific species data or enzymatic test, or if new statistical techniques were developed for handling non-comparable environmental data.

The protocol for the review was approved in June 2011 and the searches, suitability, extraction and analysis have all taken place since. Whilst more time might not have overcome the issues of handling the environmental data it might have helped with obtaining additional data sets. Several authors whose papers made the final 43, but from the published papers there were issues with data extraction were contacted, but at the time of writing only one had successfully managed to return supplemental data files.

6 Reviewer's Conclusions

Reviewing the literature published since January 2006 on the environmental impact of GM crops using a systematic process produced a data set that indicated a significant increase in environmental indicators with the adoption of GM from an expected ratio of 1, indicating no difference, to 1.31.

There was a lack of statistically significant difference between the extracted comparators, although a general trend was observed suggesting that in most of the situations investigated the adoption of GM increased the measured environmental parameters.

Environmental indicators for beneficial and deleterious environmental changes do not currently exist that could be applied to the scale attempted in this review or, for that matter, to much smaller environmental scales.

Narrative analysis of the 43 recovered papers from the systematic search process indicated that 84.6% found no adverse effects on the environment from the cultivation of GM, 10.3% reported a beneficial effect and 5.1% a deleterious impact. Whilst this is an overwhelming indication of a lack of negative impact from GM adoption the existence of more than 5% of papers indicating a deleterious effect suggested that something more than chance may be at work within the GM system.

In order to establish the comparators responsible for the variation observed within the produced data set meta-analysis was conducted. The results of the regression analysis indicate that there is no standard model to explain variation in environmental outcome.

In both cotton and maize models variables relating to the design of the study had a significant effect on outcome, but these variables were not related to trait or gene insertion and were generally either year, country specific or due to changes in cultivation practice in origin.

This review is in keeping with several that have come before, all indicating that there is no evidence to indicate a deleterious impact of GM on the environment, but that changes in agricultural management can result in unintentional changes.

7 Acknowledgements

This work was produced in response to DEFRA tender FFG 0922, to conduct a systematic review of the environmental and economic impacts of GM crops. The tender was split to produce two reviews; one economic (CEE11-02) and one environmental (CEE11-01). The sister economic review has been completed and is under review with DEFRA and the CEE. Neither DEFRA, CEE, SAC nor Innovation Management have ventures or undertakings that would profit from work pertaining to be either for or against the adoption of GM. Additionally none of the organisations have links with external companies or other bodies that could have either profited from this review or attempted to influence its outcome. In this regard this work represents an unbiased interpretation of the available data.
During some components of this review additional statistical advice was provided by Dr Gareth Hughes.

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Appendix I

Search engine Standard operating procedure and inclusion criteria and decision

Search terms used and given in the protocols were used to derive the assessment of the engines, prior to finalisation and use of the terms given in section 2 of the protocol.

1. Web of Knowledge

http://wok.mimas.ac.uk/

Click on the orange button “Click here to access Web of Knowledge”

Search terms

Search all combinations of pairs from the key word table – every term from the ‘key word one’ column combined with every term from the ‘key word two’ column. This provides 112 searches that have to be conducted.

Search tips for Web of Knowledge

To search for an exact phrase, enclose the phrase in quotation marks. For example, the query **"genetically modified"** will retrieve records that contain the exact phrase *genetically modified*. This applies only to Topic and Title searches.

Wildcards: The asterisk (*) represents any group of characters, including no character.

When you search by Topic or Title, you must use at least three characters before the asterisk, question mark, or dollar sign or your search will generate an error.

Search process for Web of Knowledge

Search “all databases”

Enter key word one in the first line and key word two in the second line (using the search terms from the tables above)

From the drop down menus in the right hand boxes for the first two lines select “title”

From the drop down menu in the right hand box for the third line, select “year published” – enter 2006-2011

For example, the first search is as follows:

Field OR Crop* OR Cultiva* NOT glasshouse NOT laboratory NOT pot* NOT microcosm*
AND
Bollgard* OR Roundup$ready OR amoflora* OR liberty$link OR Herbicide SAME toleran* OR Insect SAME resistan* OR Bt OR Genetically$modified OR GM OR Genetically$engineer* OR Transgenic* OR Biotech*

AND
Non-target OR Cross pollinat* OR Agronom* OR Pesticide OR Insecticide OR Herbicide OR Yield OR Environmen*SAME impact* OR Environment*SAME effect*OR Ecological SAME effect* OR Soil* OR Water OR Ecolo* OR Habitat* OR Ecosystem OR diversity

2006-2011 in Year Published
This search (conducted on 26th July 2011) yielded 158 hits.

On the results page in Web of Knowledge there is an option to sort results “by relevance” – this should be selected from the drop down menu (default setting is ‘by date’).

At the bottom of the page is a box “Output records”.
Under step 1, select the third option “Records”, make sure that in the box “step 2” the “plus abstract” option is ticked.
Under step 3 select “other reference software” and save the text file.

When the next page comes up and the results have been processed, click on the ‘Export’ button and save the file in the “R” drive in the folder “Defra GM Review”.

Name the file as follows:
Database name search term one AND search term two

For example
Web of knowledge genetically modified AND environ

The ISI-CE filter is required to import the text file into reference manager, but does not work perfectly. 4 of the 158 references did not transfer with a complete bibliography, although the web link did copy and remain active, allowing for file inclusion.

2. ScienceDirect

http://www.sciencedirect.com/

On the green band across the top Click on the “search” option

Search terms
Search all combinations of search statements.

Search tips for ScienceDirect
To find documents where your search terms appear together, enclose your phrase in double quotes. For example, the query **"genetically modified"** will retrieve records that contain the exact phrase *genetically modified*.

Wildcards: Use * on the end to find a root word plus all the words made by adding letters to the end of it. For example, econom*

Search process for ScienceDirect

Search “Abstract, Title, key words”

Use the Expert tag to produce a large enough dialogue box to enter the entire search statement. Follow the Science Direct search guidelines and move the AND NOT components to the end of the search statement.

For example;
Bollgard* OR Roundup$ready OR amoflora* OR liberty$link OR “Herbicide toleran*” OR “Insect resistan*” OR Bt OR Genetically$modified OR GM OR Genetically$engineer* OR Transgenic* OR Biotech* AND Non-target OR Cross pollinat* OR Agronom* OR Pesticide OR Insecticide OR Herbicide OR Yield OR “Environmen* impact*” OR “Environment* effect*” OR “Ecological effect*” OR Soil* OR Water OR Ecolo* OR Habitat* OR Ecosystem OR *diversity AND Field OR Crop* OR Cultiva* AND NOT glasshouse AND NOT laboratory AND NOT pot* AND NOT microcosm*

Include
Journals and books

Source should be selected as All sources

Subject should be selected as All sciences

Date range should be 2006 to Present

This search (conducted on 26th July 2011) yielded 105 hits.

For comparison, using the advanced, which can not accommodate the entire proposed search statement, the following modified search in titles since 2006:
Field OR Crop* OR Cultiva* AND NOT glasshouse laboratory pot* microcosm* AND Bollgard* OR Roundup$ready OR amoflora* OR liberty$link OR “Herbicide toleran*” OR “Insect resistan*” OR Bt OR Genetically$modified OR GM OR Genetically$engineer* OR Transgenic*
AND
Non-target OR Cross pollinat* OR Agronom* OR Pesticide OR Insecticide OR Herbicide OR Yield OR “Environmen* impact*” OR “Environment* effect*” OR “Ecological effect*” OR Soil* OR Water OR Ecolo* OR Habitat* OR Ecosystem OR *diversity

Resulted in 3954 hits on the same date.

On the results page click on “Export citations”

On the ‘export citations’ page, under ‘content format’ select “citations and abstracts”. Make sure the ‘export format’ option selected is ‘RIS format for Reference Manager, End Note, Pro Cite’.
Click on the ‘Export’ button and save the file in the “R” drive in the folder “Defra GM review”.

Problem: In some instances more than 1000 results will be encountered. Science Direct only provides an option to extract the first 1000 results in these instances, so the references were sorted by relevance prior to extraction. Science Direct would not run in Google Chrome.

Save each search as a separate file.

3. Copac

http://copac.ac.uk/

On the left hand side click on the green button “Search Copac” without logging in

Search terms
Search all combinations of search statements.

Search tips for Copac
For a **phrase** use quote marks. For example, the query **"genetically modified"** will retrieve records that contain the exact phrase *genetically modified*.

Wildcards: To **find variant word endings** cut the end off the search word and replace it with an asterisk *.

Search process for Copac

The search page that comes up is the ‘quick search’ page. Click on the ‘main search’ tab.

In the title word box enter the search statement terms using AND as the connector.

In the ‘date published’ box enter 2006-

Scroll down the ‘language’ box and select “English”

A search (conducted 26th July 2011) yielded 9804 hits.

Problem: There is no “relevance” sort option. The default is alphabetically by title and extraction is limited to the first 2500 hits. There is also no option for Abstract retrieval.

Export all records as “EndNote, Zotero”. (Once all records are saved to ReferenceManager).

Some search criteria in COPAC generate thousands of hits, for example any search that had Biotech* as the first term. Reversing the search terms in COPAC, for example using cost AND biotech* reduces the number of returned hits significantly from 21200 to 210. This is clearly an issue with the search engine being used by this database. Other issues have been encountered with the use of wildcards on certain keywords. If a search order is modified to reflect the issue of size of retrieval and possible relevance then we will record this within the search results.

Click on the ‘Export’ button and save the file in the “R” drive in the folder “Defra GM review”.

4. Agbioview

http://www.agbioworld.org/search/index.html

This is a business newsletter delivered electronically several times a month. It had been received and stored by Bruce Knight, Innovation Management, since 2004. On average 5 newsletters per month had been received with around 10 articles, or about 600 articles per year.
The service is provided by the US based organisation Agbioworld, www.agbioworld.com .
Agviview is compiled by Dr. C. S. Prakash, Professor in Plant Molecular Genetics and Director of the Center for Plant Biotechnology Research at Tuskegee University, Alabama.
Agbioworld supports the application of GM crops, consequently the articles selected tend not to feature publication by activist GMOs. However, many articles are responding to activist's reports.
Agbioview covers mainly English language publications from around the world. Articles vary in depth from press reports from popular newspapers to in depth study reports. All articles relate to GM crops and occasionally to the wider benefits from science based crop production.

Search terms
Search all combinations of pairs from the key word table – every term from the 'key word one' column combined with every term from the 'key word two' column. This provides 112 searches that have to be conducted.

Search tips for Agbioworld
In addition, there are several ways to modify the default search behavior.

1. **phrase search**
   The search engine supports three types of phrase search.
   - To match an exact phrase, use quotes around the phrase
     Example: "free search engine"
   - To match a near (within a couple of words) phrase, use square brackets [around the words]
     Example: [free search engine]
   - To match a far (within several words) phrase, use braces around the words
     Example: {free search engine}
2. **+ and - qualifiers**
   If you prepend a word with **+** that word is required to be on the page.
   If you prepend a word with **-** that word is required to *not* be on the page.
   Example: +always -never
3. *** wildcard**
   If a query word ends with a ***** all words on a page which start the same way as that query word will match.
   Example: gift*
4. **? wildcard**
   If a query word contains a **?** any character will match that position.
   Example: b?g
5. **boolean search**
   You can use the following boolean operators in your search: AND, OR, NOT. These operators MUST be in capital letters.
   Example: (contact AND us) OR (about AND us)

Search process for Agbioworld

Enter keyword one and keyword two into the search box

For example, the first search is:

“Genetically modified” AND environ*

This search yielded 27 hits on 1st November 2010

Problem: Accessing the links displayed in the search results displays a secondary layer of material. The method by which this material has been linked to the initial search terms is not evident and therefore we can not be sure of how this material relates to our search criteria. There appears to be no way to export results other than copy and paste the page into a word document.

A manual method of search was conducted where by all article titles were reviewed by Bruce Knight and those of relevance to this review highlighted in a list titles. From this the titles were extracted and the links to the manuscripts followed for further inclusion in the review process.

5. BCPC

http://www.bcpc.org/

This newsletter is published by the British Crop Production Council. This is delivered 2-3 times a month. It had been received and stored by Bruce Knight, Innovation Management, since late 2008. BCPC news lists web sites under a range of headings, including GM crops. Typically 20 GM crop web sites are listed each time, so about 700 per year.
The articles/web sites selected are from world- wide sources and relatively broad in scope including publications from NGOs. Many are scientific research and regulatory reports.

Search terms

Search all combinations of pairs from the key word table – every term from the ‘key word one’ column combined with every term from the ‘key word two’ column. This provides 112 searches that have to be conducted.

Search tips for BCPC

Attempt searches using the left hand of the page search box (text is faint when entered)

Search process for BCPC

A search on 01/11/2010 for the following searches; Genetically modified AND Environ, Genetically modified AND Environ*, and Genetically modified all failed to return any hits. A search for Genetically returned a single hit to the BCPC ‘The GM Crop Manual’.
The lack of value to this search retrieval meant it will not be used in subsequent electronic searches.

The newsletters were studied methodically and any articles that featured information on economics or environmental issues were short listed, extracted and saved.
Once the selection protocols were defined the saved articles were studied and only those articles that met the protocol were extracted. In many cases the published articles, particularly press reports, made reference to original documents. These original documents were then sourced through search engines.
In some cases the articles or papers covered information relevant to GM economics as well as environmental data.

6. Scirus

http://www.scirus.com/srsapp/advanced/index.jsp?q1=

Search terms
Search all combinations using the search statement strategy provided in the document

Search tips for Scirus
You can use quotation marks (“ ”) to search for an exact phrase.
Use an asterisk (*) to replace multiple characters e.g. parasit* finds parasite, parasitic, parasitology, parasitemia

Search process for Scirus

At the top of the page (right hand side) click on “preferences” and under “number of results” select display “50” results per page.
Click on save preferences

On the ‘advanced search’ page

In the first row enter the search statement 1AND 2 AND 3.
NOTE: changing the order of the statements changed the selected results. As such 120 references were retrieved. Forty from a 1 AND 2 AND 3 search, 40 from a 2 AND 3 AND 1 search and 40 from a 3 AND 2 AND 1 search.

Against “dates” enter 2006 to 2011

Limit ‘File Formats’ to PDF and WORD.

Under ‘Content Sources’ show the full list and select all apart from Science Direct to avoid duplication.

Leave everything else as default settings

At the top of the page just above the results tick the little tick box to select all 100 hits on this first page. SCIRUS will only export the first 40 hits at a time. Check the first 40 results then click on “export” checked results

This brings up a small “export results” box

Select export “citations, abstract and keywords”
Leave file format as “RIS format”
Make sure that the option “Save file to disk or open Reference Software (depends on your settings)” is selected and then click on “Export”

Save as a reference manager file in the folder in the R drive

Name the file database name keyword AND one keyword two

7. CAB Direct

http://www.cabdirect.org

Search terms

((Field OR Crop* OR Cultiva*) NOT glasshouse NOT laboratory NOT pot* NOT microcosm*)
AND
(Bollgard* OR Roundup$ready OR amoflora* OR liberty$link OR Herbicide SAME toleran* OR Insect SAME resistan* OR Bt OR Genetically$modified OR GM OR Genetically$engineer* OR Transgenic* OR Biotech*)
AND (Non-target OR Cross pollinat* OR Agronom* OR Pesticide OR Insecticide OR Herbicide OR Yield OR Environmen* SAME impact* OR Environment* SAME effect* OR Ecological effect* OR Soil* OR Water OR Ecolo* OR Habitat* OR Ecosystem OR diversity)

Search in titles produced 0 hits. Changing the search parameter to all fields, since 2006 in English returned 9342 results, but there was difficulty extracting them as marking all hits for export resulted in the system crashing repeatedly over 3 days of trying. Getting around this issue could not be resolved. As such it was decided to recover the first 1000 (as this was comparable to Science Direct). The references were ordered by relevance and the first 10 pages with 100 hits each was recovered. Titles in pages 11 and 12 were screened and none would have been taken forward to abstract review so this was deemed to have captured the majority of relevant titles.

A refined attempt using just the second and third search statements was also undertaken:
(Bollgard* OR Roundup$ready OR amoflora* OR liberty$link OR Herbicide SAME toleran* OR Insect SAME resistan* OR Bt OR Genetically$modified OR GM OR Genetically$engineer* OR Transgenic* OR Biotech*) AND (Non-target OR Cross pollinat* OR Agronom* OR Pesticide OR Insecticide OR Herbicide OR Yield OR Environmen* SAME impact* OR Environment* SAME effect* OR Ecological effect* OR Soil* OR Water OR Ecolo* OR Habitat* OR Ecosystem OR diversity)

Selected article title and from 2006 produced 544 hits.
Selecting 100 entries per page, marking all and then extracting to Reference manager 1 page at a time was successful in retrieving these references.

NOTE: Retrieval failed to work in Explorer 9 and Google Chrome was used as the internet browser to make this possible.