

Biodiversity and GM crops

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1. The needs for biodiversity – the general case

Biological diversity (often contracted to *biodiversity*) has emerged in the past decade as a key area of concern for sustainable development, but crop biodiversity, the subject of this book, is rarely considered. The author's contribution to the discussion of crop biodiversity in this volume should be considered as part of the general case for biodiversity. Biodiversity provides a source of significant economic, aesthetic, health and cultural benefits. It is assumed that the well-being and prosperity of earth's ecological balance as well as human society directly depend on the extent and status of biological diversity (Table 1). Biodiversity plays a crucial role in all the major biogeochemical cycles of the planet. Plant and animal diversity ensures a constant and varied source of food, medicine and raw material of all sorts for human populations. Biodiversity in agriculture represents a variety of food supply choice for balanced human nutrition and a critical source of genetic material allowing the development of new and improved crop varieties. In addition to these direct-use benefits, there are enormous other less tangible benefits to be derived from natural ecosystems and their components. These include the values attached to the persistence, locally or globally, of natural landscapes and wildlife, values, which increase as such landscapes and wildlife become more scarce. The relationships between biodiversity and ecological parameters, linking the value of biodiversity to human activities are partially summarized in Table 1.

Table 1 Primary goods and services provided by ecosystems

Ecosystem	Goods	Services
Agro ecosystems	Food crops Fiber crops Crop genetic resources	Maintain limited watershed functions (infiltration, flow control, partial soil protection) Provide habitat for birds, pollinators, soil organisms important to agriculture Build soil organic matter Sequester atmospheric carbon Provide employment
Forest ecosystems	Timber Fuel wood Drinking and irrigation water	Remove air pollutants, emit oxygen Cycle nutrients Maintain array of water shed functions (infiltration,

Freshwater ecosystems	Fodder	purification, flow control, soil stabilization)
	Nontimber products (vines, bamboos, leaves, etc.)	Maintain biodiversity
	Food (honey, mushrooms, fruit, and other edible plants; game)	Sequester atmospheric carbon
	Genetic resources	Generate soil
	Drinking and irrigation water	Provide employment
	Fish	Provide human and wildlife habitat
	Hydroelectricity	Contribute aesthetic beauty and provide recreation
	Genetic resources	Buffer water flow (control timing and volume)
		Dilute and carry away wastes
		Cycle nutrients
Grassland ecosystems		Maintain biodiversity
		Sequester atmospheric carbon
		Provide aquatic habitat
		Provide transportation corridor
		Provide employment
		Contribute aesthetic beauty and provide recreation
		Maintain array of watershed functions (infiltration, purification, flow control, soil stabilization)
		Cycle nutrients
		Remove air pollutants, emit oxygen
		Maintain biodiversity
Coastal and marine ecosystems		Generate soil
		Sequester atmospheric carbon
		Provide human and wildlife habitat
		Provide employment
		Contribute aesthetic beauty and provide recreation
		Moderate storm impacts (mangroves; barrier islands)
		Provide wildlife (marine and terrestrial) habitat
		Maintain biodiversity
		Dilute and treat wastes
		Sequester atmospheric carbon
Desert ecosystems		Provide harbors and transportation routes
		Provide human and wildlife habitat
		Provide employment
		Contribute aesthetic beauty and provide recreation
		Sequester atmospheric carbon
		Maintain biodiversity
		Provide human and wildlife habitat
		Provide employment
		Contribute aesthetic beauty and provide recreation
		Provide housing and employment
Urban ecosystems	space	Provide transportation routes
		Contribute aesthetic beauty and provide recreation
		Maintain biodiversity
		Contribute aesthetic beauty and provide recreation
		Contribute aesthetic beauty and provide recreation

With this introduction, the following sustainability scheme can easily be understood: The left column is really the most important one when it comes to necessities of mankind: But in order to reach sustainability in agriculture, we must adopt progressive management strategies, it will be necessary to combine the most efficient *and* sustainable agriculture production systems. Details can be seen in the fig. 1. It should be made clear that agriculture needs to become highly competitive, innovative and there is an urgent need to produce more on a smaller surface. But all efforts will be in vain, if we do not succeed to make substantial progress in the fields of socio-economics and

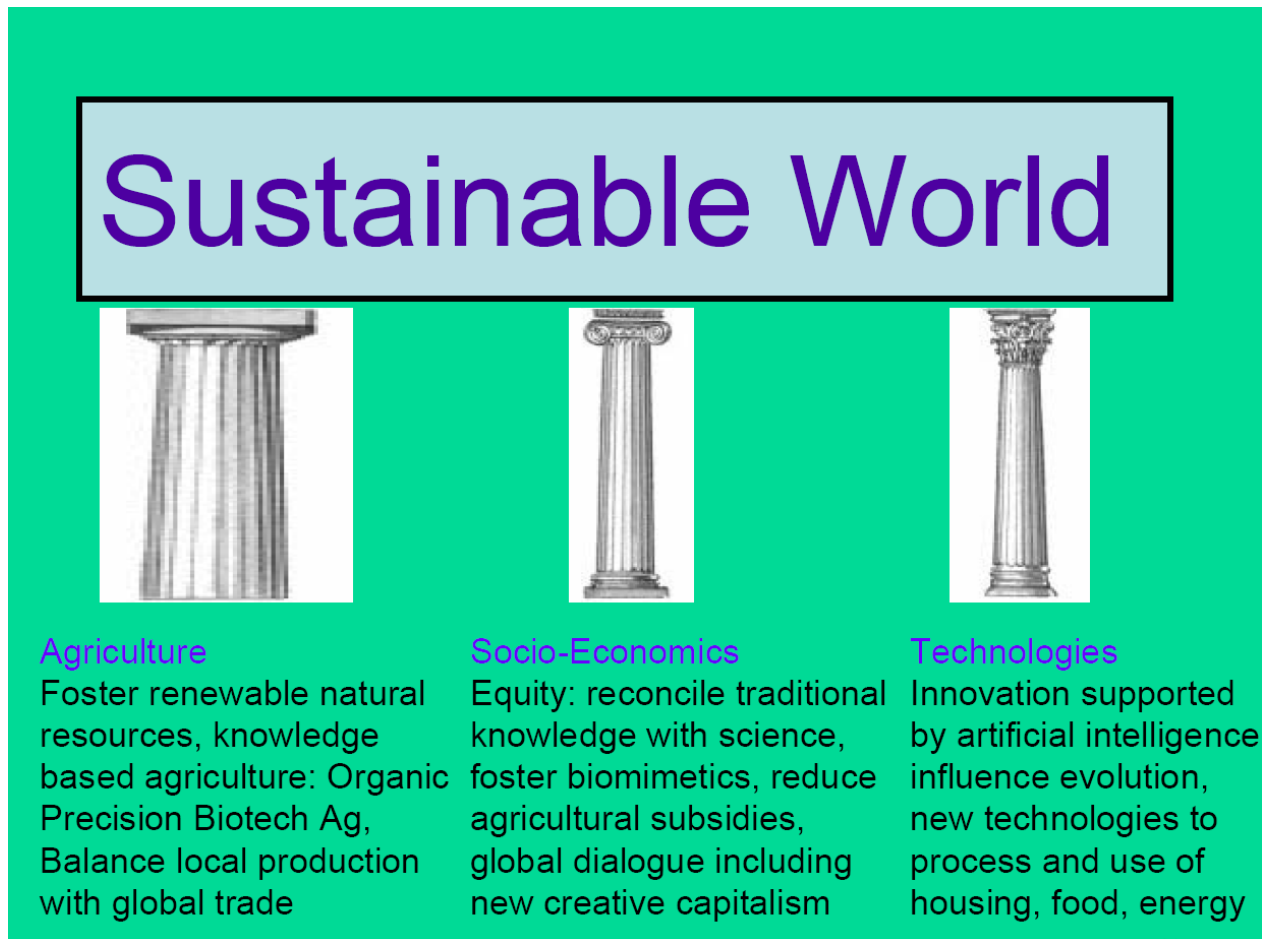


Fig. 1 A new concept of a sustainable world, in AGRICULTURE based on renewable natural resources, knowledge based agriculture and organic precision biotech-agriculture, in SOCIO-ECONOMICS based on equity, global dialogue, reconciliation of traditional knowledge with science, reduction of agricultural subsidies and creative capitalism, in TECHNOLOGIES based. Original K. Ammann 2008

Biological diversity may refer to diversity in a gene, species, community of species, or ecosystem, or even more broadly to encompass the earth as a whole. Biodiversity comprises all living beings, from the most primitive forms of viruses to the most sophisticated and highly evolved animals and plants. According to the 1992 International Convention on Biological Diversity, biodiversity means “the variability among living organisms from all sources including, terrestrial, marine, and other aquatic ecosystems and the ecological complexes of which they are part” (CBD, 1992) It is important not to overlook the various scale-dependent perspectives of biodiversity, as this can lead to many misunderstandings in the debate about biosafety. It is not a simple task to evaluate the needs for biodiversity, especially to quantify the agro ecosystem biodiversity vs. total biodiversity (Purvis & Hector, 2000; Tilman, 2000). One example may be sufficient to illustrate the difficulties: Biodiversity is indispensable to sustainable structures of ecosystems. But sustainability has many facets, among others also the need to feed and to organize proper health care for the poor. This last task is of utmost importance and has to be balanced against biodiversity per se, such as in the now classic case of the misled total ban on DDT, which caused hundreds of

thousands of malaria deaths in Africa in recent years, the case is summarized many publications, here a small selection: (Attaran & Maharaj, 2000; Attaran et al., 2000; Curtis, 2002; Curtis & Lines, 2000; Horton, 2000; Roberts et al., 2000; Smith, 2000; Taverne, 1999; Tren & Bate, 2001; WHO, 2005)

2. Types, distribution, and loss of biodiversity

2.1. Genetic diversity

In many instances genetic sequences, the basic building blocks of life, encoding functions and proteins are almost identical (highly conserved) across all species. The small unconserved differences are important, as they often encode the ability to adapt to specific environments. Still, the greatest importance of genetic diversity is probably in the combination of genes within an organism (the genome), the variability in phenotype produced, conferring resilience and survival under selection. Thus, it is widely accepted that natural ecosystems should be managed in a manner that protects the untapped resources of genes within the organisms needed to preserve the resilience of the ecosystem. Much work remains to be done to both characterize genetic diversity and understand how best to protect, preserve, and make wise use of genetic biodiversity (Batista et al., 2008; Baum et al., 2007; Cattivelli et al., 2008; Mallory & Vaucheret, 2006; Mattick, 2004; Raikhel & Minorsky, 2001; Witcombe et al., 2008).

The number of metabolites found in one species exceeds the number of genes involved in their biosynthesis. The concept of one gene - one mRNA - one protein - one product needs modification. There are many more proteins than genes in cells because of post-transcriptional modification. This can partially explain the multitude of living organisms that differ in only a small portion of their genes. It also explains why the number of genes found in the few organisms sequenced is considerably lower than anticipated.

2.2. Species diversity

For most practical purposes measuring species biodiversity is the most useful indicator of biodiversity, even though there is no single definition of what is a species. Nevertheless, a species is broadly understood to be a collection of populations that may differ genetically from one another to some extent degree, but whose members are usually able to mate and produce fertile offspring. These genetic differences manifest themselves as differences in morphology, physiology, behaviour and life histories; in other words, genetic characteristics affect expressed characteristics (phenotype). Today, about 1.75 million species have been described and named but the majority remains unknown. The global total might be ten times greater, most being undescribed microorganisms and insects (May, 1990).

2.3. Ecosystem diversity

At its highest level of organization, biodiversity is characterized as ecosystem diversity, which can be classified in the following three categories:

Natural ecosystems, i.e. ecosystems free of human activities. These are composed of what has been broadly defined as “Native Biodiversity”. It is a matter of debate whether any truly natural ecosystem exists today, as human activity has influenced most regions on earth. It is unclear why so many ecologists seem to classify humans as being “unnatural”.

Semi-natural ecosystems in which human activity is limited. These are important ecosystems that are subject to some level of low intensity human disturbance. These areas are typically adjacent to managed ecosystems.

Managed ecosystems are the third broad classification of ecosystems. Such systems can be managed by humans to varying degrees of intensity from the most intensive, conventional agriculture and urbanized areas, to less intensive systems including some forms of agriculture in emerging economies or sustainably harvested forests.

Beyond simple models of how ecosystems appear to operate, we remain largely ignorant of how ecosystems function, how they might interact with each other, and which ecosystems are critical to the services most vital to life on earth. For example, the forests have a role in water management that is crucial to urban drinking water supply, flood management and even shipping.

Because we know so little about the ecosystems that provide our life-support, we should be cautious and work to preserve the broadest possible range of ecosystems, with the broadest range of species having the greatest spectrum of genetic diversity within the ecosystems. Nevertheless, we know enough about the threat to, and the value of, the main ecosystems to set priorities in conservation and better management. We have not yet learnt enough about the threat to crop biodiversity, other than to construct gene banks, which can only serve as an ultimate ratio – we should not indulge into the illusion that large seed banks could really help to preserve crop biodiversity. The only sustainable way to preserve a high crop diversity, i.e. also as many landraces as possible, is to actively cultivate and breed them further on. This has been clearly demonstrated by the studies of Berthaud and Bellon (Bellon & Berthaud, 2004, 2006; Bellon et al., 2003; Berthaud, 2001) Even here we have much to learn, as the vast majority of the deposits in gene banks are varieties and landraces of the four major crops. The theory behind patterns of general biodiversity related to ecological factors such as productivity is rapidly evolving, but many phenomena are still enigmatic and far from understood (Schlapfer et al., 2005; Tilman et al., 2005), as for example why habitats with a high biodiversity are more robust towards invasive alien species.

3. The global distribution of biodiversity

Biodiversity is not distributed evenly over the planet. Species richness is highest in warmer, wetter, topographically varied, less seasonal and lower elevation areas. There are far more species in total per unit area in temperate regions than in polar ones, and far more again in the tropics than in temperate regions. Latin America, the Caribbean, the tropical parts of Asia and the Pacific together host eighty percent of the ecological mega-diversity of the world. An analysis of global biodiversity on a strictly

metric basis demonstrates, that besides the important rain forest areas there are other hotspots of biodiversity, related to tropical dry forests for example (Kier et al., 2005; Kuper et al., 2004; Lughadha et al., 2005).

Within each region, every specific type of ecosystem will support its own unique suite of species, with their diverse genotypes and phenotypes. In numerical terms, global species diversity is concentrated in tropical rain forests and tropical dry forests. Amazon basin rainforests can contain up to nearly three hundred different tree species per hectare and supports the richest (often frugivorous) fish fauna known, with more than 2500 species in the waterways. The submontane tropical forests in tropical Asia and South America are considered to be the richest per unit area in animal species in the world. (Vareschi, 1980).

4. The case of agro-biodiversity

Species and genetic diversity within any agricultural field will inevitably be more limited than in a natural or semi-natural ecosystem. Many of the crops growing in farming systems all over the world have surprisingly enough ancestral parent traits which lived in originally in natural monocultures (Wood & Lenne, 2001). This is after all most probably the reason why our ancestral farmers have chosen those major crops. There are many examples of natural monocultures, such as the classic stands of Kelp, *Macrocystis pyrifera*, already analysed by (Darwin, 1845), and more relevant to agriculture: It has now been recognized by ecologists that simple, monodominant vegetation exists throughout nature in a wide variety of circumstances. Indeed, (Fedoroff & Cohen, 1999) reporting (Janzen, 1998, 1999) use the term 'natural monocultures' in analogy with crops. Monodominant stands may be extensive. As one example of many, Harlan recorded that for the blue grama grass (*Bouteloua gracilis*): 'stands are often continuous and cover many thousands of square kilometers' of the high plains of central USA. It is of the utmost importance for the sustainability of agriculture to determine how these extensive, monodominant and natural grassland communities persist when we might expect their collapse. More examples are given in (Wood & Lenne, 1999), here only a few more cases: Wild species: *Picea abies*, *Spartina townsendii*, various species of Bamboos, *Arundinaria ssp*, (Gagnon & Platt, 2008), *Sorghum verticilliflorum*, *Phragmites communis*, and *Pteridium aquilinum*. Ancestral cultivars are cited extensively by (Wood & Lenne, 2001): Wild rice: *Oryza coarctata*, reported in Bengal as simple, oligodiverse pioneer stands of temporarily flooded riverbanks (Prain, 1903), Harlan described *Oryza* (Harlan, 1989) and illustrated harvests from dense stands of wild rice in Africa (*Oryza barthii*, the progenitor of the African cultivated rice, *Oryza glaberrima*). *Oryza barthii* was harvested wild on a massive scale and was a local staple across Africa from the southern Sudan to the Atlantic. (Evans, 1998) reported that the grain yields of wild rice stands in Africa and Asia could exceed 0.6 tonnes per hectare — an indication of the stand density of wild rice.

Botanists and plant collectors have according to (Wood & Lenne, 2001) repeatedly and emphatically noted the existence of dense stands of wild relatives of wheat. For example, in the Near East, (Harlan, 1992) noted that 'massive stands of wild wheats cover many square kilometers. (Hillmann, 1996) reported that wild einkorn (*Triticum monococcum* subsp. *boeoticum*) in particular tends to form dense stands, and when harvested its yields per square meter often match those of cultivated wheats under

traditional management. (Harlan & Zohary, 1966) noted that wild Einkorn 'occurs in massive stands as high as 2000 meters [altitude] in south-eastern Turkey and Iran'. Wild emmer (*Triticum turgidum subsp. dicoccoides*) 'grows in massive stands in the northeast' of Israel, as an annual component of the steppe-like herbaceous vegetation and in the deciduous oak park forest belt of the Near East (Nevo, 1998). According to (Wood & Lenne, 2001) they are the strongest examples embracing wild progenitors of wheat: (Anderson, 1998) recorded wild wheat growing in Turkey and Syria in natural, rather pure stands with a density of 300/ m².

Nevertheless, agricultural ecosystems can be dynamic in terms of species diversity over time due to management practices. This is often not understood by ecologists who involve themselves in biosafety issues related to transgenics. They still think in ecosystems close (or seemingly close) to nature. Biodiversity in agricultural settings can be considered to be important at country level in areas where the proportion of land allocated to agriculture is high: Ammann in (Wolfenbarger et al., 2004). This is the case in continental Europe for example, where forty five percent of the land is dedicated to arable and permanent crops or permanent pasture. In the UK, this figure is even higher, at seventy percent. Consequently, biodiversity has been heavily influenced by humans for centuries, and changes in agrobiological management will influence biodiversity in such countries overall. Innovative thinking about how to enhance biodiversity in general coupled with bold action is critical in dealing with the loss of biodiversity. High potential to enhance biodiversity considerably can be seen on the level of regional landscapes, as is proposed by (Dollaker, 2006; Dollaker & Rhodes, 2007), and with the help of remote sensing methods it should be possible to plan for a much better biodiversity management in agriculture (Mucher et al., 2000).

Centers of biodiversity are a controversial matter, and even the definition of centers of crop biodiversity is still debated. Harlan (Harlan, 1971) proposed a theory that agriculture originated independently in three different areas and that, in each case, there was a system composed of a center of origin and a noncenter, in which activities of domestication were dispersed over a span of five to ten-thousand kilometers. One system was in the Near East (the Fertile Crescent) with a noncenter in Africa; another center includes a north Chinese center and a noncenter in southeast Asia and the south Pacific, with the third system including a Central American center and a South American noncenter. He suggests that the centers and the noncenters interacted with each other.

There is a widespread view that centers of crop origin should not be touched by modern breeding because these biodiversity treasures are so fragile that these centers should stay free of modern breeding. This is an erroneous opinion, based on the fact that regions of high biodiversity are particularly susceptible to invasive processes, which is wrong. On the contrary, there are studies showing that a high biodiversity means more stability against invasive species, as well as against genetic introgression (Morris et al., 1994; Tilman et al., 2005; Whitham et al., 1999). The introduction of new predators and pathogens has caused well-documented extinctions of long-term resident species, particularly in spatially restricted environments such as islands and lakes. One of the (in)famous cases of an extinction of an endemic rare moth is documented from Hawaii, it has been caused by a failed attempt of biological control (Henneman & Memmott, 2001; Howarth, 1991). However, there are surprisingly few instances of extinctions of resident species that can be attributed to competition from new species. This suggests either that competition-driven extinctions take longer to occur than those

caused by predation or that biological invasions are much more likely to threaten species through inter-trophic than through intra-trophic interactions (Davis, 2003). This also fits well with agricultural experience, which builds on much faster ecological processes.

5. About the differences between transgenic and non-transgenic crops on the molecular level:

(Van Bueren et al., 2003) try to explain on the molecular level, why organic farming cannot accept genetic engineering with a number of arguments:

Following (Verhoog et al., 2003), they state that the naturalness of organic agriculture not only to the avoidance of inorganic, chemical inputs and to the application of other agroecological principles, but also implies integrity. Their definition of intrinsic integrity of plant genomes:

The general appreciation for working in consonance with natural systems in organic farming extends itself to the regard with which members of the movement view individual species and organisms. Species, and the organisms belonging to them, are regarded as having an intrinsic integrity. This integrity exists aside from the practical value of the species to humanity and it can be enhanced or degraded by management and breeding measures. This kind of integrity can only be assessed from a biocentric perspective (see below). Organic agriculture assigns an ethical value to this integrity, and encourages propagation, breeding, and production systems that protect or enhance it.

And further on:

“From a biocentric perspective, organic agriculture acknowledges the intrinsic value and therefore the different levels of integrity of plants as described above. The consequence of acknowledging the intrinsic value of plants and respecting their integrity in organic agriculture implies that the breeder takes the integrity of plants into account in his choices of breeding and propagation techniques. It implies that one not merely evaluates the result and consequences of an intervention, but in the first place questions whether the intervention itself affects the integrity of plants. From the above described itself affects the integrity of plants.”

From the above described levels of the nature of plants and its characteristics, a number of criteria, characteristics, and principles for organic plant breeding and propagation techniques are listed by the authors for exclusion: All breeding methods using chemicals or radiation, such as colchicizing or gamma radiation induced mutants, all methods not allowing a full live cycle of the plant, all methods manipulating the genome of the organisms etc.

Unfortunately, the authors completely miss the point that the structure and assembly of DNA has been changed heavily over the decades and centuries of traditional breeding. Modern wheat in all variants and traits used today – also by organic farmers – are a product of processes, where the intrinsic value of the genomic naturalness has been completely ignored and any imaginable change has been successfully integrated, from adding chromosome fragments to integrating foreign genomes and accepting radiation mutation in the case of *Triticum durum* over a long period of time, also chromosome inversions, translocations are well documented in most major crops. The reality is, whether we accept it for any kind of definition, that most of the principles advocated by (Van Bueren & Struik, 2004, 2005; Van Bueren et al., 2002; Van Bueren et al., 2003; Verhoog et al., 2003) are clearly violated by almost all existing modern crop traits and cannot be redone, unless you could theoretically go back to the ancestral traits (which have in most cases of the major crops not survived the centuries of classical breeding efforts). So, in reality, the principle of the ‘intrinsic values of the plant genome’ is a fiction and not science based.

The whole concept of violation of the intrinsic naturalness of the genome by inserting alien genes from other species across the natural species barrier is also falsified by the occurrence of a naturally transgenic grass: See the case discussed by (Ghatnekar et al., 2006) in chapter 6.2 paragraph 2).

It is also questionable to stress the overcoming of natural hybridization barriers by genetic engineering, since this has been done by traditional breeding methods in former decades: Here the example of Somatic hybridising (i.e. non-sexual fusion of two somatic cells). The advantage of this method is that by the fusion of cells with different numbers of chromosomes (for instance different species of *Solanum*) fertile products of the crossing can be obtained at once because diploid cells are being somatically fused. Polyploid plants are obtained containing all the chromosomes of both parents instead of the usual half set of chromosomes from each. For this, cells are required whose cell walls have been digested away by means of enzymes and are only enclosed by a membrane, (these are then called protoplasts). With the loss of their cell walls, protoplasts have also lost their typical shape and are spherical like egg cells. This mixture of cells to be fused is then exposed to electric pulses. In order to get from the cell mixture the 'right' product of the fusion (since fusion of two cells from similar plants can also occur) one different selectable character in each of the original plants is necessary. Only cells that survive this double selection are genuine products of fusion. (The easiest way to achieve such selectable markers is by genetic engineering, for instance by incorporating antibiotic resistance into the original plants.) Protoplast fusion has been investigated and applied to potatoes, for instance. In the EU regulations concerning the deliberate release of genetically modified organisms into the environment somatic hybrids are not considered as GMO's and do not require authorization. The most recent draft of the EU organic regulations in which the introduction of GMO's in organic cultivation is forbidden, follows the above definition. (Karutz, 1999; Koop et al., 1996).

The concept of violated intrinsic naturalness of the genomes by transgenity is also falsified by the publications of Arber (Nobel Laureate 1978). He compared designed genetic alterations (including genetic engineering) with the spontaneous genetic variation known to form the substrate for biological evolution (Arber, 2002):

"Site-directed mutagenesis usually affects only a few nucleotides. Still another genetic variation sometimes produced by genetic engineering is the reshuffling of genomic sequences, e.g. if a given open reading frame is brought under a different signal for expression control or if a gene is knocked out. All such changes have little chance to change in fundamental ways, the properties of the organism. In addition, it should be remembered that the methods of molecular genetics themselves enable the researchers anytime to verify whether the effective genomic alterations correspond to their intentions, and to explore the phenotypic changes due to the alterations. This forms part of the experimental procedures of any research seriously carried out. Interestingly, naturally occurring molecular evolution, i.e. the spontaneous generation of genetic variants has been seen to follow exactly the same three strategies as those used in genetic engineering. These three strategies are:

- (a) small local changes in the nucleotide sequences,
- (b) internal reshuffling of genomic DNA segments, and
- (c) acquisition of usually rather small segments of DNA from another type of organism by horizontal gene transfer.

However, there is a principal difference between the procedures of genetic engineering and those serving in nature for biological evolution. While the genetic engineer pre-reflects his alteration and verifies its results, nature places its genetic variations more randomly and largely independent of an identified goal. Under natural conditions, it is the pressure of natural selection which eventually determines, together with the available diversity of genetic variants, the direction taken by evolution. It is interesting to note that natural selection also plays its decisive role in genetic engineering, since indeed not all pre-reflected sequence alterations withstand the power of natural selection. Many investigators have experienced the effect of this natural force which does not allow functional disharmony in a mutated organism."

See also (Arber, 2000, 2003, 2004) in writings which confirm this important comparison on the genomic level of evolutionary and modern plant breeding processes. But there is of course, despite all the similarities, one major difference: whereas natural mutation acts completely in a natural time scale, that is, the mutants will need hundreds to hundred of thousands of years to overcome selective processes in nature until they really succeed and take over against their natural competitors, this is totally different with the transgenic crop products: they run through a R&D phase, and a regulatory process of an average of 15 to 20 years until being completely deregulated. But somewhere along this process they will be propagated to the millions in the field, covering in a evolutionary extremely short time span millions of hectares.

This basic insight of a molecular biologist has been confirmed by analysis of modern breeding processes and their real products in crops, as an example here a comparison on the genomic level between transgenic and non-transgenic wheat traits done by Shewry et al.: (Shewry et al., 2006):

“Whereas conventional plant breeding involves the selection of novel combinations of many thousands of genes, transgenesis allows the production of lines which differ from the parental lines in the expression of only single or small numbers of genes. Consequently it should in principle be easier to predict the effects of transgenes than to unravel the multiple differences which exist between new, conventionally-produced cultivars and their parents. Nevertheless, there is considerable concern expressed by consumers and regulatory authorities that the insertion of transgenes may result in unpredictable effects on the expression of endogenous genes which could lead to the accumulation of allergens or toxins. This is because the sites of transgene insertion are not known and transgenic plants produced using biolistics systems may contain multiple and rearranged transgene copies (up to 15 in wheat) inserted at several loci which vary in location between lines (Barcelo et al., 2001; Rooke et al., 2003). Similarly, this apparently random insertion has led to the suggestion that the expression of transgenes may be less stable than that of endogenous genes between individual plants, between generations and between growth environments. Although there is evidence that the expression of transgenes introduced by biolistic transformation is prone to silencing in a small proportion of wheat (Anand et al., 2003; Howarth et al., 2005), many recent reviews including, (Altpeter et al., 2005; Jones, 2005; Kohli et al., 2003; Sahrawat et al., 2003) demonstrate the utility of biolistics transformation (and other methods such as direct insertion of DNA fragments as a basis for stable genetic manipulation.”

(Baker et al., 2006; Barcelo et al., 2001) are confirming the above statements – they could be extended to other methods of transformation like direct insertion of DNA fragments (Paszkowski et al., 1984) and with some questions about the long term stability also to the agrobacterium mediated transformations (Maghuly et al., 2007). But what is really interesting us here is published and documented by (Baudo et al., 2006): Overall, genome disturbances in traditional breeding in comparable cases are measured to be greater than in transformation.

“Detailed global gene expression profiles have been obtained for a series of transgenic and conventionally bred wheat lines expressing additional genes encoding HMW (high molecular weight) subunits of glutenin, a group of endosperm-specific seed storage proteins known to determine dough strength and therefore bread-making quality. Differences in endosperm and leaf transcriptome profiles between untransformed and derived transgenic lines were consistently extremely small, when analyzing plants containing either transgenes only, or also marker genes. Differences observed in gene expression in the endosperm between conventionally bred material were much larger in comparison to differences between transgenic and untransformed lines exhibiting the same complements of gluten subunits. These results suggest that the presence of the transgenes did not significantly alter gene expression and that, at this level of investigation, transgenic plants could be considered substantially equivalent to untransformed parental lines.”

Further confirmings are coming from recent publications like (Batista et al., 2008; Baudo et al., 2006), they all come to the conclusion, that at least certain transgenic crops show demonstrably less transscriptomic disturbances than their non-transgenic counterparts.

The consequences are, that organic farming – using the argument of artificial DNA breeding disturbance, should decide for the transgenic crops in many cases. Another consequence is that transgenic crops of the first generation should never have been subjected to regulation

purely based on methodology, rather it would have been wise to have in each case a close look at the products. In the case of the Golden Rice this has serious ethical consequences, because each year lost to unreasonable and unscientific regulation causes the death of hundreds of thousands of deaths due to severe deficiency in vitamin A, especially among the children of developing countries of South Eastern Asia. In Europe this kind of unscientific regulatory basis hinders the development of transgenic crop breeding for the benefit of a more ecological production. And on top of this the organic farming industry does not shy away from false and often hypocrite propaganda against genetically engineered crops for the sake of marketing their own products.

6. Loss of biodiversity

Biodiversity is being lost in many parts of the globe, often at a rapid pace. It can be measured by loss of individual species, groups of species or decreases in numbers of individual organisms. In a given location, the loss will often reflect the degradation or destruction of a whole ecosystem. The unchecked rapid growth of any species can have dramatic effects on biodiversity. This is true of weeds, elephants but especially humans, who being at the top of the chain can control the rate of proliferation of other species, as well as their own, when they put their mind to it.

Habitat loss due to the expansion of human urbanisation and the increase in cultivated land surfaces is identified as a main threat to eighty five percent of all species described as being close to extinction. The shift from natural habitats towards agricultural land paralleled population growth, often thoroughly and irreversibly changing habitats and landscapes, especially in the developed world. Many from the developed world are trying to prevent such changes from happening in developing nations, to the consternation of many of inhabitants of the developing world who consider this to be eco-imperialism, promulgated by those unable to correct their own mistakes. A clear decline of biodiversity due to agricultural intensification is documented by (Robinson & Sutherland, 2002) for the post-war period in Great Britain.

Today, more than half of the human population lives in urban areas, a figure predicted to increase to sixty percent by 2020 when Europe, and the Americas will have more than eighty percent of their population living in urban zones. Five thousand years ago, the amount of agricultural land in the world is believed to have been negligible. Now, arable and permanent cropland covers approximately one and a half billion hectares of land, with some 3.5 billion hectares of additional land classed as permanent pasture. The sum represents approximately 38% of total available land surface of thirteen billion ha according to FAO statistics.

Habitat loss is of particular importance in tropical regions of high biological diversity where at the same time food security and poverty alleviation are key priorities. The advance of the agricultural frontier has led to an overall decline in the world's forests. While the area of forest in industrialised regions remained fairly unchanged, natural forest cover declined by 8% in developing regions. It is ironical that the most biodiverse regions are also those of greatest poverty, highest population growth and greatest dependence upon local natural resources. (Lee & Jetz, 2008)

Introduced species, another threat to biodiversity Unplanned or poorly planned introduction of non-native (“exotic” or “alien”) species and genetic stocks is a major threat to terrestrial and aquatic biodiversity worldwide. There are hundreds if not thousands of new and foreign genes introduced with trees, shrubs, herbs, microbes and higher and lower animals each year (Kowarik, 2005; Sukopp & Sukopp, 1993). Many of those survive and can, after years and even many decades of adaptation, begin to be invasive. This might be misconstrued as increasing biodiversity, but the final effect is sometimes the opposite. The introduced species often displace native species such that many native species become extinct or severely limited, such cases are known to be very serious in tropical islands (Ammann, 1997; Fowler et al., 2000)

Freshwater habitats worldwide are amongst the most modified by humans, especially in temperate regions. In most areas, introduction of non-native species is the most or second most important activity affecting inland aquatic areas, with significant and often irreversible impacts on biodiversity and ecosystem function. A classic example is the extinction of half to two thirds of the indigenous fish population in Lake Victoria after the introduction of the Nile perch *Lates niloticus*, a top predator (Schofield & Chapman, 1999). Several species of free-floating aquatic plants able to spread by vegetative growth have dispersed widely over the globe and become major pests. Water hyacinth (*Eichhornia crassipes*) is a notable example in tropical waters as is *Anarchis canadensis* = *Elodea canadensis* in temperate waters of the Northern Hemisphere.

Biodiversity should still act as biological insurance for ecosystem processes, except when mean trophic interaction strength increases strongly with diversity (Thebault & Loreau, 2005). The conclusion, which needs to be tested against field studies, is that in tropical environments with a natural high biodiversity the interactions between potentially invasive hybrids of transgenic crops and their wild relatives should be buffered through the complexity of the surrounding ecosystems. This view is also confirmed by the results of Davis (Davis, 2003). Taken together, theory and data suggest that compared to intertrophic interaction and habitat loss, competition from introduced species is not likely to be a common cause of extinctions in long-term resident species at global, metacommunity and even most community levels.

7. Interlude: the role of fundamentalist activists and scientists with a strong anti-GMO agenda in the dispute about GM crops

New technologies always cause in the introductory phase some concern, even anxiety among the population. Some nice examples from past technology introduction phases are summarized in “Hystories” (Showalter, 1997), the present situation is probably best analyzed by (Taverne, 2005b) and his latest book on the “March of Unreason” (Taverne, 2005a). It is also devastating to see, that development of modern breeding is hindered dramatically in Africa (Paarlberg, 2000), and it is one of the perpetuating myths that the multinational companies are taking over in developing countries – on the contrary, it’s

the public research which is dominant to 85% according to FAO statistics (Dhlamini et al., 2005) and (Cohen, 2005). The statistics of ISAAA show that the trend in developing countries is very positive

<http://www.isaaa.org/resources/publications/briefs/37/executivesummary/default.html>

Contrary to this constant positive trend in the development and spread of GM crops there is a widespread activity existing of various kinds of anti-GMO activists, here just a very few typical examples:

There are four main lines of resistance working frantically to reverse these positive trends:

- Scientists who publish questionable or simply flawed papers, based usually on lab protocols which do not fit to international standards, such as Irina Ermakovas rat experiments (Marshall, 2007), for more details go to the ASK-FORCE of PRRI: http://pubresreg.org/index.php?option=com_smf&Itemid=27&topic=13.0
- Activist websites like the ones of Greenpeace, producing lots of scaremonger material such as the hoax of the 1600 dead sheep in India which allegedly have eaten leaves of Bt cotton and died afterwards, a story which has been perpetuated on the websites, despite scientific evidence that the sheep died from infections. Full details on the ASK-FORCE blog of the European Federation of Biotechnology <http://www.efb-central.org/index.php/forums/>
- Lay people like Jeffrey Smith, a long time ardent member of the Maharishi cult and fanatic anti-GMO author: He publicly claimed there were 500 studies proving that yogic flying and transcendental meditation cut crime and increased IQ. His latest book is proof of the contrary: scare stories in a professional layout, with very little verifiable facts but written in a brilliant style in the mode: Throw plenty of dirt and some will be sure to stick. (Smith, 2007). An excellent documentation of many of those myths against GM crops has recently been published by Peggy Lemaux (Lemaux, 2008)
- The most problematic publications stem from scientists who filter facts, give a one-sided picture by omitting crucial data, but per se come with reproducible results and manage to get them published in peer reviewed journals, a typical example comes from a member of GENOEK from Tromsø in Norway, a group pretending to have a holistic view in contrast to most pro-GMO scientists, but actually just do the exact contrary: Ann Myhre published a paper demonstrating that the 35S promoter so often used to enhance transgene expression, shows some activity in cultures of human cells. This is – per se – a scary story, but in her paper (Myhre et al., 2006) she and her co-authors carefully avoid to tell the reader that the very same promoter is eaten daily in quantities by those who relish vegetables of Brassicaceae.

8. Three case studies on the impact of transgenic crops on biodiversity and health

8.1. The case of herbicide tolerant crops, Application of Conservation Tillage easier with herbicide tolerant crops

The soil in a given geographical area has played an important role in determining agricultural practices since the time of the origin of agriculture in the Fertile Crescent of the Middle East. Soil is a precious and finite resource. Soil composition, texture, nutrient levels, acidity, alkalinity and salinity are all determinants of productivity. Agricultural practices can lead to soil degradation and the loss in the ability of a soil to produce crops. Examples of soil degradation include erosion, salinization, nutrient loss and biological deterioration. It has been estimated that 67% of the world's agricultural soils have been degraded (World Resources Institute, 2000).

It may also be worth noting that soil fertility is a renewable resource and soil fertility can often be restored within several years of careful crop management.

In many parts of the developed and the developing world tillage of soil is still an essential tool for the control of weeds.

Unfortunately, tillage practices can lead to soil degradation by causing erosion, reducing soil quality and harming biological diversity. Tillage systems can be classified according to how much crop residue is left on the soil surface (Fawcett et al., 1994; Fawcett & Towery, 2002; Trewavas, 2001; Trewavas, 2003). Conservation tillage is defined as "any tillage and planting system that covers more than 30% of the soil surface with crop residue, after planting, to reduce soil erosion by water" (Fawcett & Towery, 2002). The value of reducing tillage was long recognized but the level of weed control a farmer required was viewed as a deterrent for adopting conservation tillage. Once effective herbicides were introduced in the latter half of the 20th century, farmers were able to reduce their dependence on tillage. The development of crop varieties tolerant to herbicides has provided new tools and practices for controlling weeds and has accelerated the adoption of conservation tillage practices and accelerated the adoption of "no-till" practices (Fawcett & Towery, 2002). Herbicide tolerant cotton has been rapidly adopted since its introduction in (Fawcett et al., 1994). In the US, 80% of growers are making fewer tillage passes and 75% are leaving more crop residue (Cotton Council, 2003). In a farmer survey, seventy-one percent of the growers responded that herbicide tolerant cotton had the greatest impact on soil fertility related to the adoption of reduced tillage or no-till practices (Cotton Council, 2003). In soybean, the growers of glyphosate tolerant soybean plant higher percentage of their acreage using no-till or reduced tillage practices than growers of conventional soybeans (American Soybean Association, 2001). Fifty-eight percent of glyphosate-tolerant soybean adopters reported making fewer tillage passes versus five years ago compared to only 20% of non-glyphosate tolerant soybean users (American Soybean Association, 2001). Fifty four percent of growers cited the introduction of glyphosate tolerant soybeans as the factor which had the greatest impact

toward the adoption of reduced tillage or no-till (American Soybean Association, 2001). Today, the scientific literature on “no-tillage” and “conservation tillage” has grown on more than 6500 references, a selection of some 1200 references from the last three years are given in the following link:

<http://www.botanischergarten.ch/Tillage/Bibliography-No-conservation-Tillage-2006-20080626.pdf>

Several important reviews have been published in recent months, the all tell a positive story regarding the overall impact of herbicide tolerant crops and the impact on the agricultural environment:

Here just a few examples and statement:

(Bonny, 2008): In a comprehensive review Bonny describes the unprecedented success of the introduction of transgenic Soybean in the United States.

It is worthwhile to show one of the graphs about the statistics of glyphosate use, thus correcting some of the legends spread by opponents, sometimes coming in seemingly sturdy statistics like those of (Benbrook, 2004) stating that the herbicide and pesticide use has grown ever since the introduction of transgenic crops. But a closer, more differentiated look reveals this to be an “urban legend”: (Carpenter & Gianessi, 2000).

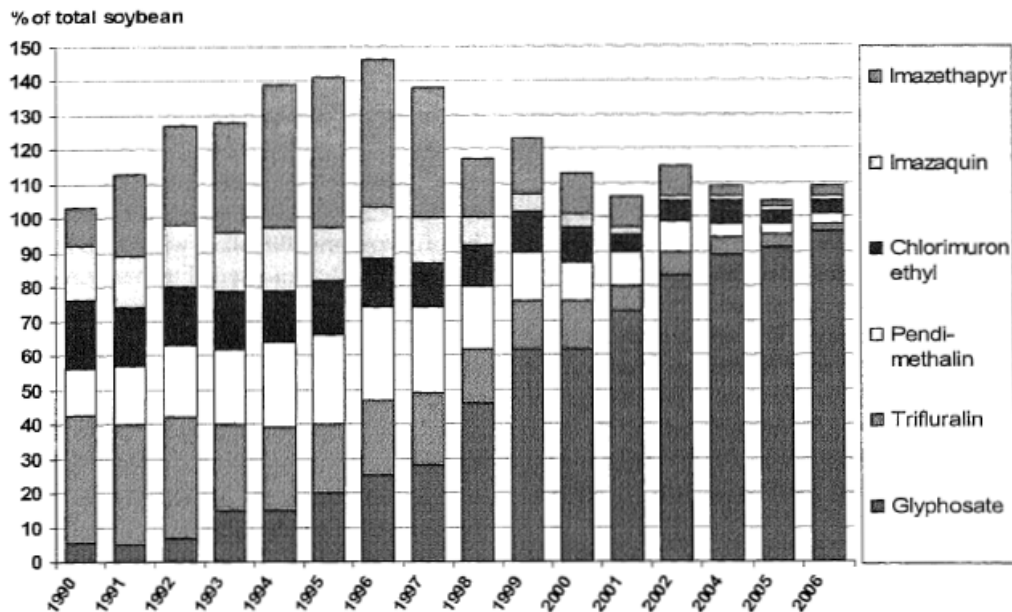


Fig. 2 1. Main herbicides used on total soybean acreage, 1990-2006 (as % of soybean surface treated by each herbicide) (From USDA NASS, 1991-2007). With the development of glyphosate-tolerant soybean, this herbicide is used far more extensively. Indeed, it replaces the herbicides used previously; the Figure shows only a few of the latter. From (Bonny, 2008):

“A comparison of transgenic versus conventional soybean reveals that transgenic glyphosate-tolerant soybean allows both the simplification of weed control and greater work flexibility. Cropping transgenic soybean also fits well with conservation tillage. Transgenic soybean has an economic margin similar to conventional soybean, despite a higher seed cost. The next section describes the evolution of the use of herbicides with transgenic soybean, and some issues linked to the rapid increase in the use of glyphosate. At the beginning a smaller amount of herbicides was used, but this amount increased from 2002, though not steadily. Nonetheless, the environmental and toxicological impacts of pesticides do not only depend on the amounts applied. They also depend on the conditions of use and the levels of toxicity and ecotoxicity. The levels of ecotoxicity seem to have somewhat decreased. The success of transgenic soybeans for farmers has led to a higher use of glyphosate as a replacement for other herbicides, which has in turn led to a decline in its effectiveness. However, the issue here is not only genetic engineering in itself, but rather the management and governance of this innovation.”

(Cerqueira et al., 2007) also emphasize the benefits, despite some green propaganda from Brazil and Argentina, but point also to some potential problems with the evolution of glyphosate resistant weeds:

“Transgenic glyphosate-resistant soybeans (GRS) have been commercialized and grown extensively in the Western Hemisphere, including Brazil. Worldwide, several studies have shown that previous and potential effects of glyphosate on contamination of soil, water, and air are minimal, compared to those caused by the herbicides that they replace when GRS are adopted. In the USA and Argentina, the advent of glyphosate-resistant soybeans resulted in a significant shift to reduced- and no-tillage practices, thereby significantly reducing environmental degradation by agriculture. Similar shifts in tillage practiced with GRS might be expected in Brazil. Transgenes encoding glyphosate resistance in soybeans are highly unlikely to be a risk to wild plant species in Brazil. Soybean is almost completely self-pollinated and is a non-native species in Brazil, without wild relatives, making introgression of transgenes from GRS virtually impossible. Probably the highest agricultural risk in adopting GRS in Brazil is related to weed resistance. Weed species in GRS fields have shifted in Brazil to those that can more successfully withstand glyphosate or to those that avoid the time of its application. These include *Chamaesyce hirta* (erva-de-Santa-Luzia), *Commelina benghalensis* (trapoeraba), *Spermacoce latifolia* (erva-quente), *Richardia brasiliensis* (poaia-branca), and *Ipomoea* spp. (corda-de-viola). Four weed species, *Conyza bonariensis*, *Conyza canadensis* (buva), *Lolium multiflorum* (azevem), and *Euphorbia heterophylla* (amendoim bravo), have evolved resistance to glyphosate in GRS in Brazil and have great potential to become problems.”

These findings are also published in an earlier study with a worldwide scope looking at the herbicide tolerant crops of the Western Hemisphere by some of the same authors (Cerqueira & Duke, 2006) with the same outcome as above.

More pertinent review papers on soil erosion and other agronomic parameters have been published in relationship with the new agricultural management of herbicide tolerant weeds:

(Anderson, 2007; Bernoux et al., 2006; Beyer et al., 2006; Bolliger et al., 2006; Causarano et al., 2006; Chauhan et al., 2006; Etchevers et al., 2006; Gulvik, 2007; Knapen et al., 2007; Knowler & Bradshaw, 2007; Peigne et al., 2007; Raper & Bergtold, 2007; Thomas et al., 2007; Thompson et al., 2008; Wang et al., 2006).

8.2. The Case of Impact of Bt maize on non-target organisms

In a study on environmental impact of Bt-maize on the environment, a book project of now 350 pages, the author also has included a commentary chapter for over 180 scientific studies dealing with non-target organism which could be harmed by the cultivation of Bt maize. Observing strictly the baseline comparison with non-Bt maize cultivation, it can be said that there is not a single publication pointing to detrimental effects of Bt maize compared to other maize traits. Four meta studies have been

published recently with more or less stringent selection of data published in scientific journals, and all those meta analysis do not show any sign of regulatory problems. (Chen et al., 2008; Duan et al., 2008; Marvier et al., 2007; Wolfenbarger et al., 2008) (Wolfenbarger et al., 2008) is singled out here since it is the best meta-analysis existing so far, the selection criteria are clearly defined on all levels and based on a carefully filtered dataset, actually a subset of the database published by (Marvier et al., 2007) on the net under www.sciencemag.org/cgi/content/full/316/5830/1475/DC1

In total, the database used contained 2981 observations from 131 experiments reported in 47 published field studies on cotton, maize and potato. Maize has been studied in the following two comparison categories (including also data on potato and cotton).

- The first set of studies contrasted Bt with non-Bt plots, neither of which received any additional insecticide treatments. This comparison addresses the hypothesis that the toxins in the Bt plant directly or indirectly affect arthropod abundance. It also can be viewed as a comparison between the Bt crop and its associated unsprayed refuge (Gould, 2000).
- The second set of studies contrasted unsprayed Bt fields with non-Bt plots that received insecticides. This comparison tests the hypothesis that arthropod abundance is influenced by the method used to control the pest(s) targeted by the Bt crop. (The third set of studies contrasted fields of Bt-crops and non-Bt-crops both treated with insecticides, a category which did not occur in the here included studies of maize.)

Great care was taken to eliminate redundant taxonomic units and multiple development stages of the same species, with a preference of the least mobile development stage, also the datasets are all derived from the same season.

In contrast to the following study by (Marvier et al., 2007) the statistical analysis was not done with the original taxonomic units, rather the authors decided to use an additional descriptor, six '*functional guilds*' (herbivore, omnivore, predator, parasitoid, detritivores, or mixed). More details can be read in the original publication, as a whole, database robustness and sensitivity of the datasets have been thoroughly discussed and careful decisions have been made in order to get maximum quality of the meta analysis.

"In maize, analyses revealed a large reduction of parasitoids in Bt fields. This effect stemmed from the lepidopteran-specific maize hybrids, and examining the 116 observations showed that most were conducted on *Macrocentrus grandii*, a specialist parasitoid of the Bt-target, *Ostrinia nubilalis*. There was no significant effect on other parasitoids, but *M. grandii* abundance was severely reduced by Bt maize. Higher numbers of the generalist predator, *Coleomegilla maculata*, were associated with Bt maize but numbers of other common predatory genera (*Orius*, *Geocoris*, *Hippodamia*, *Chrysoperla*, were similar in Bt and non-Bt maize."

The conclusion is rather simple: Bt maize is better for the environment, and in almost all field studies the non-target insects, including a whole range of butterflies have a better survival chance than in non-Bt crop fields.

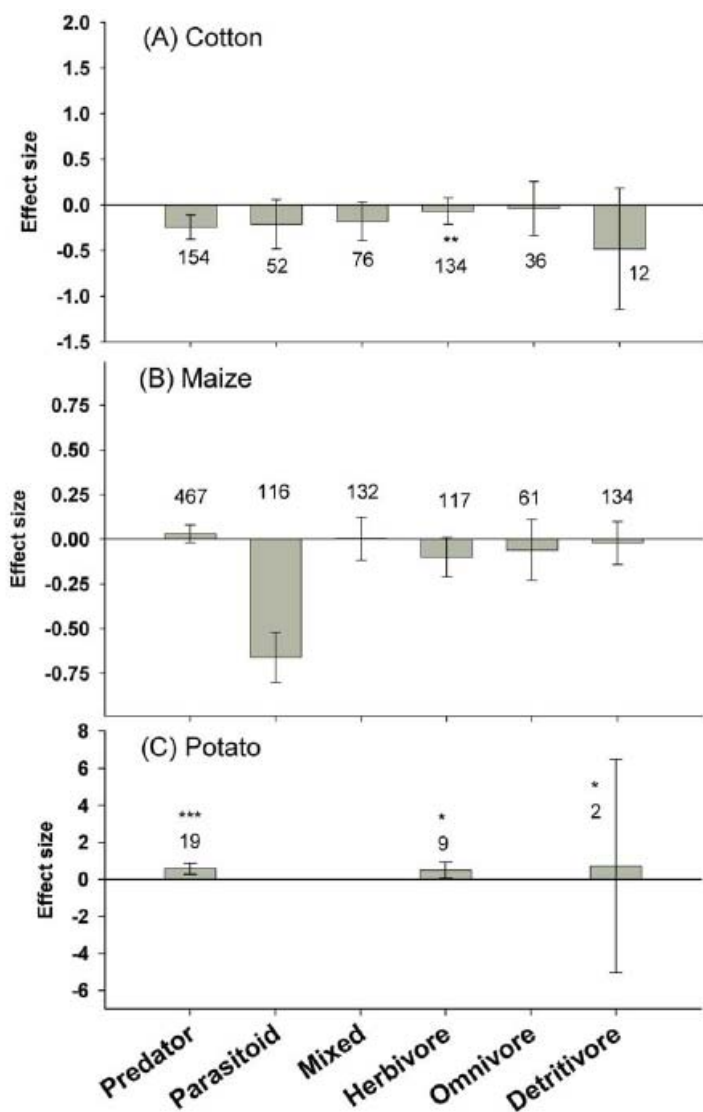


Fig. 3 The effect of Bt crops on non-target functional guilds compared to unsprayed, non-Bt control fields. Bars denote the 95% confidence intervals, asterisks denote significant heterogeneity in the observed effect sizes among the comparisons (* ,0.05, ** ,0.01, *** ,0.001), and Arabic numbers indicate the number of observations included for each functional group. doi:10.1371/journal.pone.0002118.g001. Fig. 1 from (Wolfenbarger et al., 2008)

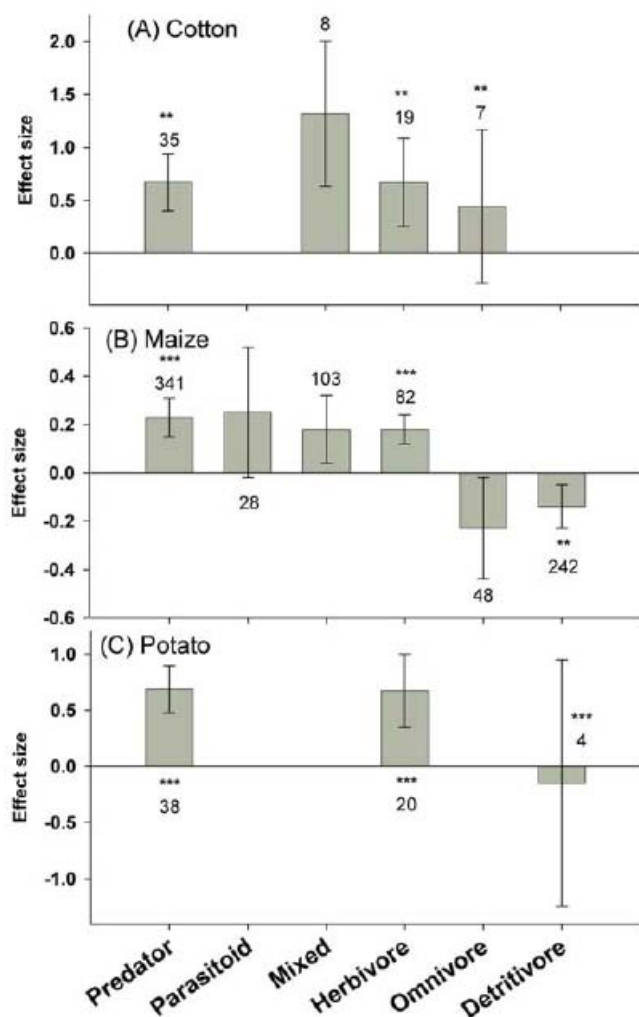


Fig. 4 The effect of Bt crops on non-target functional guilds compared to insecticide-treated, non-Bt control fields. Bars denote the 95% confidence intervals, asterisks denote significant heterogeneity in the observed effect sizes among the studies (*,0.05, **,0.01, ***,0.001), and Arabic numbers indicate the number of observations included for each functional group. doi:10.1371/journal.pone.0002118.g002. Fig. 2 from (Wolfenbarger et al., 2008)

“In maize, the abundance of predators and members of the mixed functional guild were higher in Bt maize compared to insecticide-sprayed controls (Fig. 2b). Significant heterogeneity occurred in predators, indicating variation in the effects of Bt maize on this guild. For example, we detected no significant effect sizes for the common predator genera *Coleomegilla*, *Hippodamia* or *Chrysoperla*, but the predator *Orius* spp. and the parasitoid *Macrocentrus* were more abundant in Bt maize than in non-Bt maize plots treated with insecticides. Partitioning by taxonomic groupings or the target toxin (*Lepidoptera* versus *Coleoptera*) did not reduce heterogeneity within predators. However, insecticides differentially affected predator populations. Specifically, application of the pyrethroid insecticides lambda-cyhalothrin, cyfluthrin, and bifenthrin in non-Bt control fields resulted in comparatively fewer predators within these treated control plots. Omitting studies involving these pyrethroids revealed a much smaller and homogeneous effect size. Predator abundance in Bt fields was still significantly higher compared with insecticide-treated plots, but the difference was less marked without the pyrethroids (Fig. 3). Compared to the subset of controls using pyrethroids, Bt maize was particularly favorable to *Orius* spp.”

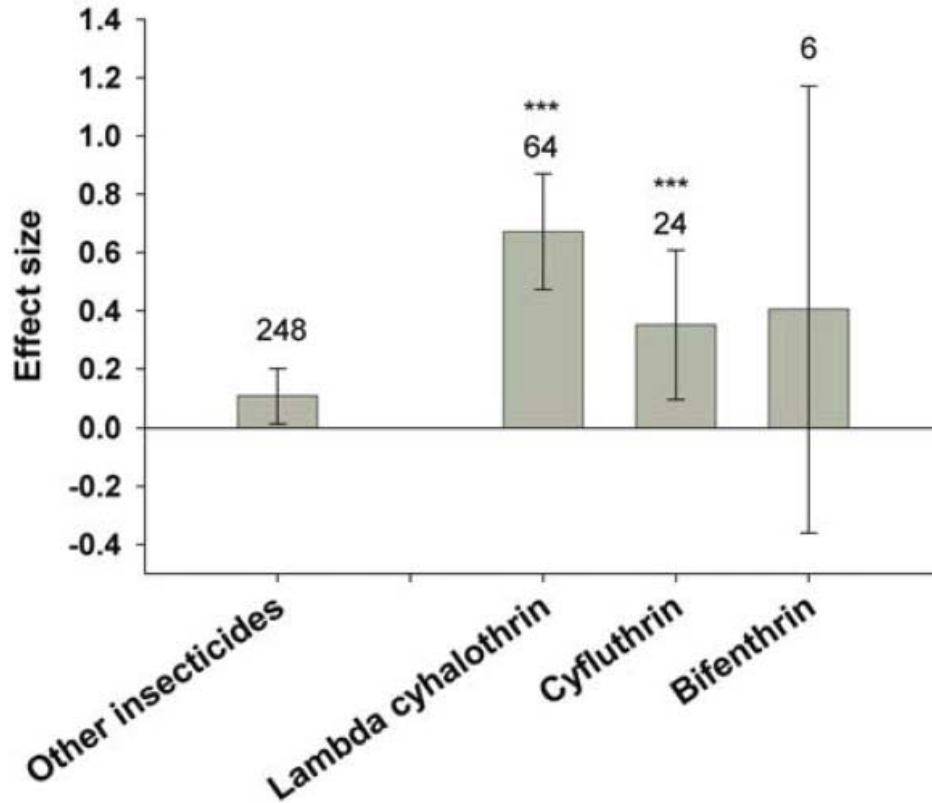


Fig. 5 Effects of Bt maize vs. control fields treated with a pyrethroid insecticide on predatory arthropods. Bars denote the 95% confidence intervals, asterisks denote significant heterogeneity in the observed effect sizes among the studies (* ,0.05, ** ,0.01, * ,0.001), and Arabic numbers indicate the number of observations included for each functional group. doi:10.1371/journal.pone.0002118.g003 . Fig. 3 from (Wolfenbarger et al., 2008)**

“Bt-maize favored non-target herbivore populations relative to insecticide-treated controls, but there was also significant heterogeneity, some of which was explained by taxonomy. Aphididae were more abundant in insecticide sprayed fields and Cicadellidae occurred in higher abundance in the Bt maize. In contrast to patterns associated with predators and detritivores, type of insecticide did not explain the heterogeneity in herbivore responses. The pyrethroid-treated controls accounted for 85% of the herbivore records. Individual pyrethroids had variable effects on this group, and none yielded strong effects on the herbivores.

An underlying factor associated with the heterogeneity of the herbivore guild remained unidentified, but many possible factors were eliminated (e.g., Cry protein target, Cry protein, event, plot size, study duration, pesticide class, mechanism of pesticide delivery, sample method, and sample frequency).

An underlying factor associated with the heterogeneity of the herbivore guild remained unidentified, but many possible factors were eliminated.”

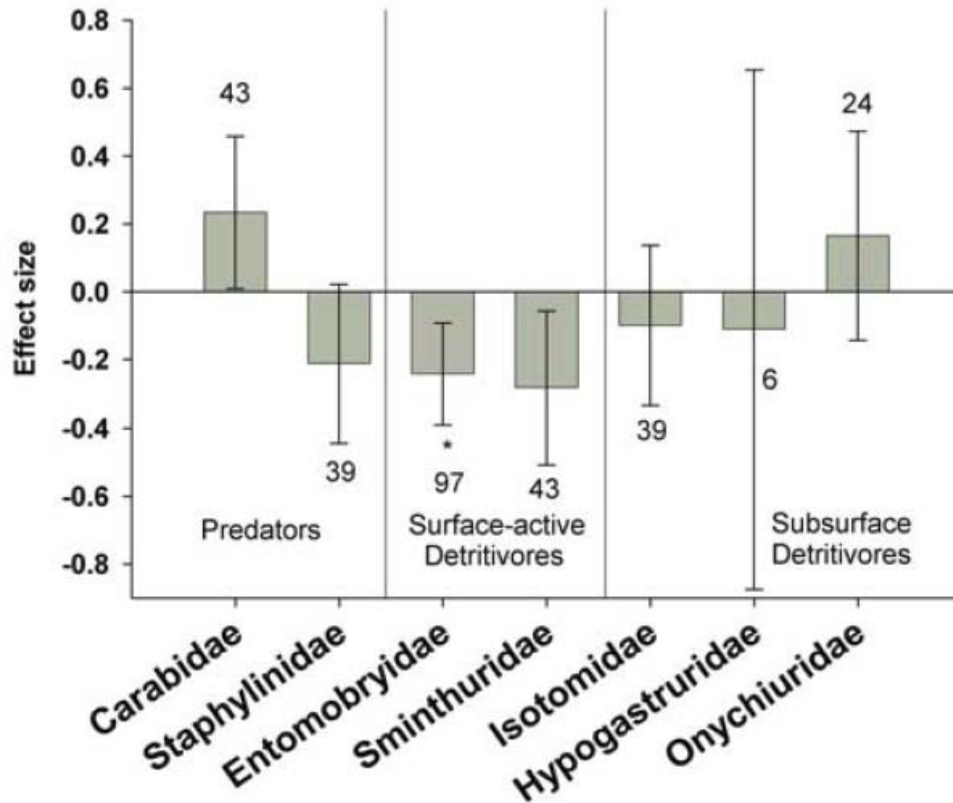


Fig. 6 Effect of Bt crops vs. insecticide-treated, non-Bt control fields on soil-inhabiting predators and detritivores. Bars denote the 95% confidence intervals, asterisks denote significant heterogeneity in the observed effect sizes among the studies (*, 0.05, **, 0.01, *, 0.001), and Arabic numbers indicate the number of observations included for each functional group. doi:10.1371/journal.pone.0002118.g004. Fig. 4 from (Wolfenbarger et al., 2008)**

“The “mixed” functional group was more abundant in Bt maize ($E = 0.1860.14$, $n = 103$) compared with non-Bt maize treated with insecticides. The majority of this functional group is comprised of carabids ($n = 33$), nitidulids ($n = 26$), and mites ($n = 23$).

For potatoes, the abundance of predators ($E = 0.6960.30$, $n = 38$), but not herbivores, was significantly higher in the Bt crop (Fig 2c). Responses within each functional group were variable but sample sizes were too low to further partition this significant heterogeneity.

Predator-non target herbivore ratio analyses.

No significant change in predator-prey ratios was detected in cotton or potato; in maize there was a significantly higher predator- prey ratio in Bt maize plots than in the insecticide controls ($E = 0.6360.42$, $n = 15$). Significant heterogeneity for the predator: prey response existed in all three crops, but again sample sizes were too small to explore the cause of this variability.

Predator-detritivore analyses.

The higher abundance of detritivores in sprayed non-Bt maize appeared to be driven primarily by two families of Collembola with a high proportion of surface-active species (Entomobryidae: $E = 20.2460.15$, $n = 97$;

Sminthuridae: $E = 20.2860.23$, $n = 43$, Fig. 4). Three other families, Isotomidae, Hypogastruridae, and Onychiuridae, with more sub-surface species, were similar in Bt and non-Bt fields. We would expect surface-active collembolans to be more vulnerable to surface-active predators, and we detected a significantly lower abundance in one predator of Collembola (Carabidae: $E = 0.2360.22$, $n = 43$) but not in another (Staphylinidae: $E = 20.2160.23$, $n = 39$, Fig 4). The other two detritivore families occupy different niches than Collembola and responded differently to insecticide treatments. The abundance of Japygidae (Diplura) was unchanged ($E = 20.1160.35$, $n = 9$), but that for Lathridiidae (Coleoptera) was higher in Bt maize ($E = 0.7660.70$, $n = 6$), suggesting a direct negative effect of insecticides on this latter group. Lathridiid beetles, although being surface-active humusfeeders, are larger and more motile than Collembola and thus may be less vulnerable to predators and more vulnerable to insecticides.”

As a whole, the study of Wolfenbarger et al. et al. did not reveal any negative effects, confirming for a large amount of data and publications the environmental benefits of the Bt maize tested.

8.3. Bt corn has much less cancer causing mycotoxins than conventional corn

Bt corn is definitely healthier: Many publications have demonstrated that Bt maize has less mycotoxins with their bad reputation of cancerogeneity.

In a worldwide review, (Placinta et al., 1999) summarized the situation on mycotoxins in animal feed (including a comprehensive list of literature).

“Three classes of *Fusarium* mycotoxins may be considered to be of particular importance in animal health and productivity.

Within the trichothecene group, deoxynivalenol (DON) is widely associated with feed rejection in pigs, while T-2 toxin can precipitate reproductive disturbances in sows.

Another group comprising zearalenone (ZEN) and its derivatives is endowed with oestrogenic properties.

The third category includes the fumonisins which have been linked with specific toxicity syndromes such as equine leukoencephalomalacia (ELEM) and porcine pulmonary oedema.”

It is important to know that storage conditions are heavily influencing the fumonisin content of the maize cobs, as was shown by (Fandohan et al., 2003; Gressel et al., 2004; Olakojo & Akinlosotu, 2004) in Africa: the storage conditions are often poor and foster fungal infection dramatically, also due to post-harvest weevils.

It seems logical to fight fumonisin producing fungi with fungicides, but this is obviously not an easy task according to (D'Mello et al., 1998; D'Mello et al., 2001; D'Mello et al., 1999). There are no feasible solutions ready – except the ones offered by the Bt crops. Also the use of fungicide sprays does not really bring considerable remedy. It is interesting to note that D'Mello deems most promising to develop *Fusarium* resistant crops, in order to avoid the clearly detrimental effects of pigs reacting on high fumonisin levels in feed.

Many studies in epidemiological human medicine have proven the clear pathogenicity of fumonisins: Here the important critical review of many pertinent papers: (Marasas et al., 2004). They found and cite numerous studies which demonstrate that fumonisins are potential risk factors for neural tube defects, craniofacial anomalies, and other birth defects arising from neural crest cells because of their apparent interference with folate utilization.

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