the impact of agricultural biotechnology on biodiversity

a review

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Landscape contrasts caused by man in its constant strive for food: Grazing cattle above, pristine temperate rainforest below in New Zealand, photo K. Ammann

Executive Summary ↺

This paper gives an overview of biodiversity and how it is impacted by agricultural biotechnology, building upon chapters on the impact of biotechnology on biodiversity for the European Federation of Biotechnology (Braun & Bennett, 2001) and UNESCO (Braun & Ammann, 2002). Biodiversity encompasses the fundamental bases of life on earth, including genetic, species and ecosystem diversity. There is a need to better understand biodiversity in terms of its fundamental components (genes and taxa), the interrelatedness of these components (ecology), their importance for human life and life in general, and the factors that threaten biodiversity. Within the tropics, Biodiversity is still concentrated in unmanaged habitats. In temperate zones, particularly in the European Union, almost 50% of the landscape is agricultural, and agricultural lands contain a significant portion of the biodiversity in these zones. The greatest threats to biodiversity are destruction and deterioration of habitats, particularly in tropical developing countries, and introductions of exotic species. Maintaining biodiversity requires addressing these threats.

Many of the factors affecting biodiversity are related directly or indirectly to the needs of agricultural production, and it is important to consider how these impacts could be mitigated. Increasing human population and limited arable land have demanded increased agricultural productivity leading to more intensive agricultural practices on a global basis. In response, higher yielding crop varieties have been coupled with increased inputs in the form of fertilizers, irrigation, and pesticides and more intensive practices such as greater tillage of soil and fewer crop rotations and fallows. More recently, technological advances have led to the development of genetically modified (GM) crops with insect resistance and herbicide tolerance that have a demonstrated potential to enhance productivity. These technologies have been broadly adopted in some farming systems, replacing broad-spectrum insecticides in some systems and facilitating reductions in tillage in others.

Agricultural impacts on biodiversity can be divided into impacts on in-field biodiversity and impacts on natural (off-site) biodiversity. Intensive agriculture has negative impacts on both species and genetic biodiversity within agricultural systems, primarily because of low crop and structural diversity but also through pesticide use and tillage. These impacts can be addressed by encouraging diversification of agricultural systems, and by reducing broad-spectrum insecticide use and tillage, both of which GM crops can achieve in some systems. Agricultural impacts on natural biodiversity primarily stem from conversion of natural habitats into agricultural production and from irrigation. Transport of fertilizers and pesticides into aquatic systems also causes significant habitat deterioration through eutrophication and toxicity. Increasing the efficiency of agricultural production can reduce these impacts, as can minimizing off-site movement of fertilizers and pesticides by reducing tillage and total agricultural inputs. Technologies such as GM crops are important in this respect. Benefits of GM crop growing related to biodiversity are already visible in sound field experiments and can be improved through enhanced management.

Overall, creating agricultural systems with lower impact on offside biodiversity and maintenance of high levels of inside biodiversity will require us to utilize all available technologies while simultaneously encouraging appropriate farmer practices. This also means that agricultural and conservation policy should work together in order to develop appropriate markets.

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Section 1

Basics of Biodiversity

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Definition of Biodiversity

Biological diversity is a term that may refer to diversity in a gene, species, community of species, or ecosystem. It is often contracted to *biodiversity* and used broadly with reference to the total biological diversity in an area or 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 Convention on Biological Diversity, biodiversity means “the variability among living organisms from all sources including, *inter alia,* terrestrial, marine, and other aquatic ecosystems and the ecological complexes of which they are part” (CBD, 1992). It is important not to oversee the various scale-dependent perspectives of biodiversity, as described in the paragraphs below, since this can be the source of many misunderstandings in the debate of biosafety. It is not a simple task to define biodiversity, nor to quantify it: (Tilman, 2000), (Purvis & Hector, 2000)

There are many websites dealing with biodiversity and its definition, amongst which:

GBIF, Global Biodiversity Information Facility (GBIF, 2003)

BioCase, A Biological Collection Access Service for Europe (BioCase, 2003),

Natural Science Collections Alliance (Alliance, 2003),

European Community Biodiversity Clearing House Mechanism (European Community, 2003)

Euro+Med Plant Base (Euro+Med, 2003) with an European perspective.

European Federation of Biotechnology, Section Biodiversity (EFB, 2003)

The present section will look at biodiversity at all levels but the paper will then focus on gene and species diversity, particularly in terrestrial and freshwater environments.

Genetic, Species and Ecosystem Diversity ↺

Genetic diversity

Genes are the basic building blocks of life. In many instances genetic sequences, functions and the proteins encoded by the genes are almost identical (highly conserved) across all species. The importance of genetic diversity is noted in the combination of genes within an organism (the genome), the variability in phenotype that they produce as well as their resilience and survival under selection. As such, it is widely believed that ecosystems, natural ecosystems in particular, should be managed in a way that protects the untapped resource of genes within their host organisms. Today, much work remains to be done to both characterize genetic diversity and understand how best to protect and make wise use of it. (Raikhel & Minorsky, 2001).

It becomes obvious that 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. It turns out that there are many more proteins than genes in cells because of post-transcriptional modification. This would now also explain the multitude of living organisms which differ in only a small portion of their genes. Also it explains why the number of genes discovered in the few organisms sequenced is considerably lower than anticipated.

Species diversity ↺

For most practical purposes, species are the most useful units for biodiversity research and species diversity is the most useful indicator of biodiversity. There is no single definition of what a species is and species-level taxonomy can change with new data as well as new approaches. Nevertheless, a species could broadly be defined as a collection of populations that may differ genetically from one another to a greater or lesser degree, but whose individuals are facultative able to mate and produce 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, many of these being undescribed insects (Table 1).

Table 1: Estimated numbers of described species and possible global total

Kingdoms	Phyla	Described species	Estimated total
Bacteria		4,000	1,000,000
Protoctista		80,000	600,000
Animalia			
	Craniata (vertebrates) total	52,000	55,000
	Mammals	4,630	
	Birds	9,946	
	Reptiles	7,400	
	Amphibians	4,950	
	Fishes	25,000	
	Mandibulata (insects & myriapods)	963,000	8,000,000
	Chelicerata (arachnids etc)	75,000	750,000
	Mollusca	70,000	200,000
	Crustacea	40,000	150,000
	Nematoda	25,000	400,000
Fungi		72,000	1,500,000
Plantae		270,000	320,000
TOTAL		**1,750,000**	**14,000,000**

(Source:UNEP World Conservation Monitoring Center 2000) (Groombridge & Jenkins, 2000)

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 anthropogenic management 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 since human activity has influenced most regions on earth.

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 typically abut managed ecosystems.

The third broad classification of ecosystems are “managed ecosystems”. Such systems can be managed 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 they function, how different ecosystems might interact with each other, and which ecosystems are critical to the services most vital to life on Earth. The role of the forests for water management is crucial due to acute threats through urbanisation, in particular also the dry tropical forests. 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. Nevertheless, we know enough about the threat status and the value of the main ecosystems in order to set priorities in conservation and better management (World Resources Institute, 2000) Theory behind patterns of biodiversity related to ecological factors is rapidly evolving, but many phenomena are still enigmatic and far from understood (Gaston, 2000)

Let’s sum up with the words of Lyn Margulis:

> “What is life? It is a linguistic trap. To answer according to the rules of grammar, we must supply a noun, a thing. But life on Earth is more like a verb. It is a material process, surfing over matter like a strange slow wave. It is a controlled artistic chaos, a set of chemical reactions so staggeringly complex that more than 4 billion years ago it began a sojourn that now, in human form, composes love letters and uses silicon computers to calculate the temperature of matter at the birth of the universe.” (Margulis, 1995)

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 (Figure 1). Latin America, the Caribbean, Asia and the Pacific host together 80% of the ecological mega-diversity of the world.

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. The Amazon basin contains for example 87 to nearly 300 different tree species per hectare and supports the richest fish fauna known, with more than 2500 species. The forests in Asia and South America are considered to be especially rich in animal species.

Species and genetic diversity within any agricultural field will be more limited than in a natural or semi-natural ecosystem. Nevertheless, agricultural ecosystem can be dynamic in terms of species diversity over time due to the amount of management. Biodiversity in agricultural settings is extremely important at country level in areas where the proportion of land allocated to agriculture is high. This is the case in Europe for example, where 45% of the land is dedicated to arable and permanent crop or permanent pasture (FAOSTAT, 2003). In the UK, this figure is even higher, at 70%. Consequently, biodiversity is to a large degree influenced by man since centuries, and changes in agrobiological management will influence biodiversity in such countries overall. Instead of lamenting the loss of single rare birds (which anyway may be the product of agricultural activity to a great extent) it would be important to think along innovative lines to enhance biodiversity in general.

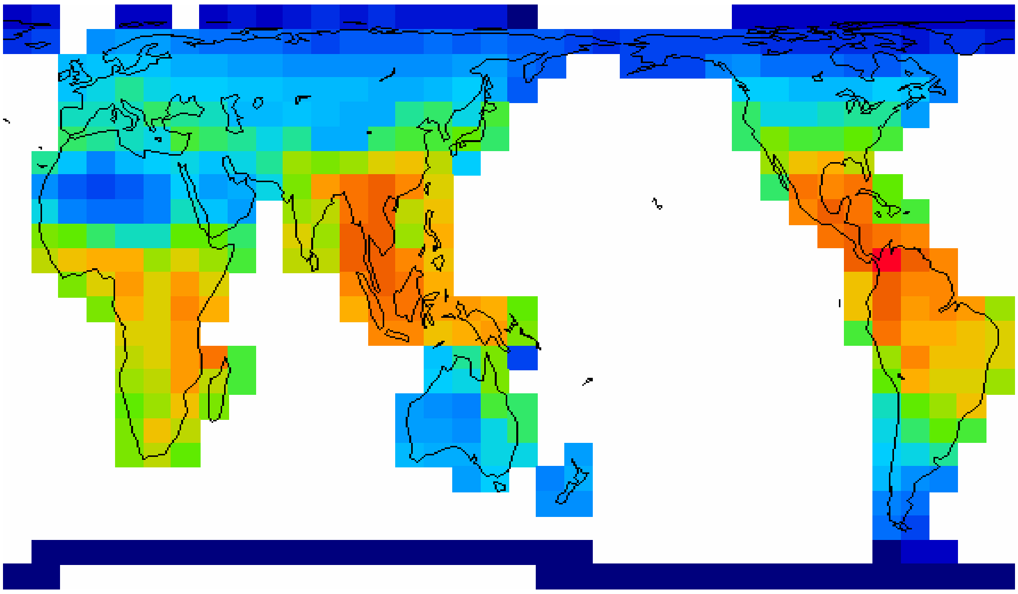

Figure 1 Global biodiversity value: a map showing the distribution of some of the most highly valued terrestrial biodiversity world-wide (mammals, reptiles, amphibians and seed plants), using family-level data for equal-area grid cells, with red for high biodiversity and blue for low biodiversity (Williams et al., 2003).

Loss of Biodiversity ↺

Threats to global biodiversity

Loss of biodiversity is occurring 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. Recently the Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA, 2003) of the Convention on Biological Diversity ranked threats to global biodiversity in the following manner:

Habitat loss: Probably the most serious of all threats to biodiversity

Introduction of exotic species

Further: flooding, lack of water, climate changes, salination etc., all of which may be either natural or man-made (not dealt with in this report).

The United Nations Environment Program, in their 1997 Global State of the Environment report (UNEP, 1997), described regional environmental trends as shown in Figure 2.

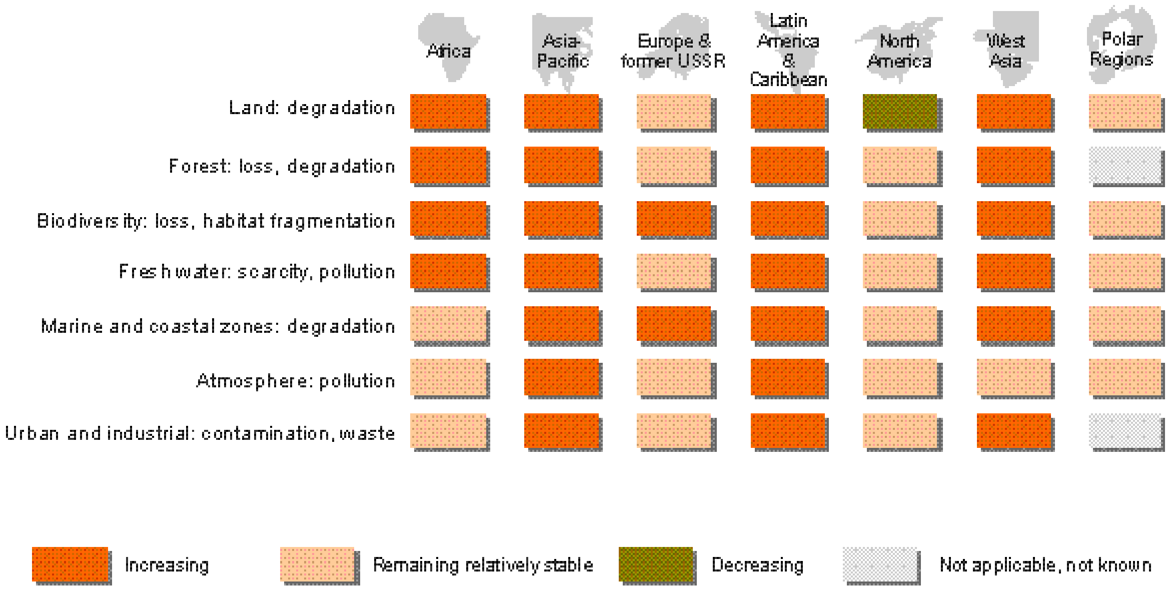

Figure 2: Regional environmental trends in habitat loss (UNEP, 1997).

The unchecked rapid growth of human population has had dramatic effects on biodiversity worldwide. Habitat loss due to the expansion of human activities is identified as a main threat to 85% of all species described in the IUCN Red List (IUCN, 2000). Main factors are urbanisation and the increase in cultivated land surfaces.

The shift from natural habitats towards agricultural land must have been dramatic in past times. the following map illustrates this: The spread of wheat in Europe must have changed habitats and landscapes thoroughly and irreversibly:

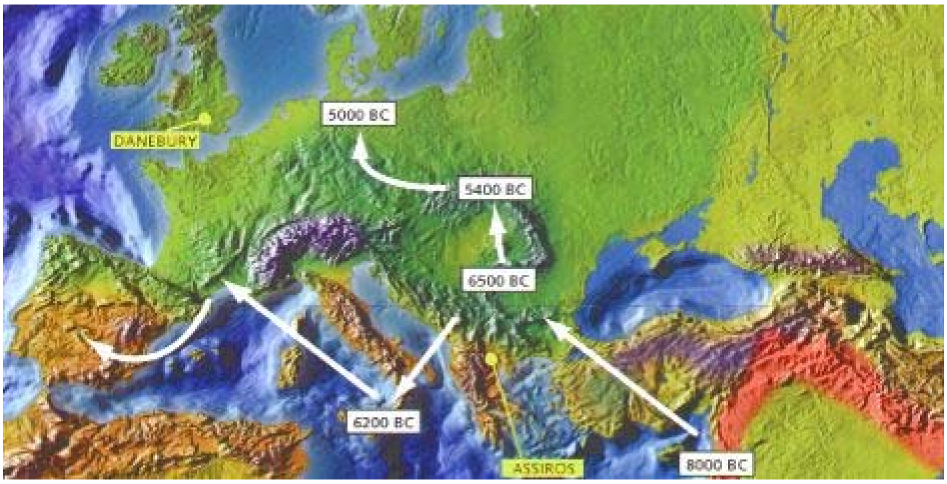

Figure 3: Spread of wheat in Europe (Brown & Johnes, 2003)

Agriculture had far-reaching effects on human society, spreading across Eurasia and leading to increased populations and eventually to civilisations such as those of classical Greece and Rome. But most of this happened centuries before the invention of writing, so it is only through archaeology that we can try to understand prehistoric agriculture. (Chapin et al., 1998; Chapin et al., 2000)

Today, more than half of humankind lives in urban areas, a figure predicted to increase to 60% by 2020 when Europe, Latin America and North America will have more than 80% 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. In 2000, arable and permanent cropland covered approximately 1,497 million hectares of land, with some 3,477 million hectares of additional land classed as permanent pasture (Figure 3). The sum represents approximately 38% of total available land surface (13,062 million ha, according to (FAOSTAT, 2003).

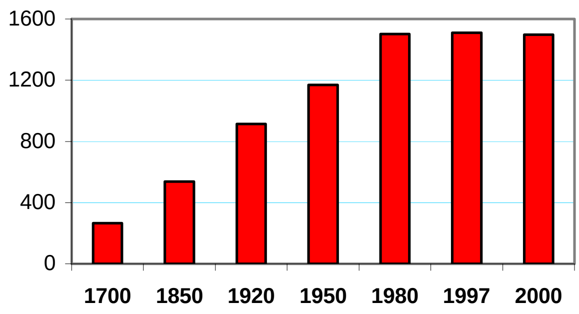

Figure 4: Land converted to arable and permanent cropland, in a time axis from 1700 to now, in million hectares (FAOSTAT, 2003)

Habitat loss is of particular importance in regions of high biological diversity where at the same time food security and poverty alleviation are key priorities (e.g. some parts of Latin America and Asia Pacific for example). Forests are a good example: the impacts of development activities and the advance of the agricultural frontier has led to an overall decline in the world's forests and woodlands of approximately 2% between 1980 and 1990. While the area of forest in industrialised regions remained fairly unchanged, natural forest cover declined by 8% in developing regions

(UNEP, 1997). It is a bitter irony, that the most biodiverse regions are also those of greatest poverty, highest population growth and greatest dependence upon local natural resources.

Introduction of exotic species ↺

Unplanned or poorly planned introduction of non-native species and genetic stocks is a major threat to terrestrial and aquatic biodiversity worldwide. According to (Sukopp & Sukopp, 1993) there are hundreds if not thousands of new and foreign genes introduced with trees, shrubs, herbs, microbes and higher and lower animals each year. Many of those survive and can, after years and even many decades of adaptation, begin to be invasive. (Starfinger et al., 1998)

Terrestrial areas most affected by the introduction of exotic species include forests, Mediterranean regions as well as similar types of natural vegetation in the Cape Province of South Africa, parts of Chile, Southern Australia and California, grasslands and savannas and agricultural lands. One of the most extreme examples is seen in the pampas of Argentina, a flat grassland with a moderate climate, from which nearly all the native grasses have disappeared and have been replaced by European plants. Islands and other areas having evolved unique ecosystems are particularly at risk (CBD-ALIEN, 2003)

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 haplochromine cichlid fish population in Lake Victoria after the introduction of the Nile perch *Lates niloticus,* a top predator. (Schofield & Chapman, 1999). Also, several species of free-floating aquatic plants able to spread by vegetative growth have dispersed widely over the globe and become major pests, as a notable example in the Northern Hemisphere *Elodea canadensis,* Elodea, Common Waterweed.

Loss of biodiversity in the agricultural environment ↺

In an agricultural context, a rapid decline in species, varieties and genetic diversity has been brought about by the success of new commercial varieties. Reported losses of over 80% of varieties in species such as apple, maize, tomato, wheat and cabbage have occurred worldwide (UNEP World Conservation Monitoring Centre, 2003). Studies in population genetics raised concern over genetic erosion and the recognition of the importance of plant genetic material in the development of new varieties led to the establishment in the 1970's of the International Plant Genetic Resources Institute in Rome (FAO, 2003; IPGRI, 2003) and increased efforts to collect germplasm for *ex-situ* collections. The strong decrease in the number of butterfly species in Flanders (north Belgium) in the 20th century is illustrated by (Maes & Van Dyck, 2001) using data from a national butterfly mapping scheme. Nineteen of the 64 indigenous species went extinct and half of the remaining species are threatened at present. Flanders is shown to be the region with the highest number of extinct butterflies in Europe. More intensive agriculture practices and expansion of house and road building increased the extinction rate more than eightfold in the second half of the 20th century.

Terrestrial but also aquatic biodiversity within and around agricultural fields, as discussed in Chapter 3, has also been strongly influenced by agricultural practices. (Tilman, 1999; Tilman et al., 2002) Fertilisers, pest control chemicals, tillage and even crop rotation have been shown to profoundly impact the richness and diversity of agricultural ecosystems. (Beringer, 2000; Ross et al., 2002). Habitat fragmentation may have a more adverse effect in combination with disturbance.

Importance of Biodiversity ↺

Biological diversity has emerged in the past decade as a key area of concern for sustainable development. It 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. (CBD, 1992), see Preamble.

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. In agriculture, biodiversity 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 scarcer.

Generally, it is assumed that higher biodiversity results in higher productivity for biomass (Edwards & Abivardi, 1998; Hector et al., 1999; Pfisterer & Schmid, 2002; Symstad et al., 1998)

For more information about biodiversity and its relationship to ecological parameters go to:

From the following table it will be clear to the reader, that the value of biodiversity is linked to most human activities:

Primary Goods and Services Provided by Ecosystems

Ecosystem	Goods	Services
Agroecosystems	▪ 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 ▪ Fuelwood ▪ Drinking and irrigation water ▪ Fodder ▪ Nontimber products (vines,bamboos, leaves, etc.) ▪ Food (honey, mushrooms, fruit, and other edible plants; game) ▪ Genetic resources	▪ Remove air pollutants, emit oxygen ▪ Cycle nutrients ▪ Maintain array of watershed functions (infiltration, purification, flow control, soil stabilization) ▪ Maintain biodiversity ▪ Sequester atmospheric carbon ▪ Moderate weather extremes and impacts ▪ Generate soil ▪ Provide employment ▪ Provide human and wildlife habitat ▪ Contribute aesthetic beauty and provide recreation
Freshwater Systems	▪ Drinking and irrigation water ▪ Fish ▪ Hydroelectricity ▪ Genetic resources	▪ Buffer water flow (control timing and volume) ▪ Dilute and carry away wastes ▪ Cycle nutrients ▪ Maintain biodiversity ▪ Provide aquatic habitat ▪ Provide transportation corridor ▪ Provide employment ▪ Contribute aesthetic beauty and provide recreation
Grassland Ecosystems	▪ Livestock (food, game, hides, fiber) ▪ Drinking and irrigation water ▪ Genetic resources	▪ Maintain array of watershed functions (infiltration, purification, flow control, soil stabilization) ▪ Cycle nutrients ▪ Remove air pollutants, emit oxygen ▪ Maintain biodiversity ▪ Generate soil ▪ Sequester atmospheric carbon ▪ Provide human and wildlife habitat ▪ Provide employment ▪ Contribute aesthetic beauty and provide recreation
Coastal Ecosystems	▪ Fish and shellfish ▪ Fishmeal (animal feed) ▪ Seaweeds (for food and industrial use) ▪ Salt ▪ Genetic resources	▪ Moderate storm impacts (mangroves; barrier islands) ▪ Provide wildlife (marine and terrestrial) habitat ▪ Maintain biodiversity ▪ Dilute and treat wastes ▪ Provide harbors and transportation routes ▪ Provide human and wildlife habitat ▪ Provide employment ▪ Contribute aesthetic beauty and provide recreation

Figure 5 Primary Goods and Services provided by the Ecosystems (World Resources Institute, 2000)

Ever since the first Stockholm Report of the United Nations Environmental Programme (UNEP, 1972), biodiversity has been indirectly on the global agenda. In view of the importance of biodiversity for the future of mankind, several international agreements aimed at relieving some of the pressure on selected important resources have been reached. These include for example the numerous regional fishery management schemes, the Convention on International Trade in Endangered Species (CITES), and more recently the Convention on Biological Diversity (CBD, 1992).

Convention of Biological Diversity (CBD)

The Convention of Biological Diversity CBD was negotiated under the auspices of the United Nations Environment Programme (UNEP) and entered into force on 29 December 1993. The convention has three goals: promote the conservation of biodiversity, the sustainable use of its components, and the fair and equitable sharing of benefits arising out of the utilization of genetic resources.

A radical change brought about by the CBD is the recognition that States have a sovereign right over biodiversity within their own territory: previously organisms were considered to be the common heritage of mankind. Living organisms or their products may, under the terms of the CBD, only be removed from a country under mutually agreed conditions.

The CBD is a comprehensive approach to biodiversity conservation of both wild and domesticated species. It aims at conservation at the genetic, species and ecosystem levels. As reviewed by (Buhenne-Guilmin & Glowka, 1994), action is delegated to the national level obliging States to assess biodiversity, enact legislation for its conservation *in situ* and *ex situ*, and to enforce legislation within national boundaries.

Section 2 Agricultural Practices

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World food production almost doubled in the thirty-five years from 1961-1996 (FAOSTAT, 2003); (Tilman, 1999; Tilman et al., 2002). This was accomplished with only a 1.1 fold increase in cultivated lands and was made possible due to dramatic changes in agricultural practices including use of fertilisers and pest control compounds, implementation of specific agricultural practices, shifts to higher yielding varieties and adoption of new technologies. The following section will review current common agricultural practices that are used to increase productivity.

Agricultural inputs ↺

The productivity of crop plants is challenged by abiotic and biotic stresses. Abiotic stresses include nutrient deficiencies, water challenges, temperature extremes, as well as soil acidity, alkalinity and salinity. Fertilization and irrigation are two important tools for addressing some of these problems. Nitrogen and phosphorous fertilizers are commonly applied. In fact, the doubling in world food production cited above was accompanied by a 6.87 fold increase in nitrogen fertilization and a 3.48 fold increase in phosphorous fertilization. In that same time, water challenges were met by increasing irrigated lands by 1.68 fold (FAOSTAT, 2003; Tilman, 1999).

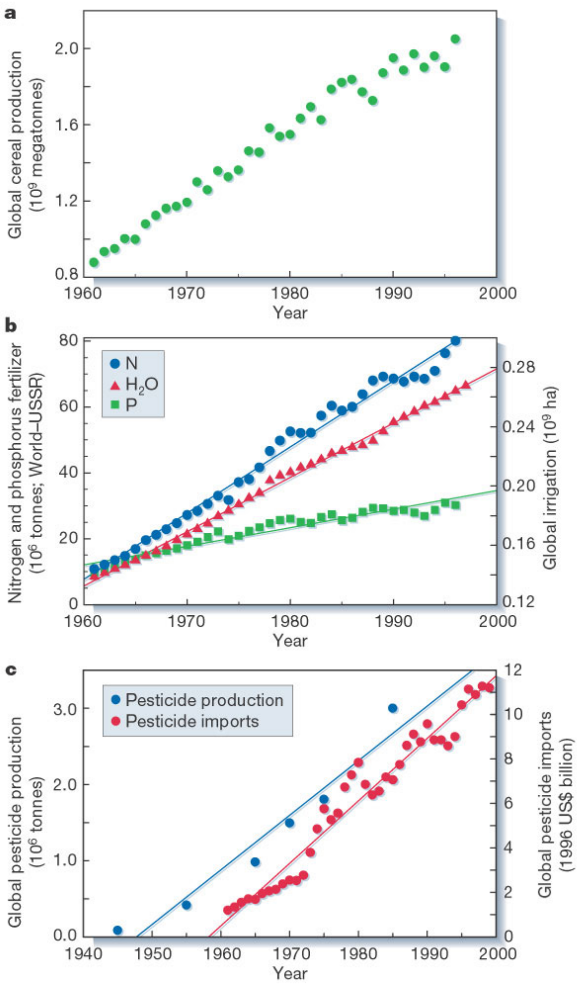


Figure 6: Agricultural trends over the past 40 years. a, Total global cereal production; b, total global use of nitrogen and phosphorus fertilizer (except former USSR not included) and area of global irrigated land; and c, total global pesticide production[3] and global pesticide imports (summed across all countries). Parts b and c modified from (Tilman et al., 2001)

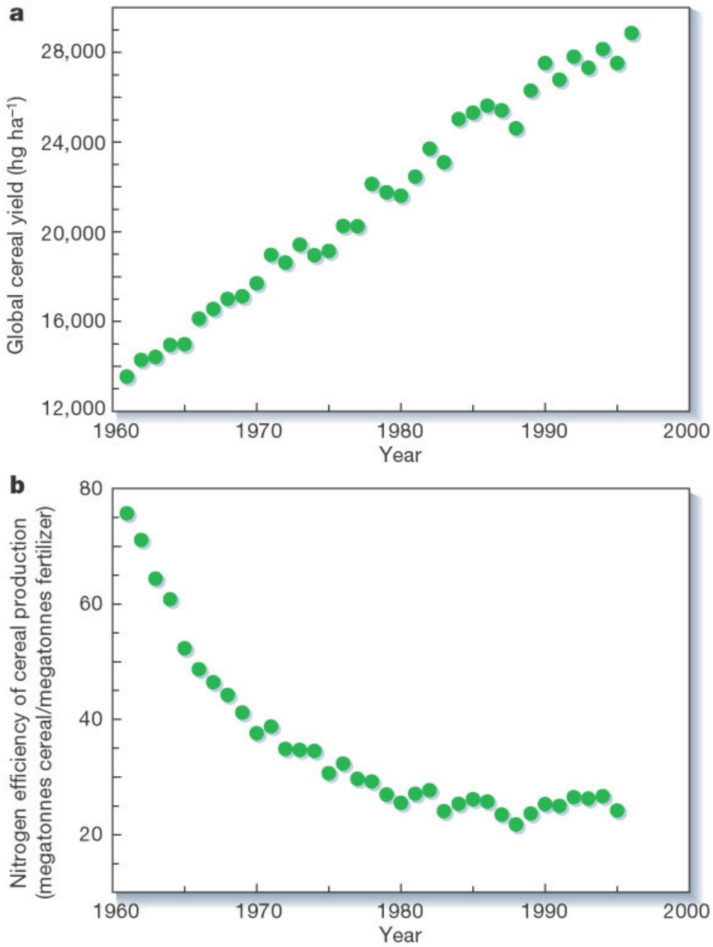


Figure 7: Diminishing returns of fertilizer application imply that further applications may not be as effective at increasing yields. a, Trends in average global cereal yields; b, trends in the nitrogen-fertilization efficiency of crop production (annual global cereal production divided by annual global application of nitrogen fertilizer) (FAOSTAT, 2003)

Biotic stresses include weeds, insects and plant pathogens such as fungi, viruses and bacteria. A number of pesticides are commonly used to control these pests. Nevertheless, between 35-42% of the world's food and fibre is lost by pests despite the use of 2.5 million metric tons of pesticides (Oerke, 1994; Oerke & Dehne, 1997; Pimentel, 2001);. Weeds cause 10-13% loss, insects 13-16% and pathogens 12-13%. Without pesticides or other pest control measures, it has been estimated that the losses would increase to 70% with an economic loss of $400 billion USD per year (Oerke & Dehne, 1997). Pest control measures are a positive economic investment for farmers yielding a return of $3-4 USD for each dollar invested (Pimentel & Lehman, 1993).

Weeds are a major problem in many crops so herbicides are an important tool in these crops. Over 90% of US soybean acres and 70% of Brazilian and Argentine soybean acres are treated with herbicides (Oerke & Dehne, 1997). For maize, over 95% of US acres are treated with herbicides (USDA-NASS, 2002). Herbicide tolerant crops can provide an opportunity to reduce herbicides in such systems. In the US, an average 10% reduction in herbicide usage was seen with herbicide tolerant soy from 1995-1998 (Hin et al., 2001). A more recent study found a reduction of 28.7 million pounds of active ingredient in herbicide tolerant soya in the US in 2001 (Carpenter, 2001).

In the EU, a standard maize herbicide program uses approximately 1740 g of active ingredient per hectare but this amount could be reduced by 30-60% if GM crop technology were adopted (Phipps & Park, 2002). Similar levels of herbicide reductions were projected for winter oil seed rape (for UK) and sugar beet (for Denmark) of GM crops with herbicide tolerance were adopted in these countries (Phipps & Park, 2002). Still, the most important contribution to a more sustainable practice is the shift from more toxic herbicides to glyphosate, (Carpenter et al., 2002)

Control of other pests is critical in a number of crops. High levels of insecticide are used to control ravaging insects in many of the world's cotton growing areas for example, reducing crop losses in some regions from 35 – 39% to 13% or less (Oerke, 2002) , (James, 2002). Adoption of insect protected cotton has impacted the level of insecticides used on this crop in many areas (James, 2002). In the US, the estimated savings in metric tons (MT) of active ingredient are 848 in 2001 (Gianessi et al., 2002), 1224 MT in 1999 and 907 MT in 1998 (Carpenter, 2001). In China, an 80% reduction in kg of formulated product used was seen due to the adoption on GM cotton (Huang et al., 2003). Introducing GM cotton in Spain would lead to a 60% reduction in volume of pesticide used and nearly a 40% reduction in active ingredient used (Phipps & Park, 2002).

Cultural Practices ↑

Crop rotation

Crop rotation is a very common practice as a means of controlling pests. Since some pest species rely on specific crops as hosts, then rotating to another crop can reduce populations of such pests. Crop rotation has been applied in virtually all agricultural strategies, from classic and historic agriculture such as the one still in place in certain actively protected localities in the Swiss Valais (Waldis, 1987) . The maize/soybean rotation in the United States as a means of controlling corn rootworm is one example of such a rotation designed to aid in pest control efforts. Another example is that of glyphosate-tolerant Roundup Ready ® soybeans which are often rotated with such crops as corn, winter wheat, spring cereals and dry beans (OECD, 2000). An interesting study from Canada shows enhancement of some agricultural parameters after 8 years in the second rotation cycle: Nitrate fertilizer requirement decreased, and wheat yield was 22% higher, under no tillage conditions as compared to conventional tillage. (Soon & Clayton, 2002). A comprehensive list of some 200 documents on crop rotation is given by (FAO Agriculture 21, 2003) after performing a search with 'crop rotation'.

Tillage

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; Trewawas, 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 gyphosate-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)

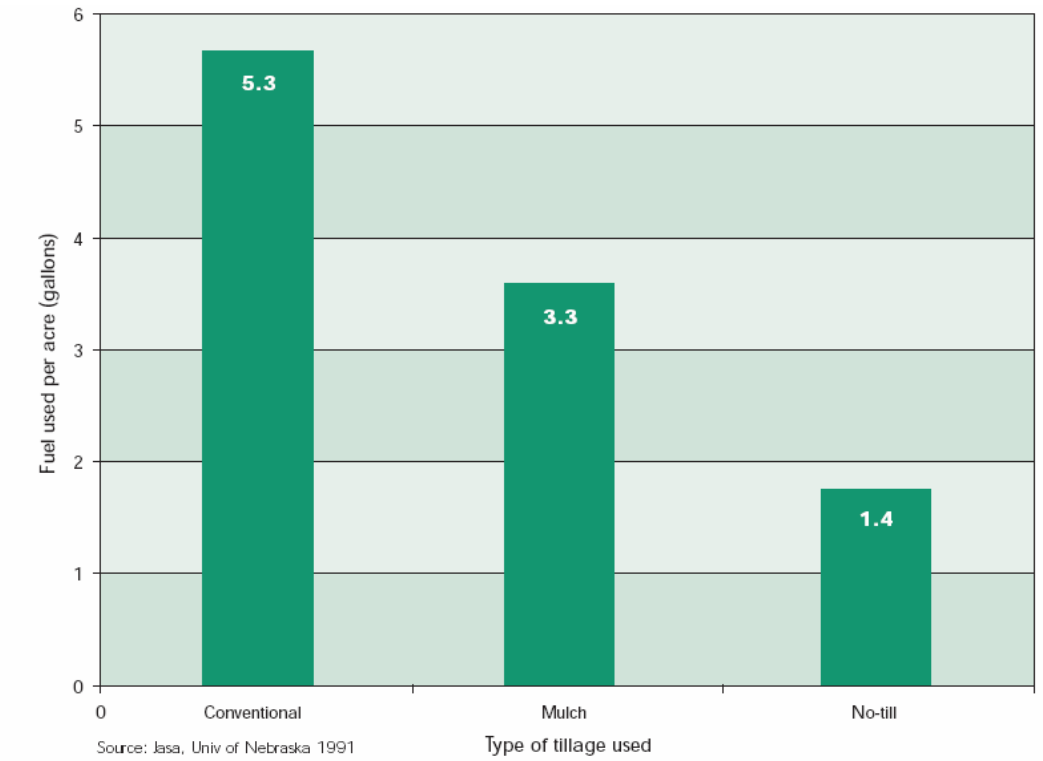


Figure 8: Tillage System versus Fuel Consumption per Acre (Fawcett & Towery, 2002) (Fig. 9-12)

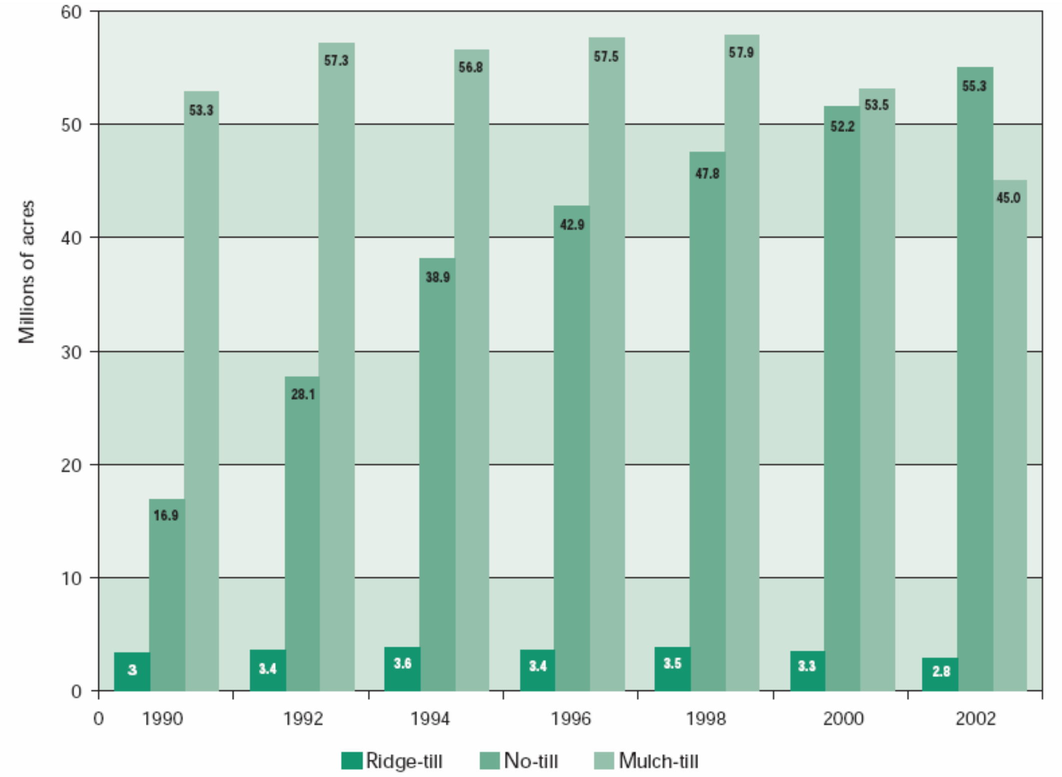


Figure 9: Conservation Tillage Adoption in the U.S. (1990 – 2002) (Fawcett & Towery, 2002)

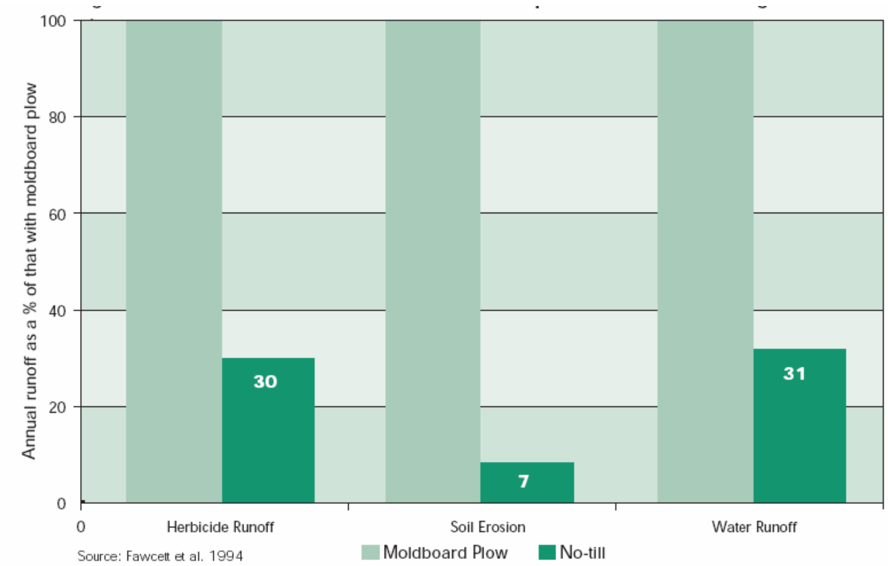


Figure 10: Runoff and Erosion in No-till Watersheds Compared to Conventional Tillage Watersheds (Fawcett & Towery, 2002)

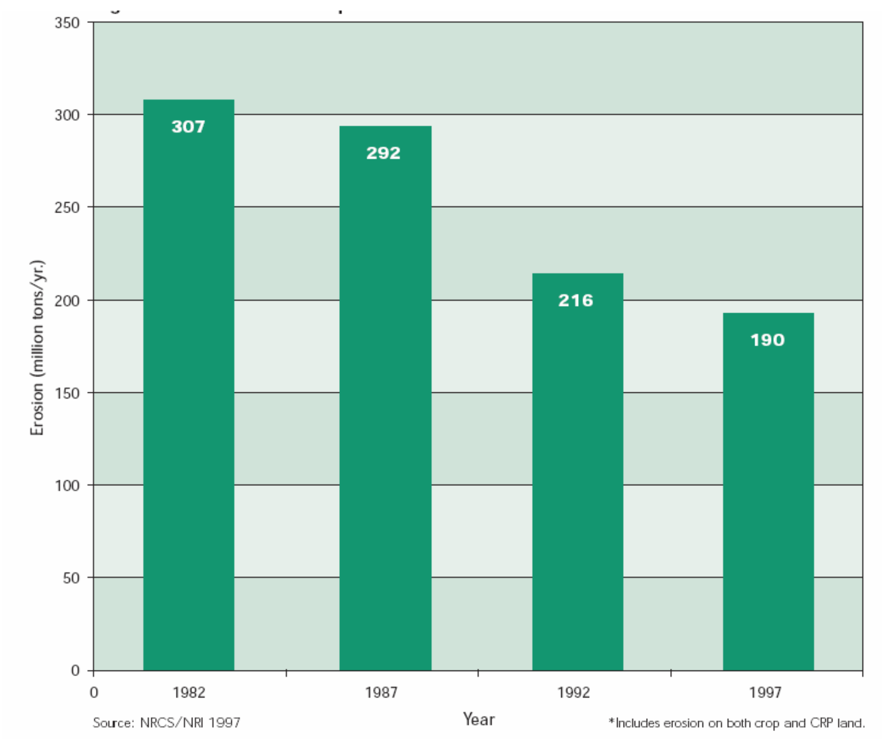


Figure 11: Soil Erosion from Cropland: incl. Conservation Reserve Prgramme land

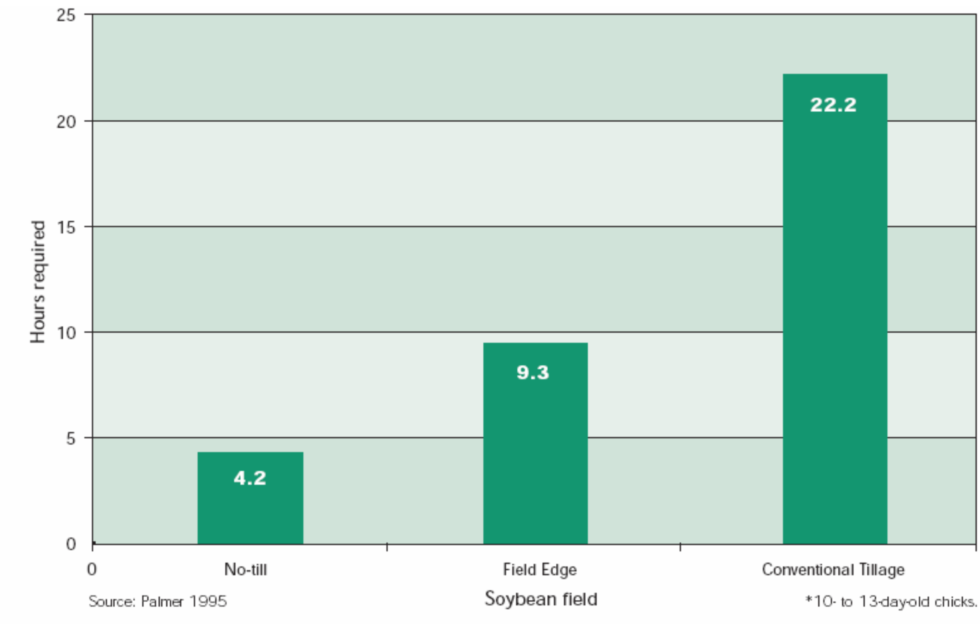


Figure 12: Time needed for Bobwhite Quail Chicks to Satisfy Daily Inect Requirements (Fawcett & Towery, 2002)

Under no-tillage crop production, the soil remains relatively undisturbed and plant litter decomposes at the soil surface, much like in natural soil ecosystems. Cultivation is known to reduce the number and diversity of microarthropod (Acarina and Collembola) populations from levels observed under natural forest or grassland vegetation. Long term experiments undertaken by (Winter et al., 1990) showed three treatments (Conventional Tillage CT, No Tillage NT and No Tillage covered with bromegrass) with different arthropode data ($P < 0.05$), with bromegrass, NT and CT soils containing respectively, 15.9, 12.4, and 5.8 microarthropods x 1000 m-2 of which 84, 69, and 70% were Acarina. Microarthropods and soil organic- C were more concentrated in the surface 5 cm of soil in NT than CT. However, the soil under bromegrass contained 1.3 times more microarthropods (99% were Acarina) than under continuous NT and CT corn. This again demonstrates the crucial importance of soil cover made possible with NT (in this experiment with bromegrass Bromus inermis). Thus, when examined to a depth of 15 cm, 19 years of NT corn did not increase the size of the microarthropod populations compared to CT, whereas production of bromegrass hay for 3-4 years following long-term continuous CT corn did increase microarthropod numbers.

Germplasm

Crop varieties ↺

In agriculture, 7'000 species of plants are used by farmers somewhere in the world, but only 30 species provide 90 percent of our calorific intake (Heywood, 2003). The top three crops are wheat, rice and maize (corn) occupying 230 million hectares, 151 million hectares and 140 million hectares, respectively, which is 35% of all global cropland. Each of the three major crops originated in different regions of the world. Wheat originated in the Near East, rice in both eastern Asia and western Africa and maize in the Americas. Within these dominant crop species, there are many hundreds of thousands of varieties (landraces, cultivars) adapted to local climates, farming practices, and cultural predilections like taste, colour, structure, ability to store the products etc. Much of this large crop diversity is important for providing the initial material for breeding. However, it must be recalled that the genetic diversity found in crops and farm animals is in most cases much less broad than the genetic diversity observed in plants or animals living in the wild, which points to the importance of wild species for agricultural breeding programs.

A major factor in the doubling of food production was the introduction of improved varieties, (Evenson & Gollin, 2003; Pfeiffer, 2003) for review of breeding improvements in the Green Revolution, a brief discussion of which follows).

For both rice and wheat, these repeated crossings led to varieties with four important characteristics: (1) higher yield; (2) fast maturation; (3) semi dwarf growth habitat and (4) resistance to disease. Once these characteristics were introduced, crossings to local varieties produced crops that are regionally adapted for optimized growth and consumer desires. The improved varieties were not just new seeds, but required the adoption of a suite of new agricultural tools. These tools included inputs such as fertilizers and pesticides, equipment for irrigation and tillage. The new technology package was important to optimize the output of the new varieties and thus realize the tremendous gains in productivity seen with the Green Revolution.

Evolution of plant breeding ↺

For most major crops, breeder's collections are sufficiently large to provide an adequate source of additional genetic material. Material from landraces and con-specific wild populations (primary gene pools) are also frequently called upon. The FAO has estimated that 30 – 40% of productivity gains overall have relied on genetic contributions from landraces (FAO, 2000) . The secondary gene pool, consisting of related species in the wild or in cultivation, has also provided important and economically valuable contributions to major crops. However, the difficulty of crossing different species using conventional methods has until now limited the use of this genetic resource. Gene transfer technology has the potential to avoid some of the difficulties limiting conventional techniques and brings the possibility of introducing into cultivars traits from an unlimited gene pool.

Such processes could perhaps provide new economic incentives to conserve agricultural biodiversity. However, novel genes have the potential to speed up the evolution of crops in a much more targeted way. Their potential to cause detrimental effects on environmental and food safety is considerable, if unwisely used and improperly tested. A careful comparison to so called ‘traditional’ breeding methods reveals a grey zone from methods used for centuries towards methods used in recent decades with a growing potential to breach the natural hybridization boundaries. Some of those more potent methods have been used widely for many decades and have never caused any harm to environmental and food safety.

Genetically modified (GM) crops are the latest development stage in a long row of breeding methods, and certainly the list will become longer in the years to come. Thirteen significant steps can be discerned in the developments of methods for plant breeding before reaching true transformation through genetic engineering, as described in the box below:

13 Steps in plant breeding from mass selection to genetic engineering, after (Karutz, 1999)

1. Selection of characteristic, homogenous varieties from traditional local or indigenous origin (e.g. land races) that generally exhibit more or less variable populations, by testing the offspring.

2. Crossing of homogenous varieties to create new variability followed by subsequent selection.

3. Intentional introduction by crossing in of desired traits, for instance resistances. (Even if ‘genes’ such as ‘mlo’ or ‘Lr 27’ (Singh et al., 2000) are in question the manipulations are carried out with pollen and ears of grain - not with DNA).

4. Artificial infection of plants in greenhouse or field by means of contact with neighbouring infected plants or a concentrated liquid spray of fungal spores. This is done to select for resistance. (On account of the high cost this is not widely practised).

5. Intentional use of the heterosis effect in hybrid breeding. (This often requires preparatory steps: some years of inbreeding if cross-pollinated species are involved, or in the case of self-pollinated species, the artificial production of male sterility – cytoplasmic, chemical or by genetic engineering.)

6. Crossing to introduce characters from more distantly related species. (This often necessitates the cultivation of the crossed embryos in a nutrient medium Embryos left in the seeds die because of incompatibility. This is called ‘embryo rescue’ (Becker, 1993).

7. Colchicinising (treating with the toxin of the autumn crocus, *Colchicum autumnale*), to double the number of chromosomes). In many vegetable and fodder crops this enables a stronger expression of certain traits it can affect a range of characters. It also facilitates the crossing of two different species or even families, because it can render fertile the sterile offspring of crosses. The most well known example in practice is Triticale, a new species of grain, resulting from crossing wheat (Triticum) and rye (Secale), two different families. (Bayerische Landesanstalt & für Landwirtschaft (LfL), 2003), (Schmid, 1985)

8. Inducing mutations with chemicals or ionising radiations and subsequent selection. This method enjoyed a certain boom 10 to 30 years ago but is not much used nowadays since the mutations are mostly disadvantageous and modern breeding methods have become more directed. There exist however, short-strawed strains of wheat that were obtained in this way (Fossati et al., 1986), and see also (FAO/IAEA Programme, 2003) where you will discover 548 seed propagated crops which have undergone gamma mutation programmes. Bread wheat has undergone gamma radiation breeding programmes extensively.

9. Anther culture. Self-fertile heterozygotes whose progeny in the next generation would normally diversify, to genetically fix the haploid chromosome set of the pollen . The pollen or the unfertilised ovule must be placed on a special sterile nutrient medium, fused by treating with colchicine and raised to become haploid plants, followed by subsequent colchicinising. Thus with one stroke one obtains a homogenous plant which would otherwise only be achieved by many generations of selection. Anther culture is established mostly in barley

and potatoes. With wheat and maize it is still at the experimental stage. (Bayerische Landesanstalt & für Landwirtschaft (LfL), 2003).

10. In-vitro-selection. If seedlings or tissue fragments can be selected in culture dishes for resistance against a fungal toxin, the cost of field trials is less because many plants will be discarded from the outset. For many traits, such methods are very successful and great efforts are being made to introduce them into routine breeding. Selection for traits: (Safarnejad et al., 1996), selection for proteins: (Hanes & Pluckthun, 1997) and a number of other, usually non-quantitative plant characters.

11. 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. (Koop et al., 1996).

12. Marker-assisted selection. For the purpose of diagnosis, DNA from all the plants from which selection is to be made, is isolated and, with the help of enzymes, broken up into smaller or larger pieces. Presently there are a number of modified methods, but the principle is the same. One looks out for bands that correlate statistically with the particular feature. Once such 'markers' have been found one has a simple criterion for selection. At the present time many breeders consider it to be *the* investment for the future that will bring about the greatest changes during the next decade. In the coming years it will be integrated into practically all the major breeding programmes. It will accelerate the process of breeding. Selection will be automated and take place in the laboratory. It will be possible to reduce field selection trials drastically. Also for complex traits inherited as polygenes the method would promise a speeding up of selection. This method certainly implies working with isolated DNA, but without invasion of the genome of the plant and is therefore not seriously disputed. Nevertheless, one must be aware that much genetic engineering with bacteria was and is necessary to establish marker-assisted selection. (Stein et al., 2001)

13. Gene transfer. With gene transfer there are also many degrees of departure from the 'natural' according to the origin of the genes and the technology employed in the transfer. (de la Riva et al., 1998), (Potrykus, 1990)

Genetically Modified (GM) Crops ↺

Early history

Since all genes consist of DNA, and the information in this DNA molecule is read in the same way in all organisms in order to make proteins, it is in principle possible to take any (single) gene from any organism and transfer it into any other organism so that the recipient produces a protein normally only made in the donor. The resulting organism is called a Genetically Modified Organism (GMO). From the time this simple strategy was devised (Cohen et al., 1973) and (Morrow et al., 1974), it took molecular biologists about a decade until the first GM crop plants were made in 1985. Ten years later, the first GM crop appeared in supermarkets in the USA, the "FlavrSavr" tomato with a delayed ripening process. The FDA's review of the Flavr Savr was requested by the tomato's developer, Calgene Inc. of Davis, California, in August, 1991. The company later submitted a food additive petition on the use of the kan-r gene in the development of new varieties of tomato, cotton, and rapeseed. In 1990-92, the U.S. Department of Agriculture granted Calgene permission to begin large-scale production of the new tomato (FDA, 1990), with final approval by fax (!) May 1994. (Maryanski, 1999). Agronomic traits followed in 1996 with the introduction of herbicide tolerant soybean and insect-resistant cotton.

Biotechnology and plant breeding ↺

Biotechnology is a valuable tool in plant breeding from 2 different aspects: as a tool to transfer new genes into crop varieties and introduce desired characteristics (as discussed previously), or as a tool for acquiring knowledge.

Molecular taxonomy, the foundation of plant breeding

Today, biological research can hardly be conducted without using biotechnology in one way or another. Taxonomy and conservation use molecular markers to identify species, much in the same way as in forensic medicine to identify criminals. This is useful for *ex situ and in situ* conservation of plants. In seed banks and conservation projects, genetic fingerprints are used to establish the origin of a seed or the relatedness of one plant variety to another. There are many texts on the use of molecular biology methods in conservation, (Jacobsen & Dohmen, 1990), (Fay, 1992), (Drilling & Ostazeski, 2003), (Students, 1999), (Frankham, 2003), (Lledó et al., 1996).

Biotechnology also is used for important phylogenetical studies in plant systematics; the application of various methods has led to breakthroughs in systematic botany: Results of the application of modern biological and statistical methods can be seen in (Stevens, 2003), a website on phylogenetic trees of the flowering plants, and a textbook: (Hollingsworth et al., 1999). It is even possible to use the invaluable collections of herbarium plants in pressed and dried condition as a good source for DNA studies (Missouri, 2003). Molecular data, in this case DNA sequences, provide a new dimension to the understanding of relationships and classification. These are of particular importance when interpretations of data from sources such as morphology, anatomy and palynology (the study of pollen) conflict. DNA data help to resolve such conflict, and lead to a clearer definition of relationships among flowering plants. This, in turn, provides a better understanding of the evolution of plant structures and breeding systems, since molecular data surprisingly well match the non-molecular ones, as has been shown by a thorough analysis (Bremer et al., 1998) (Nandi et al., 1998). A striking example of how molecular data can help find the correct place in the vascular plant system for the completely isolated genus Medusagyne, a monotypic endemic tree from the Seychelles, has been given by (Fay et al., 1997): The data revealed indeed that Medusagyne and some African genera of Ochnaceae showed the same shape of medusagyne-like styli, which would not have been discovered without the molecular lead.

Biotechnology provides more precision and speed to plant breeding ↺

Biotechnology has proven useful for following genetic markers in plant breeding. For instance plant varieties can be crossed by conventional means, and, by analysing a few cells of the newly sprouted plant, one can predict some of the expected properties of the progeny, by looking at the presence or absence of certain genes. This enables one to predict a phenotypic property, which will only show up later in life, for instance the crop's expected resistance to an infectious plant disease.

Molecular knowledge can significantly reduce the time to select useful varieties, i.e. one does not need to wait until flowering or maturation with high-throughput screening, it adds to the selection process with the application of marker genes and certainly provides much more advantages than can be described in this study, (Messmer et al., 2000). For more information visit the website of the Max Planck Institute in Koeln: (Max Planck, 2003)

The availability of genome sequences is a boost to research. The first two complete plant genome sequences determined were those of *Arabidopsis* and rice. The 120 million base pairs (MBP) of the small Brassicaceae *Arabidopsis* were sequenced by an international academic consortium and the data made public. The 430 MBP sequence of rice was completed only a few weeks later by an industrial group lead by Syngenta, and will be available by contract to other researchers. Syngenta intends to make the data available free of charge for research directly benefiting subsistence farmers. The public sector sequencing of rice through an international consortium is expected to be completed in 2004. It will hopefully become common practice for companies to make their basic discoveries publicly available, to everyone's benefit. The Monsanto company has also opened up some of its rice sequencing data. An easy way to follow up the progress is to check the Genomics Gateway of (Nature, 2003 ff). The efforts in the public sector have crystallized in the initiative on intellectual property rights by the major agricultural universities in the United States and other public-sector institutions to establish a new paradigm in the management of IP to facilitate commercial development of such crops. (Atkinson, 2003)

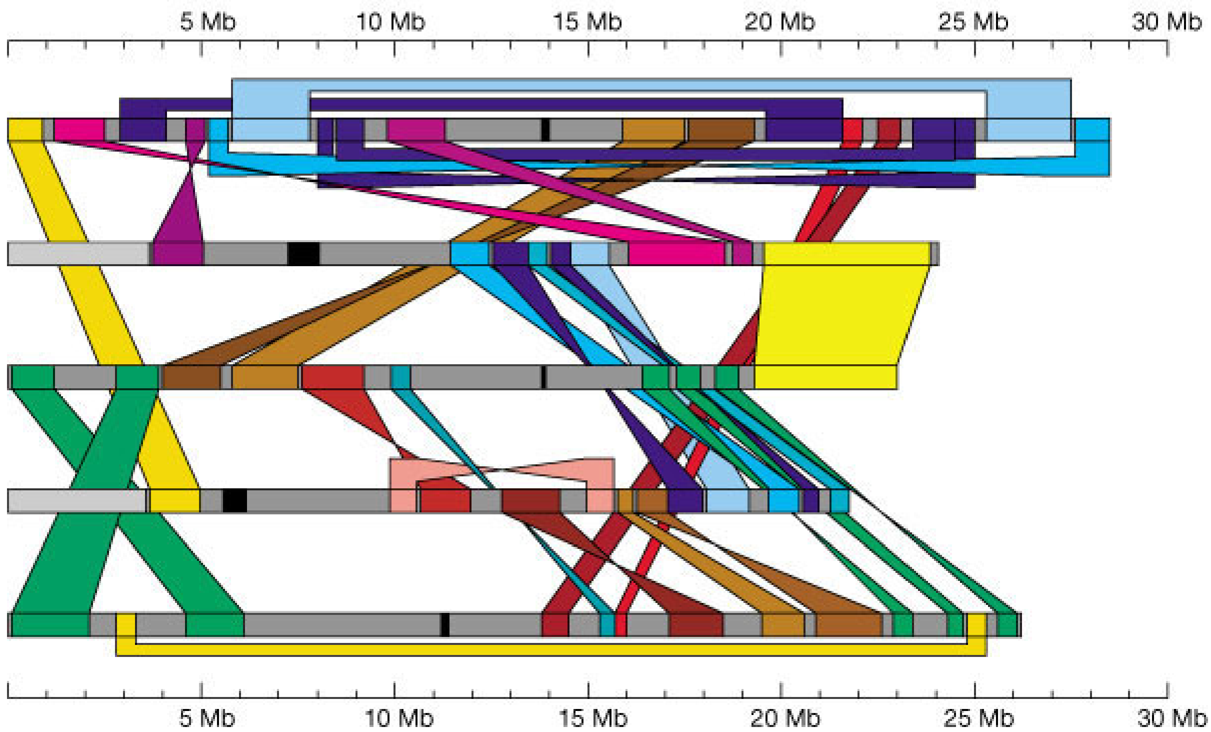


Figure 13: Segmentally duplicated regions in the *Arabidopsis* genome. Individual chromosomes are depicted as horizontal grey bars (with chromosome 1 at the top), centromeres are marked black. Coloured bands connect corresponding duplicated segments. Similarity between the rDNA repeats are excluded. Duplicated segments in reversed orientation are connected with twisted coloured bands. The scale is in megabases.

(The Arabidopsis Initiative, 2000)

Global adoption ↺

The adoption of GM crops is, in a worldwide view, a story without precedent in speed and distribution compared to the adoption of any traditional breed. (James, 2002) compiled information on adoption rates globally. In 2002, four countries grew 99% of the global transgenic crop area.

The USA led the world with 39.0 million hectares (66% of global total) Argentina followed with 13.5 million hectares (23%), Canada 3.5 million hectares (6%) and China 2.1 million hectares (4%). China showed the greatest growth with a 40% increase in its insect resistant cotton area from 1.5 million hectares in 2001 to 2.1 million hectares in 2002. This represents 51% of the total cotton area of 4.1 million hectares in China. Argentina increased its GM crop area by 14% from 11.8 million hectares in 2001 to 13.5 million hectares in 2002. South Africa increased its growing by 20% to 0.3 million hectares in 2002. The US and Canada both showed a growth rate of 9%. GM cotton area in Australia decreased by half in 2002, due to the very severe drought conditions. India, Colombia and Honduras grew transgenic crops for the first time in 2002. Overall, The number of countries that grew GM crops increased from 13 to 16 in 2002 – 9 developing countries, 5 industrial and 2 Eastern Europe countries (James, 2002).

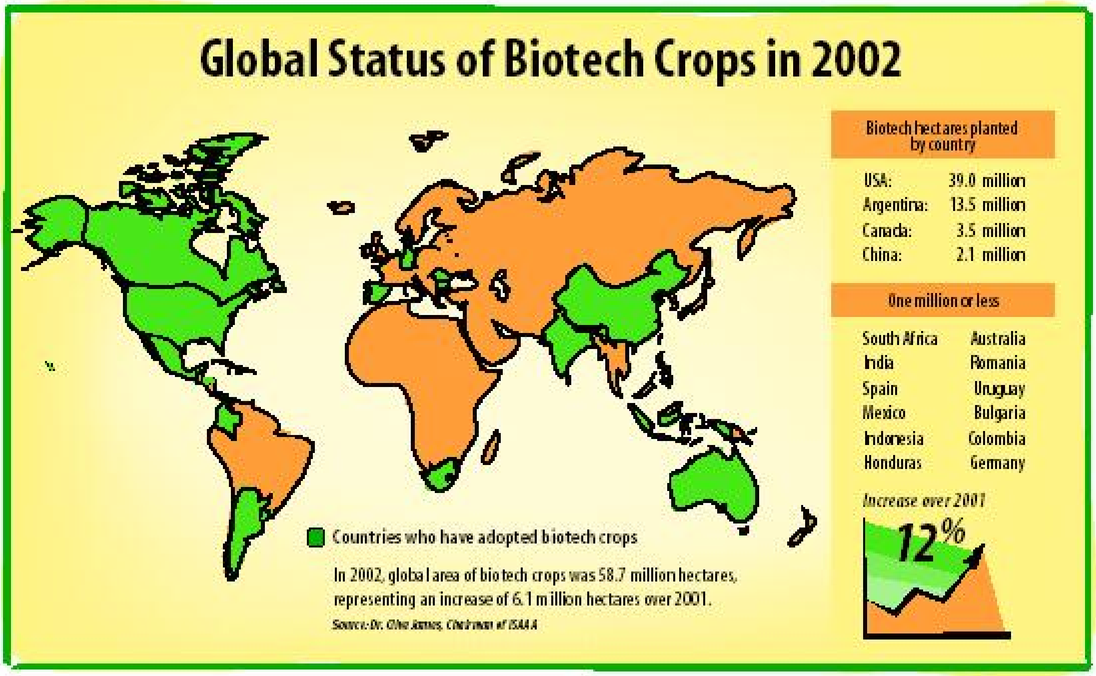


Figure 14: Global Status of Biotech Crops in 2002 (James, 2003)

Current GM crop products ↺

Clive James from the IAAS also tracked the type of crops being grown globally (James, 2002). In 2002, the principal GM crops were: soybean occupying 36.5 million hectares (with 51% of all soybean transgenic), cotton at 6.8 million hectares (12% of all cotton was GM); canola at 3.0 million hectares (12% of canola now GM) and maize at 12.4 million hectares (9% of maize now GM). Herbicide tolerance has consistently been the dominant trait followed by insect resistance. In 2002, herbicide tolerance was deployed in soybean, corn, cotton and canola and occupied 75% or 44.2 million hectares of the global 58.7 million hectares. Herbicide tolerant soybean was the single biggest trait/crop with 36.5 million hectares. Insect protected crops were offered in maize and cotton and covered 10.1 million hectares of the global transgenic area in 2002. Bt maize covered 7.7 million of those hectares. Stacked gene combinations with both herbicide tolerance and insect protected traits in the same product were offered in both cotton and maize and occupied 4.4 million hectares in 2002. A small amount of GM crops – squash and papaya - with virus resistance was also grown in 2002. The present day situation is characterized further by two facts: 99% of the acreage is in the four major crops (maize, soybeans, canola and cotton with one or both of the two major traits (Bt and Herbicide tolerance). On the other hand, there are hundreds of crops and traits tested in laboratory and field experiments. (Agbios Database, 2003).

Future GM crop products ↺

In the future, it is expected that there will be many more categories than just crops with herbicide and pest-tolerance, and viral resistance. Future crops will offer additional benefits, for example improved nutrition and quality traits, drought tolerance, or improved food production efficiency. Crops will be designed to produce valuable pharmaceutical ingredients and will be optimized for renewable energy. It is not easy to predict trends, but through the study of ongoing projects some research tendencies can be understood. A large number of GM crops with enhanced nutritional values are in the development stage and will only come to the market in a few years from now (Bouis, 1996; Vonbraun et al., 1990). They are likely to show benefits for the consumers and some may be of particular interest to farmers in tropical countries. Development will show in the next years whether the widespread events like Bt and Roundup Ready ® herbicide tolerance can be deregulated under certain conditions. It will also be necessary to give thought to a shift in regulatory strategies: It might be justified in the years to come to give more emphasis to trait oriented views instead of sticking uniquely to process oriented legislation (Miller, 2002).

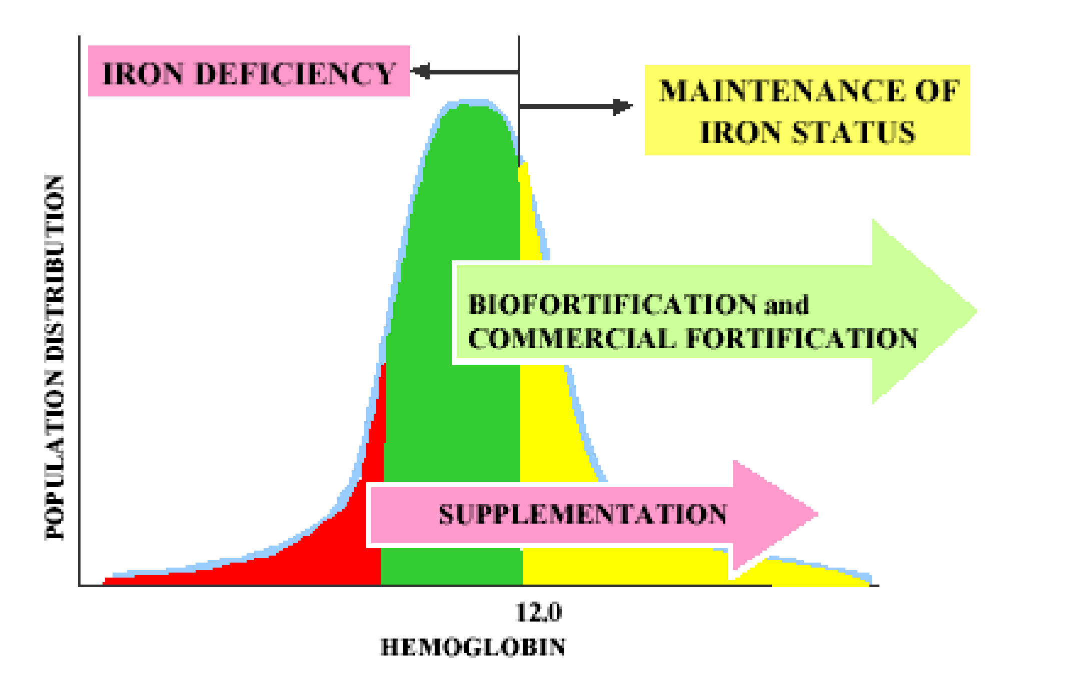


Figure 15: Biofortification improves status for those less deficient and maintains status for all at low cost.

(IFPRI - CIAT, 2002)

One of the best-known traits is fortified rice known as the Golden Rice (Potrykus, 2001). Two rice varieties, with anticipated consumer benefits are those containing Pro-Vitamin A and/or an increased level of iron in the product, which were developed by Potrykus and Beyer (Beyer et al., 2002), a development beginning in the early nineties (Peterhans, 1990). Despite traditional preventive measures (distribution of free vitamin A, encouragement to eat more fruit and vegetables), worldwide there are 130 million young people who are vitamin A-deficient. An estimated 250’000 to 500’000 vitamin A-deficient children become blind every year, half of them dying within 12 months of losing their sight. (WHO, 2002). A bowl of 200-300 g of this cooked rice is, according to latest data, enough to overcome the vitamin A-deficiency to a significant degree (Beyer et al., 2002). Similarly, iron-deficiency, particularly prevalent in pregnant women, can potentially be alleviated by rice containing an increased amount of iron in its endosperm. Such rice varieties have been successfully developed in the laboratory. In the last two years the lab plants have been completely redesigned for field use. First field trials are under way, but the project is still a few years from commercialization, for both scientific and political reasons. (King, 2002a). It is anyway economically highly beneficial to develop fortified crop varieties: high priority has to be assigned to research in modern plant breeding, in good coordination with many other strategies to fight malnutrition (Pinstrup-Andersen, 2002; Pinstrup-Andersen & Cohen, 2003).

There are many other research projects on breeding crops for nutritional fortification, e.g.: Cassava, potato, maize, beans etc. (Welch, 2002), (King, 2002a; King, 2002b). It emerges now clearly with the most recent breeding technologies at hand, that bio-fortification will change the scene also in the developing world. It is time to forget about the bifurcation between genetically engineered and non-engineered crops, what is needed are programmes focussed on the breeding success, not on the technology. As long as some of the major biofortified crops can go free of licensing fees into agricultural production of the developing world, there will be huge benefits documented in the future. (IFPRI - CIAT, 2002)

Section 3

The Impacts of Agricultural Practices on Biodiversity

↺

The following section discusses the impacts of common agricultural practices on biodiversity, and ways in which some of these impacts can be mitigated. As presented in Section 1, biodiversity can be quantified in several different, equally important ways, thus agricultural impacts on biodiversity are considered both in terms of species and genetic diversity. Within each of these categories, the impacts on agricultural biodiversity and natural biodiversity are addressed separately because the impacts of agriculture are different on these two types of habitat. This distinction could can be thought of as on-site and off-site impacts of agricultural practices.

Impacts on Species Biodiversity

Agricultural biodiversity ↺

General impacts of modern intensive agriculture

Modern agricultural practices have been broadly linked to declines in biodiversity in agro-ecosystems. This has been found to be true for a wide variety of taxonomic groups, geographic regions and spatial scales. More specifically, various researchers have found significant correlations between reductions in biodiversity at various taxonomic levels and agricultural intensification. For example, a review of published studies on arthropod diversity in agricultural landscapes found species biodiversity to be higher in less intensely cultivated habitats (Duelli et al., 1999). Similarly, analysis of 30 years of monitoring records demonstrated that the abundance of aerial invertebrates at a location in rural Scotland was negatively correlated with a suite of agricultural variables that represent more intensive agriculture; that is, arthropod populations are lowest where agriculture is the most intensive (Benton et al., 2002). In this same study, the abundance of various farmland bird species was, in turn, positively correlated with arthropod abundance in the same year and the previous year. Comparable studies have found similar impacts on bird species throughout the United Kingdom and European Union (EU). Across Europe, declines in farmland bird diversity are correlated with agricultural intensity and declines in the European Union have been greater than in non-Member States (for example, see (Donald et al., 2002a; Donald et al., 2002b).

These effects of agricultural intensification undoubtedly reflect a large number of factors which are addressed individually in the following sections, including the cropping pattern, the frequency of tillage, the amount and nature of fertilizers used, and the amount and nature of pesticides applied (particularly insecticides and herbicides). However, it should be kept in mind that all of these factors are interrelated to a greater or lesser degree, often causing negative synergies (Chapin et al., 2000) There is no doubt that many human, social and cultural factors have to be taken into account, but nevertheless, in all cultures the practice is uncontested that habitat conversion is acceptable to provide for our own needs more food and settlement. (Dale, 2002) emphasize in a review, “that the kinds of potential impacts of GM crops fall into the classes familiar from the cultivation of non-GM crops (invasiveness, weediness, toxicity or biodiversity. It is likely, however, that the novelty of some of the products of GM crop improvement will present new challenges and perhaps opportunities to manage particular crops in creative ways.”

Crop diversity ↺

Intensive agricultural systems typically and also logically have limited crop diversity. Many such systems are monocultures at least at the level of individual fields, and are relatively homogenous even at the regional level. Low crop diversity generally will mean both limited botanical diversity and limited structural diversity. (Robinson & Sutherland, 2002) analyzed changes in agriculture and biodiversity in Britain since the 1940s. They found a consistent reduction in landscape diversity, as reflected in a 65% decline in the number of farms. Farms had become more specialized and efficient. This also was associated with the removal of 50% of hedgerows and a reduction in winter stubbles. (Kläge, 1999) demonstrates in a detailed study on the vegetation of winter stubbles how rare and threatened some of those plants are: Members of a vanishing community of ‘weeds’. Hedgerows and similar non-cropped habitat are important sources of food and shelter for a variety of birds and invertebrates.

Reductions in landscape diversity lead to lower faunal diversity in intensively managed agro-ecosystems than in more diverse agricultural systems or in natural habitats. For example, (Robinson & Sutherland, 2002) found major declines in organisms associated with farmland in Britain and northwest Europe, particularly in habitat specialists. As an illustration, biodiversity declines in bird species were related to reduced food availability in the non-breeding season. They concluded that reduced habitat diversity was of particular important in the 1950s and 1960s, while reduction in habitat quality may be more important now. Similarly, a review of the available literature on arthropod diversity found that structural biodiversity in agricultural areas is correlated with functional and species biodiversity of the above-ground insect fauna (Duelli et al., 1999)

Tillage ↺

more about Tillage: ↶

Intensive tillage leads to frequent disturbances of the agricultural landscape, increases energy loss from agricultural fields, and increases problems of soil erosion and run-off from agricultural fields. All of these factors adversely affect the quality of agricultural habitats, with significant consequences for agricultural biodiversity. When (Witmer et al., 2003) studied corn, soybean and wheat cropping systems in the Mid- Atlantic region of the United States, they found that ground-dwelling and foliage-dwelling beneficial arthropods were least abundant, and pests were most abundant, in the simplest, most intensively managed continuous corn system. In general, ground-dwelling species were more abundant in no-till than in deep-tilled crops. This suggests that shifts toward conservation tillage and no-till will benefit agricultural biodiversity. As discussed in Section 2, such shifts have been occurring recently in many cropping systems as farmers recognize the environmental and economic benefits of conservation tillage practices.

The community structure of Arbuscular Mycorrhizal Fungi (AMF) in the field soil was significantly affected by tillage treatment. However, no significant differences in AMF diversity were detected among different soil tillage treatments. AMF community composition in trap cultures was affected much (Jansa et al., 2002; Jansa et al., 2003). Trends in AMF results show clearly an advantage for the no-till strategy: Fig. 11, benefits for biodiversity.

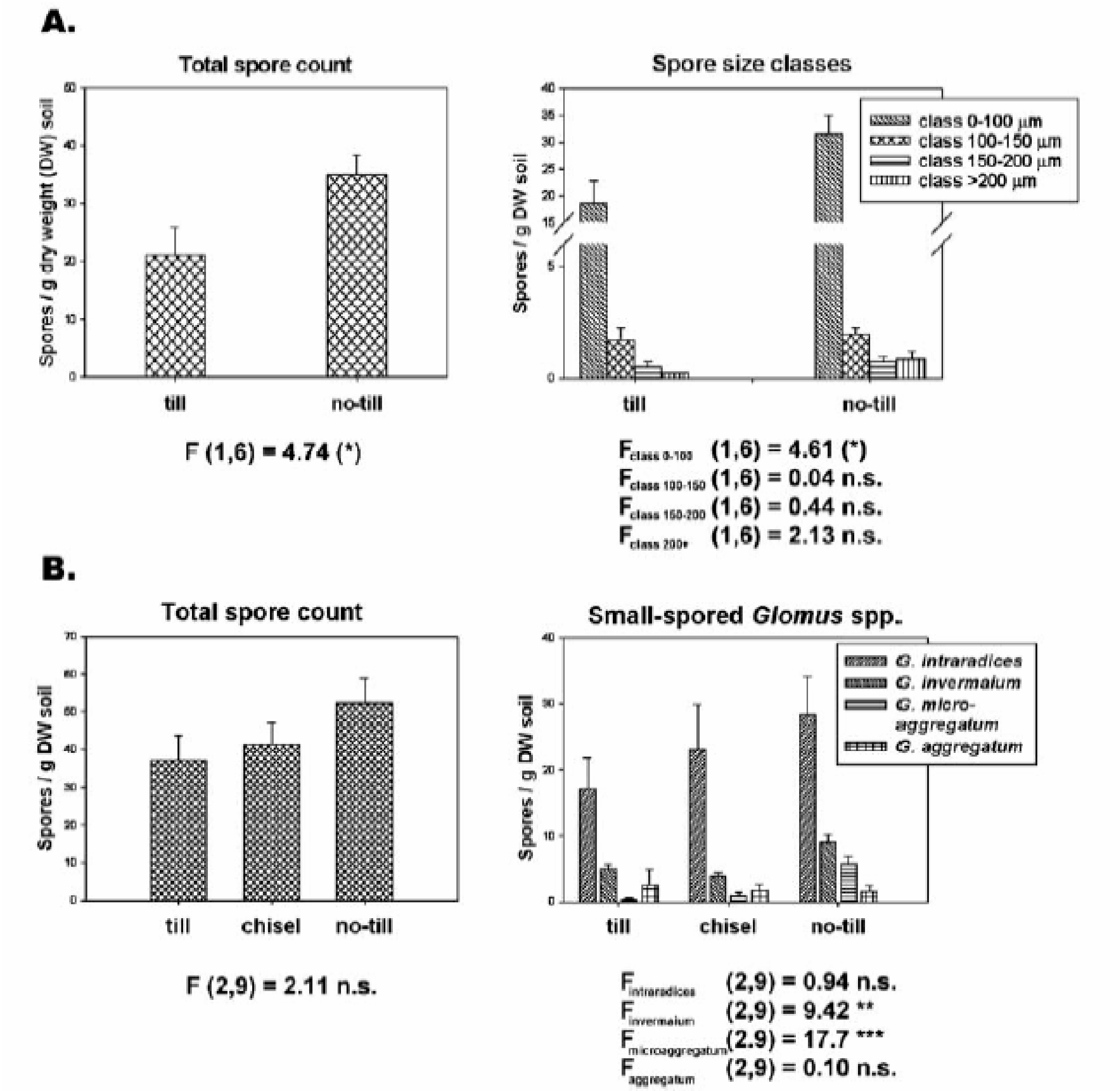


Figure 16: from (Jansa et al., 2002): Spore counts in field soils after a rapeseed season (1999), when only two tillage treatments were compared (A), and spore counts in soils following maize season (2001), where three tillage treatments were compared (B). *F*-values following ANOVAs are given. Statistical significance of results is shown (*n.s.* not significant (*P*=0.1); (*) *P*<0.1; * *P*<0.05; ** *P*<0.01)

Pesticide use ↺

Adverse effects of pesticide use in agriculture are well-documented (Pimentel & Lehman, 1993). Conventional insecticides generally reduce diversity through direct toxic effects. Many of the widely used classes of conventional insecticides, including organophosphates and pyrethroids, have been shown to adversely affect a broad range of non-target species, including species of economic importance. Local extinctions are common where these insecticides are frequently used. Such insecticides have been shown to eliminate important predator and parasitoid species from agricultural systems. (Pimentel et al., 1993) These impacts on natural enemies have been shown to lead to flare-ups in secondary pest species, some of which were not previously economically important. In a few cases, insecticides directly stimulate the population growth of non-target pest species, e.g. pyrethroids have such an effect on some mite and aphid species. In addition, the toxic effects of insecticides can lead to food chains effects because of decreased food availability for higher trophic levels and bioaccumulation of the insecticides. For example, organ chlorine use and ingestion by earthworms has led to die-offs of birds feeding on these species. Replacing broad-spectrum insecticides with more specific, softer alternatives is necessary to avoid these impacts.

Some herbicides also can be toxic to invertebrates. However, the more important effects of herbicide use with respect to biodiversity are to reduce non-crop plant (weed) populations and weed seed production in agricultural fields. Where herbicide use is intensive, adverse impacts may be seen on various vertebrate and invertebrate species that depend upon these plant (weed) species for food or shelter. Where invertebrate populations are strongly affected, consequences for higher trophic levels also may occur.

Benbrooks recent claim of increased pesticide (Benbrook, 2003) use due to the advent of genetically engineered crops does not hold up to close scrutiny. According to Wayne Parrott Benbrook doesn't always provide all the pertinent details, nor are all his assumptions necessarily valid. He consistently ignores the fact that amount of active ingredient and environmental impact are not the same thing. (Parrott, 2004). While there are definitely cases where the amount of active ingredient use has increased, overall environmental impact has decreased, compare the USDA-ERSs study (Fernandez-Cornejo & McBride, 2002) (The section on Adoption and Pesticide Use is the most relevant to the topic).

Impacts of genetically modified (GM) crops on biodiversity ↺

The use of GM crops can positively impact agricultural species biodiversity if those GM crops allow the management of weeds and insect pests in a more specific way than chemical herbicides and pesticides. In particular, the adoption of insect resistant Bt crops, expressing highly specific Bt proteins, represents an opportunity to replace broad-spectrum insecticide use. The insecticidal proteins expressed in Bt crops such as Bt maize and Bt cotton are so narrow in their activity that they have little or no activity against non-target organisms. Furthermore, the toxins are expressed within the plant tissues, minimizing the exposure of animals that do not feed on the crop plants. As a consequence, considering the large number of field studies that have been conducted, few or no differences have been seen with respect to community structure or individual species abundances where fields of Bt crops have been compared to conventional crops that have not been treated with insecticides. Where they have been calculated, indices of species diversity and community structure have not differed significantly for Bt corn fields compared to untreated conventional corn fields (e.g., (Lozzia et al., 1999; Lozzia, 1999) (Dively & Rose, 2002) or for Bt cotton fields compared to conventional cotton fields (Fitt & Wilson, 2003; Naranjo & Ellsworth, 2002; Naranjo et al., 2002; Xia et al., 1999). The only species that have been observed to be significantly and consistently less abundant in fields of Bt crops relative to fields of conventional crops are the target pests and their specific parasites. In studies where the conventional crop fields have been sprayed for the target pest species of the Bt crop (as it routinely occurs in most crop systems), many non-target species have been observed to be adversely impacted, leading to significantly lower non-target populations in sprayed conventional fields as compared to Bt crop fields. With corn fields, this is particularly obvious for foliage-dwelling species because of the method of application of these insecticides, but ground-dwelling species like carabids and cursorial spiders are also often affected, directly or indirectly, by the insecticidal sprays and are apparently not affected by Bt corn (Candolfi et al., 2003; Candolfi et al., 2004); (Dively & Rose, 2002). The team study of Candolfi was particularly impressing (summary and Fig. 17 – 19).

„A faunistic study investigating the potential side-effects of corn (Zea mays) genetically modified to express a truncated Cry1Ab protein derived from Bacillus thuringiensis subsp. kurstaki, on non-target arthropods was carried out under field conditions. The communities of non-target arthropods in the soil, on the leaves and flying in the crop area were monitored throughout the growing season. Water-treated, untransformed corn served as a control, and a spray application of a bacterial Bt insecticide (Delfin WG) and a synthetic insecticide (Karate Xpress) used to control the European corn borer (Ostrinia nubilalis; Lepidoptera: Pyralidae) acted as positive reference treatments. Results were analyzed using a principal response curve. Significantly lower infestations by the lepidopteran target species O. nubilalis were observed in the Bt-corn plots compared to the control. No effects of Bt-corn on the communities of soil dwelling and non-target plant dwelling arthropods were observed. A trend towards a community effect on flying arthropods was observed with lower abundance of adult Lepidoptera, flies in the families Lonchopteridae, Mycetophilidae and Syrphidae, and the hymenopteran parasitoids Ceraphronidae. Effects were weak and restricted to two sampling dates corresponding to anthesis. A short but statistically significant effect of Karate Xpress and Delfin was observed on the community of plant dwellers and a prolonged effect of Karate Xpress on the soil dwellers."

Some typical figures from this experiment:

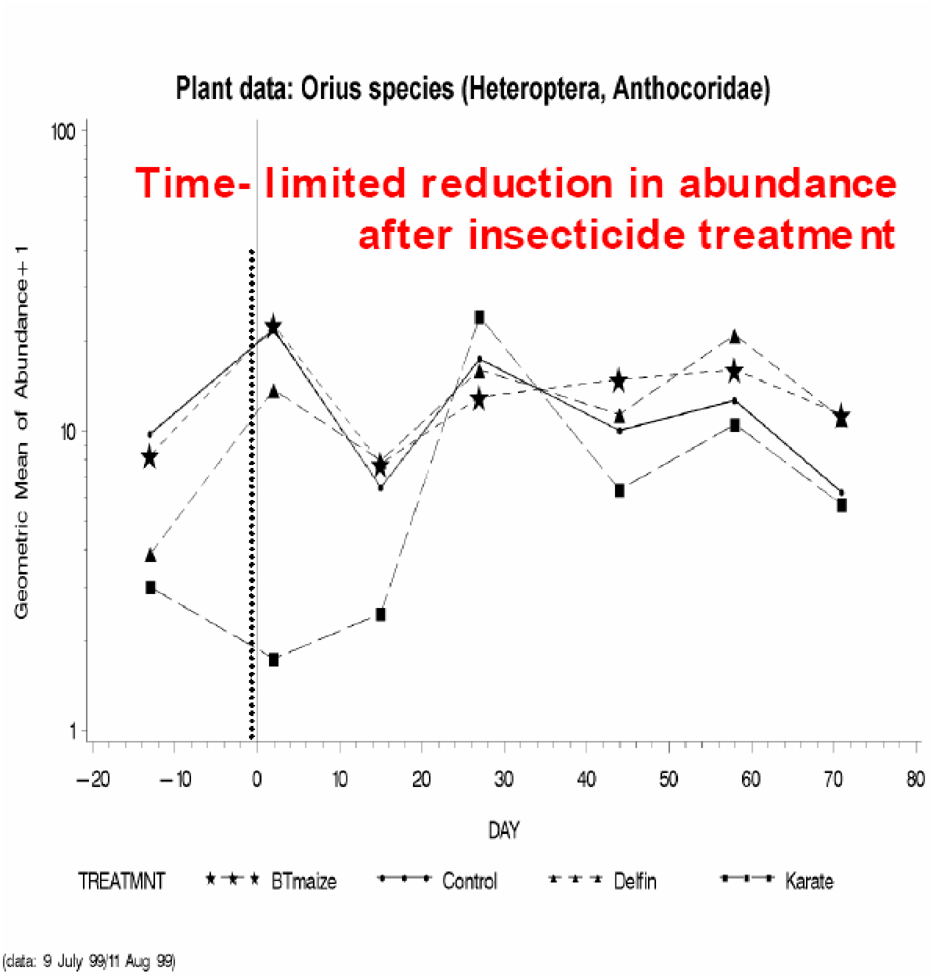


Figure 17: Plant data on non-target insects after Bt-, water- and insecticide treatment: Orius spec. (Heteroptera, Anthocoridae), data from (Candolfi et al., 2004)

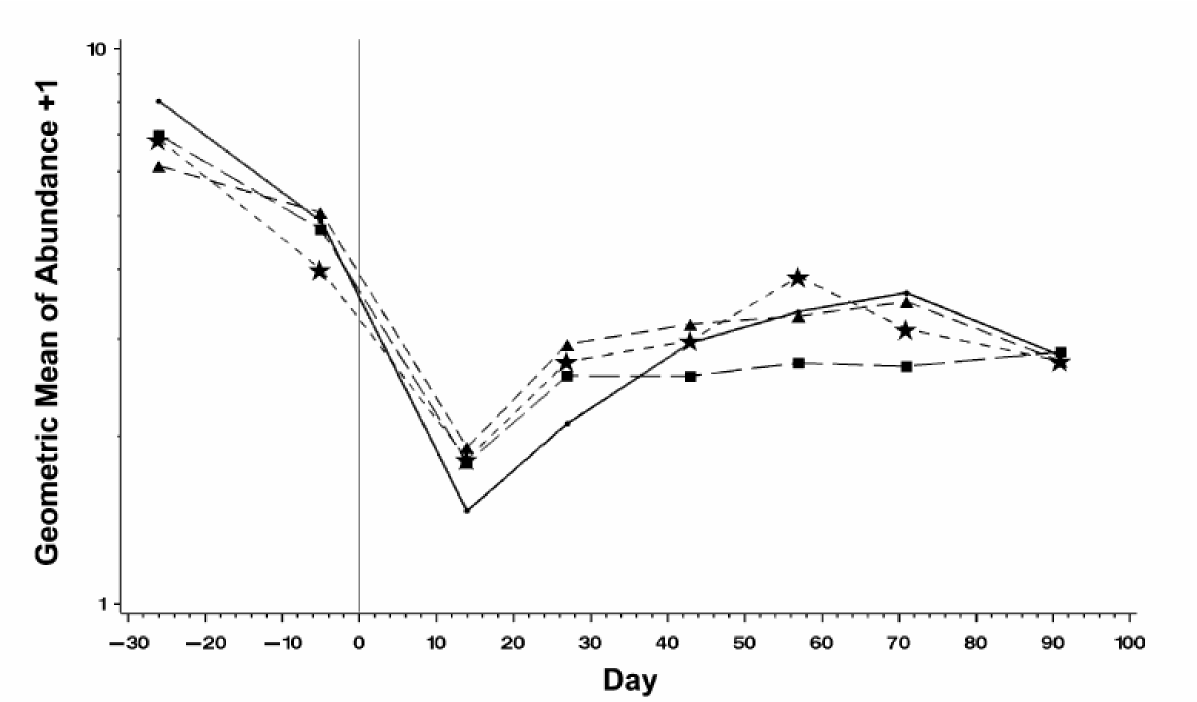


Figure 18: Population density of Alopecosa sp. (Araneae: Lycosidae). Plotted are the geometric means of abundance _/1 per trap against time: (●) untransformed corn (control); (✱) Bt-corn; (▲) untransformed corn treated with Delfin; (■) untransformed corn treated with Karate Xpress; Day 0, spray day. No statistically significant differences between treatments and the control were observed (Tukey test, P_/0.05). (Candolfi et al., 2004)

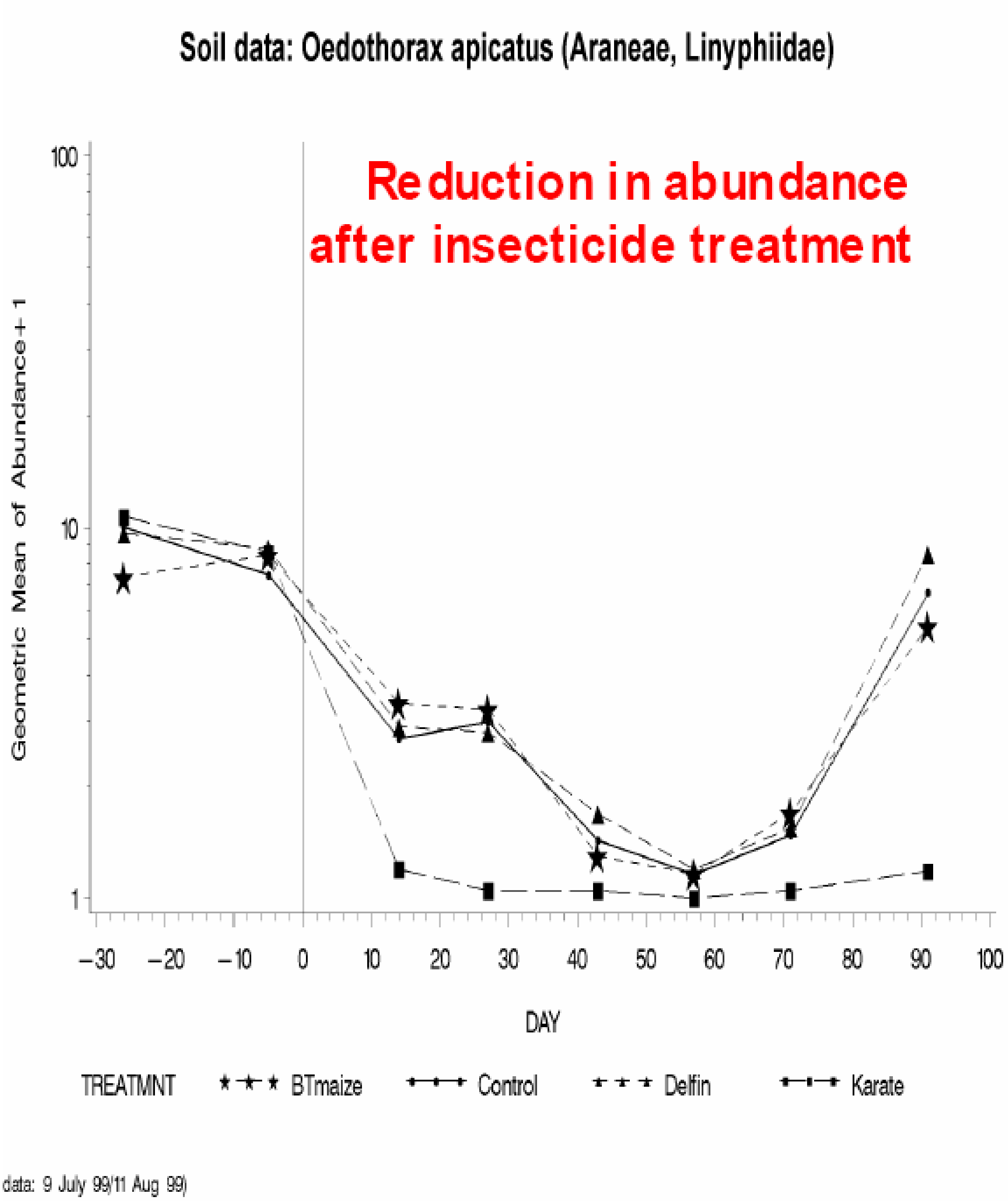


Figure 19: Soil data on non-target insects after Bt-, water- and insecticide treatment: Oedothorax apicatus (Araneae, Linyphiidae), data from (Candolfi et al., 2004). See the published graphs in (Candolfi et al., 2004)

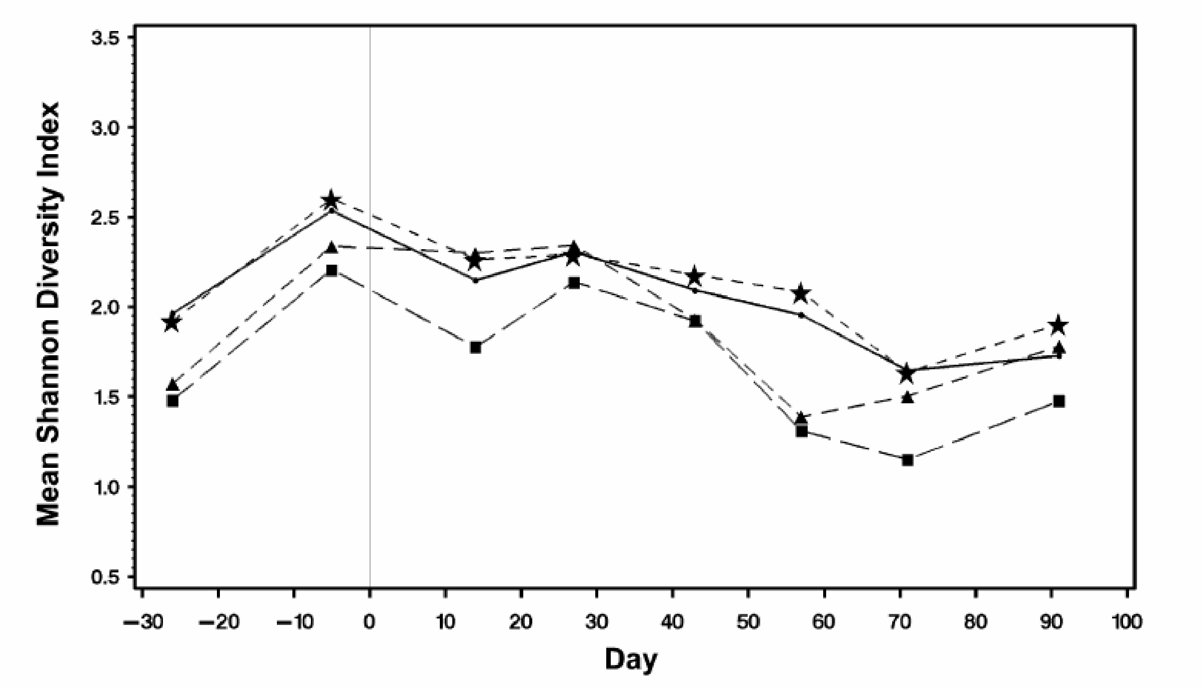


Figure 20 Shannon diversity indices of soil dwelling taxa per trap collected with the pitfall traps throughout the sampling season: (●) untransformed corn (control); (✱) Bt-corn; (▲) untransformed corn treated with Delfin; (■) untransformed corn treated with Karate Xpress; Day 0, spray day. No statistically significant differences between treatments were observed (Tukey test, P_/0.05). (Candolfi et al., 2004)

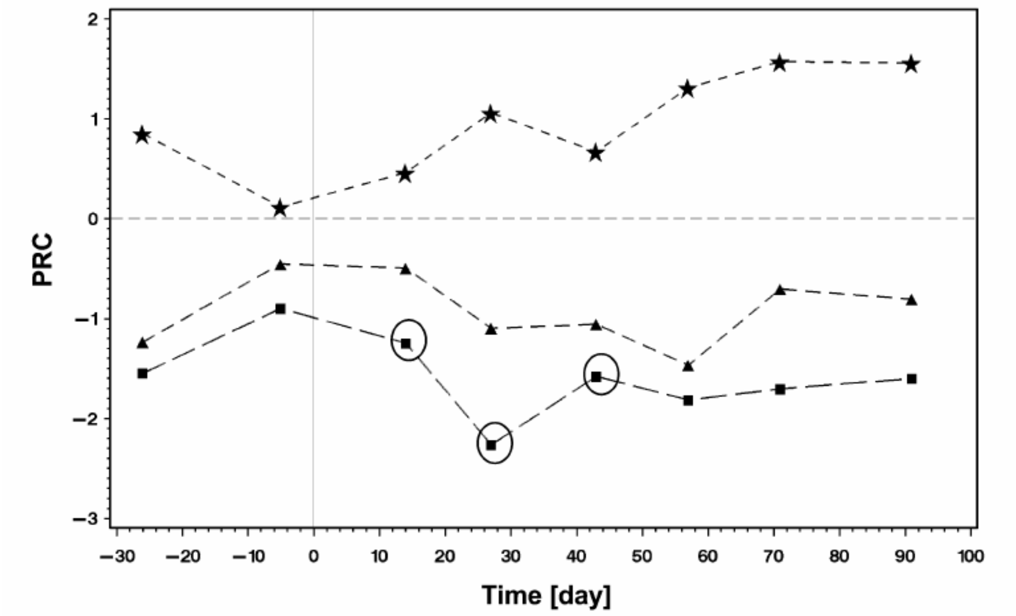


Figure 21 Principal response curve analysis for soil dwelling organinsms: zero line of the y-axis_/ untransformed corn (control); (✱) Bt-corn; (▲) untransformed corn treated with Delfin; (■) untransformed corn treated with Karate Xpress; Day 0, spray day. Statistically significan treatment effects when compared to control are circled (goodness of fit R2_/0.74, goodness of prediction Crossvalidation/Jacknife R2_/0.62). (Candolfi et al., 2004)

Contributions to Principal Response Curves for the 14 taxa contributing strongest to the PRC:

Taxa	Contribution to PRC
Diplopoda	+ 0.2163
Sminthuridae (Collembola)	– 0.2121
Entomobryoidea (Collembola)	– 0.1864
Phalangium opilio (Opiliones: Phalangiinae)	+ 0.1450
Harpalus rufipes (Coleoptera: Carabidae)	– 0.0910
Acari	– 0.0881
Pterostichus melanarius (Coleoptera: Carabidae)	+ 0.0689
Harpalus aeneus (Coleoptera: Carabidae)	– 0.0679
Oedothorax apicatus (Araneae: Linyphiidae)	+ 0.0642
Elateridae (Coleoptera)	– 0.0548
Chilopoda	+ 0.0510
Poecilus cupreus (Coleoptera: Carabidae)	– 0.0427
Linyphiidae juvenile (Araneae)	– 0.0261
Isopoda	– 0.0227

Figure 22 PRC analyses showed significant treatment effects (goodness of fit R2_/0.65, goodness of prediction Crossvalidation/Jacknife R2_/0.50) of Karate Xpress and Delfin when compared to the control treatment 2 days after application (Figure 8 in (Candolfi et al., 2004)). Main contributors to the PRC were parasitic wasps in the Eulophidae and Proctotrupoidea (Hymenoptera), the bugs Orius sp. (Heteroptera: Anthocoridae), Nabis ferus (Heteroptera: Nabidae) and Deraeocoris sp. (Heteroptera: Miridae), the leafhopper Z. scutellaris, thrips (Thysanoptera), the ladybird beetle Scymnus sp. (Coleoptera: Coccinellidae), soldier beetles (Coleoptera: Cantharidae),phorid flies (Diptera: Phoridae), and several spider taxa (Araneae: Linyphiidae, Theridiidae), phorid flies (Diptera: Phoridae), and several spider taxa (Araneae: Linyphiidae, Theridiidae, Thomisidae) (see Figure 8 for single taxa contribution to PRC). (Candolfi et al., 2004)

Similarly, a variety of studies of Bt cotton in the United States, Australia and China have all demonstrated that populations of many non-target species are higher in Bt cotton fields than in sprayed conventional cotton fields (Fitt & Wilson, 2003; Head et al., 2001; Naranjo et al., 2002; Xia et al., 1999). Likewise, work on potato fields in the north-eastern US has revealed larger populations of many generalist predators in Bt potato fields than in conventional potato fields treated with appropriate broad-spectrum insecticides (Reed et al., 2001). In contrast to Newleaf potatoes and microbial Bt formulations, however, the broad-spectrum insecticide, permethrin, had much broader and more severe unintended impacts on non-target arthropods. Debates over potential environmental risks associated with large scale use of transgenic Bt crops have been based largely on philosophical arguments, conjectural ecological theories, and limited laboratory studies (Hilbeck et al., 1999); but ecological studies with robust field data have been recently published, see above.

The years long controversy on the fate of the Monarch butterfly larvae in the US cornfields seems to be solved: A Nature publication of (Losey, 1999) and lab experiment results on forced fed predators (Hilbeck et al., 1998; Hilbeck et al., 1999) extensive field work demonstrated no significant impact (Fitt & Wilson, 2003; Gatehouse et al., 2002; Hansen & Obrycki, 2000; Hellmich et al., 2001; Hodgson, 1999; Oberhauser et al., 2001; Ortman et al., 2001; Pleasants et al., 2001; Sears, 2000; Sears et al., 2001a; Sears & Boiteau, 1989; Sears et al., 2001b; Sears & Shelton, 2000; Shelton & Sears, 2001; Stanley-Horn et al., 2001; Zangerl, 2001). It was Rachel Carson herself who named Bt proteins as a possible way out of the pesticide crisis which she described in her famous ‘The Silent Spring’, and one can only wonder what she would have said about the Bt toxin instead of being sprayed in large, but rapidly decomposing quantities, built genetically into the corn borer infested crops (Carson, 1962 - 2002). Recently, lab work on predators like Chrysoperla has revealed, that under more realistic conditions of a much lower concentration of Bt toxins even the forced feeding does not really harm the non-target insects studied (Romeis et al., 2004). But the controversy seems to continue: although not directly referring to the latest publiction of Romeis: Andow and Hilbeck still claim that the case of Bt toxins affecting non-target insects is not solved (Andow & Hilbeck, 2004).

Several conceptual models show the way forward on risk assessment of GM crops related to long term and possible indirect toxic effects on ecosystems.

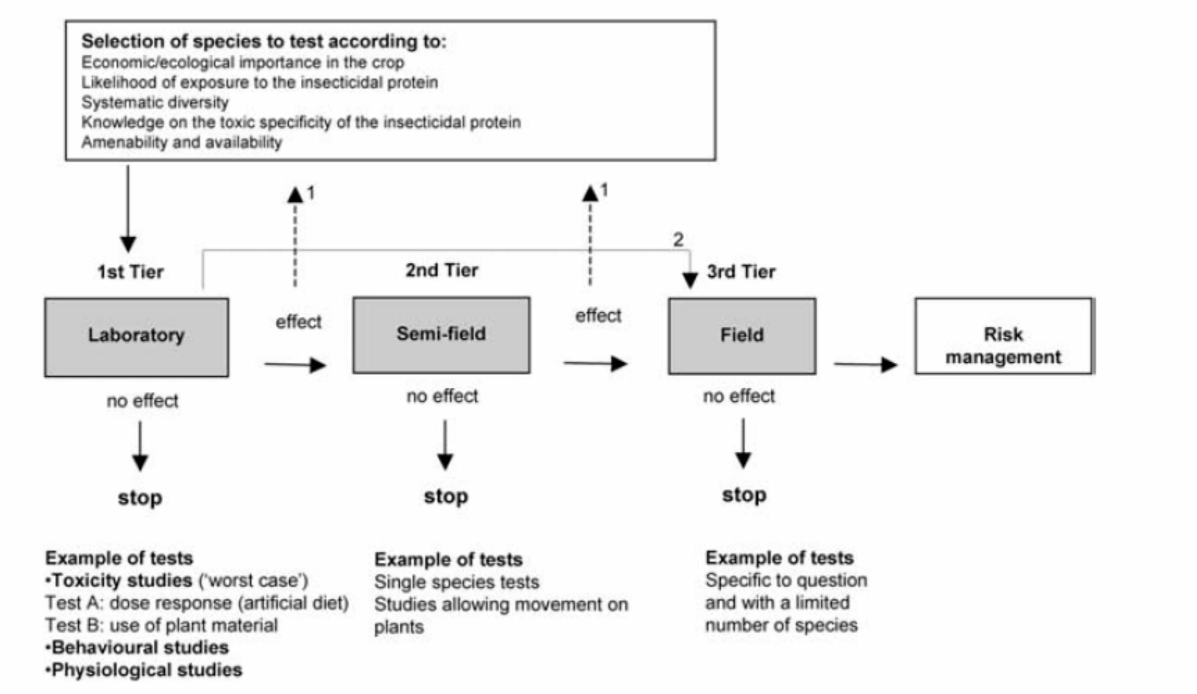


Figure 23: Monitoring concept proposed by (Dutton et al., 2003)

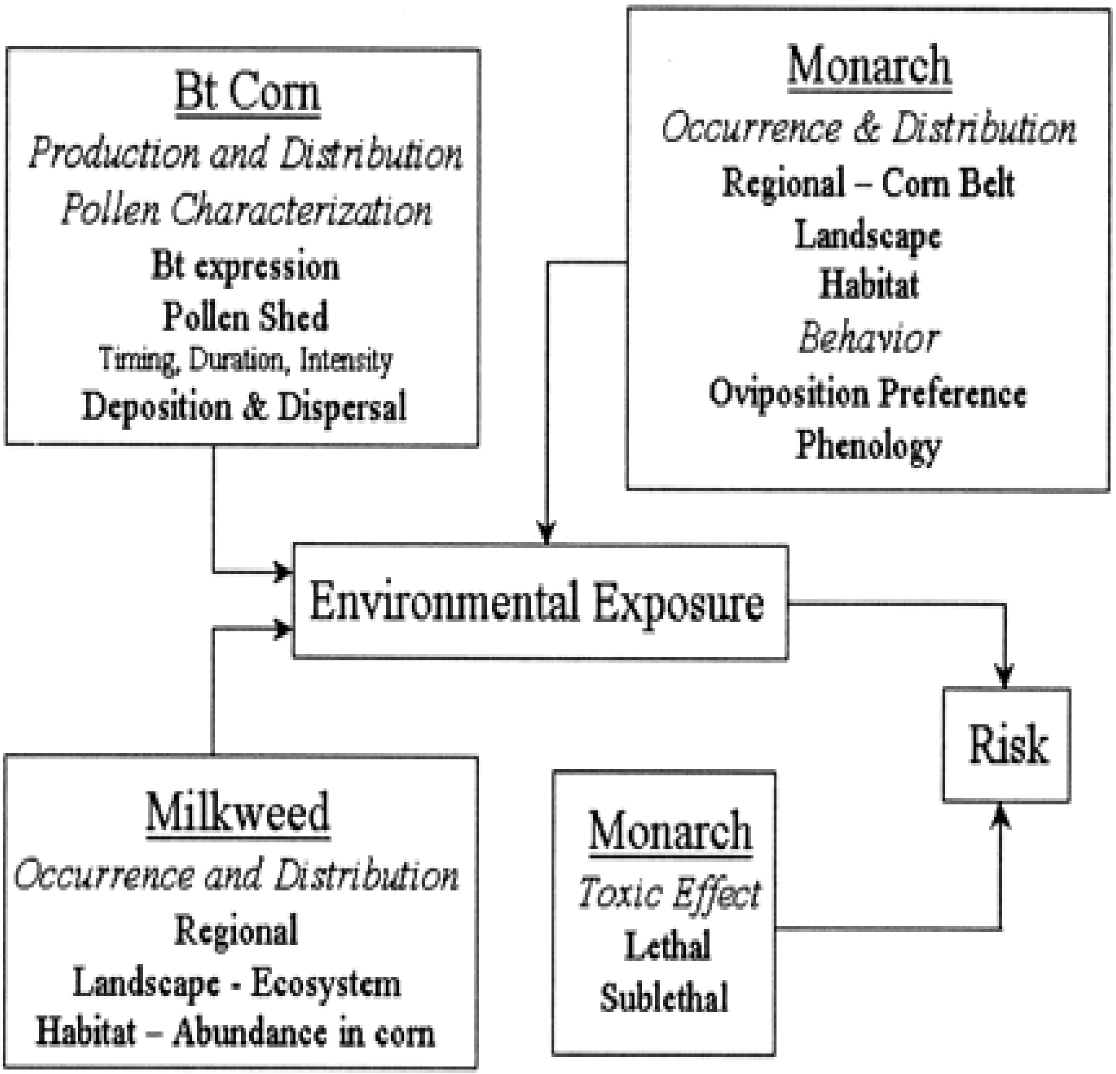


Figure 24: Conceptual model of components of risk assessment of the impact of *Bt* corn pollen on populations of the monarch butterfly. (Sears et al., 2001a)

Table 2 Ecological risk assessment framework for Bt and Roundup Ready crops

Risk = Hazard x Probability of Occurrence (Exposure)

Hazard		Exposure	
Characterization	Data	Routes	Data
Genetic instability	Molecular analysis, efficacy and protein expression	Pollen movement	Outcrossing studies (where relevant) and breeding data
Invasiveness (weediness)	Extensive agronomic and field data including growth, morphology, and yield	Seed dispersal Presence of wild relatives	Biology of crop, morphological data Biogeographical analysis
Non-target effects	Toxicity tests, compositional analyses, bird and fish studies (8 additional lab tests for Bt crops)	Protein expression	ELISA and/or western blots
Altered interactions with insects and microorganisms	Multi-site field data (baseline resistance data for Bt crops)		

Figure 25: Ecological risk assessment framework for Bt and Roundup Ready crops (Nickson & Head, 2000)

Table 3 Additional toxicity/feeding testing of Bt proteins (in addition to mouse, quail and fish done for all products)

Honey bees	Larvae
	Adults
Beneficial insects	Ladybird beetle adult
	Parasitic wasp adult
	Green lacewing larvae
Soil organisms	Earthworms
	Collembola
Aquatic animals	*Daphnia magna*

Figure 26: Additional toxicity/feeding testing of Bt proteins (in addition to mouse, quail and fish done for all products) (Nickson & Head, 2000)

We should all keep in mind that for the present day generation of Bt crops much has been already done and it is not necessary to invent the weel from scratch in every single region. It is time to rethink the familiary concept , here just two opposite views: A positive one from the US: (Hokanson et al., 1999), and a negative one from Europe: (Damgaard & Loekke, 2001)

Figure 27: Risk assessment concept of a biotech company in two steps (Nickson & Head, 2000)

Figure 28:Monarch Butterfly, Missouri Botanical Garden, September 2003, photo K.Ammann

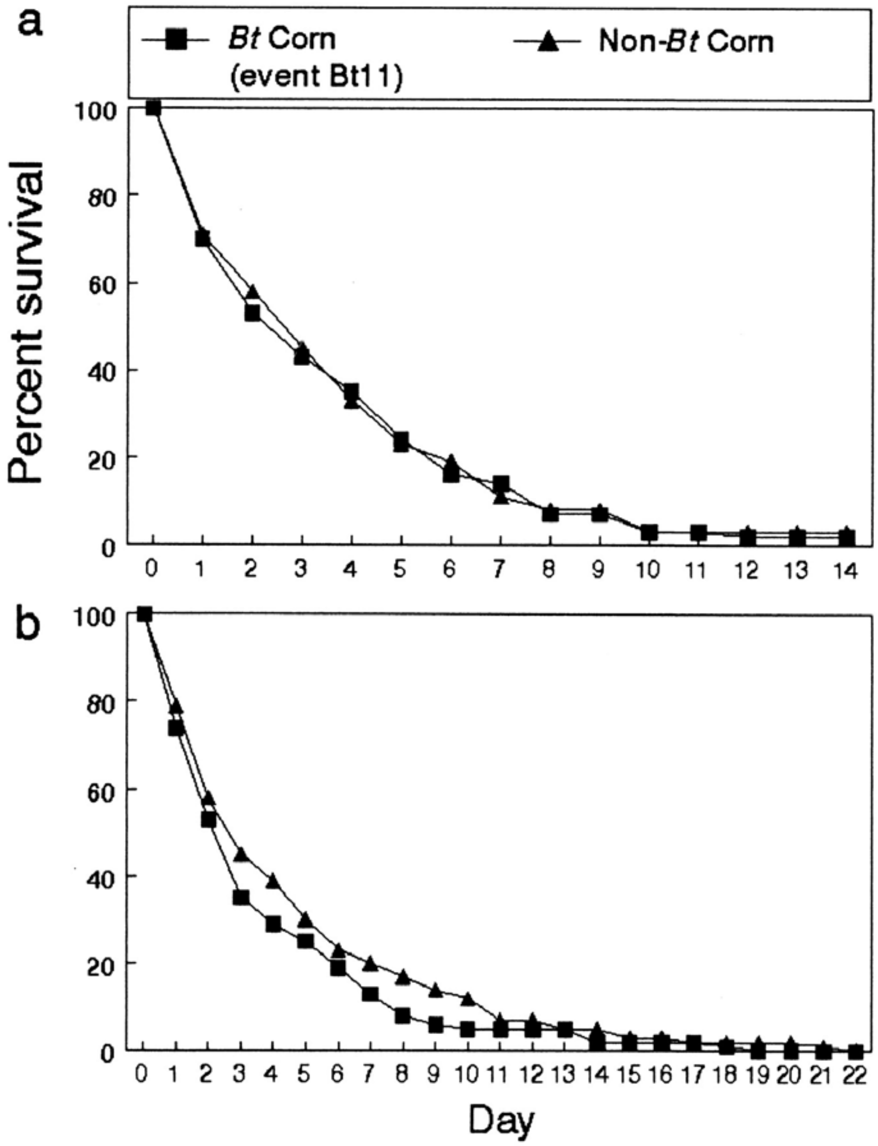


Figure 29: Survival curves for monarch larvae placed in and near *Bt* and non-*Bt* corn fields. (*a*) Iowa. (*b*) New York. The survival curves of larvae pooled over the three Bt corn sites were not significantly different from those in non-Bt (Fig. 13a). In New York, trends in survivorship were also statistically the same for cohorts of larvae feeding for 22 days on milkweeds in Bt and non-Bt fields (Fig. 13b). (Stanley-Horn et al., 2001)

Herbicide tolerant crops are not expected to directly affect agricultural biodiversity because of the nature of the proteins expressed but they may lead to changes in practices that could affect biodiversity. Herbicide tolerant crops facilitate shifts toward reduced tillage, as observed for soybean and cotton in the United States. As noted earlier, such shifts can be beneficial to agricultural eco-systems.

In addition, herbicide tolerant crops permit greater flexibility in herbicide application practices, particularly the timing of applications. If these practices lead to more intensive and higher level weed control, then biodiversity may be adversely affected (Watkinson et al., 2000). However, herbicide tolerant crops also can encourage herbicide application practices that benefit wildlife. For example, studies on herbicide tolerant sugar beet in the UK and Denmark have shown that leaving weeds untreated in the agricultural field for a longer period allow arthropod populations to increase to higher levels than are seen in conventional fields, without affecting crop yield (Dewar et al., 2002). These weeds and the associated arthropods provide valuable food and habitat for farmland birds and other wildlife. Such a practice is not feasible with conventional sugar beets. Soil fertility can be enhanced with appropriate use of broad spectrum herbicide tolerant sugar beets (Elmegaard & Pedersen, 2001; Strandberg & Pedersen, 2002).

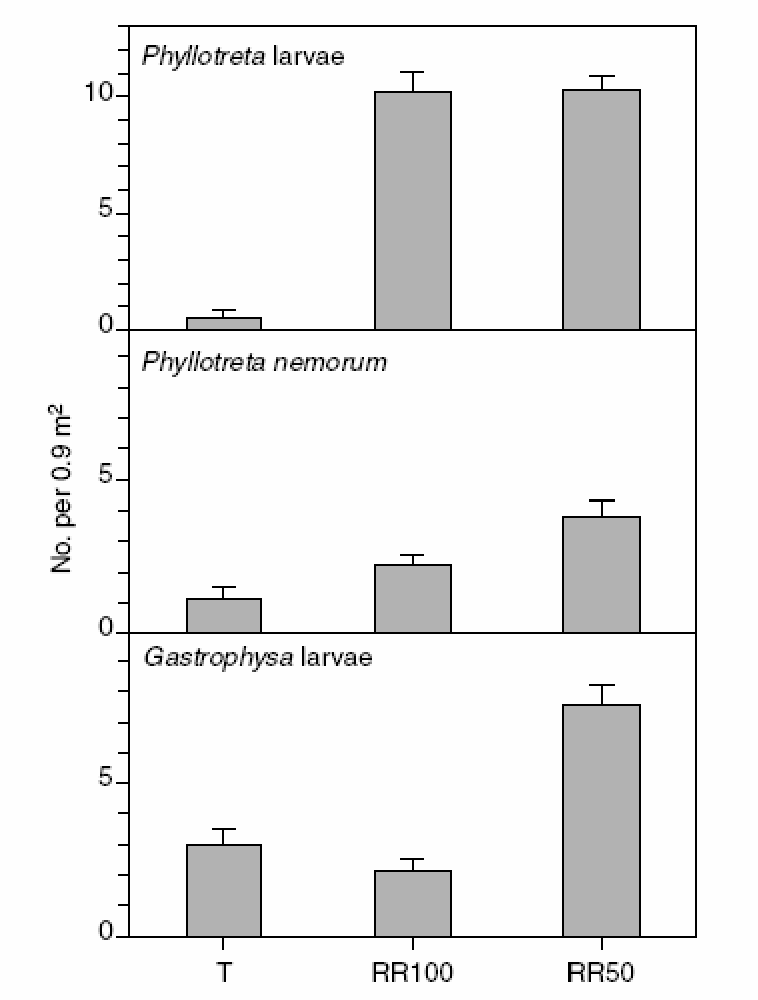


Figure 30: Density of *Gastrophysa polygoni* larvae, flea beetle larvae and *Phyllotreta nemorum* in the traditional (T) fodder beet plot, RR100 plot and RR50 plot at Skejby. Bars indicate standard error of means. (Elmegaard & Pedersen, 2001)

For a more thorough analysis of the benefits and also the controversy see Chapter The scientific controversy about GM crops VI: Generalities Interpreting Science and the example of non-target insects in fields of transgenic and non-transgenic crops

The fate of Bt toxin in the soil

It has been shown that Bt toxin is released into the rhizosphere soil with decaying litter and through root exudates from Bt corn (Stotzky, 1999). The insecticidal toxin produced by B. thuringiensis subsp. kurstaki remains active in the soil, where it binds rapidly and tightly to clays and humic acids. The bound toxin retains its insecticidal properties as determined by bioassays: the toxin is protected for some time against microbial degradation by being bound to soil particles, persisting in various soils for at least 234 days (the longest time studied). Unlike the bacterium, which produces the toxin in a precursor form, Bt corn contains an inserted truncated cry1Ab gene that encodes the active toxin. The toxins do not appear to have any consistent effects on organisms in soil (earthworms, nematodes, protozoa, bacteria, fungi) or on micro organisms *in vitro* (Koskella, 2002; Saxena et al., 1999; Saxena & Stotzky, 2001). A multiseason monitoring in six fields in the USA did not reveal any effect on various bioassays with soil organisms, using soil matter including degrading leafs (Head et al., 2002).A recent study (Zwahlen et al., 2003a; Zwahlen et al., 2003b) is focussing on bioassays with degrading leaf litter of two near isolines of Bt- and non-Bt-maize under controlled conditions. The study concludes that possible subtle, long-term toxic effects should be tested in long term monitoring in the post-commercialization phase. However, (Hector et al., 2000) suggest to critically reassess litterbag experiments data in their interdependency on a multitude of factors. These possible effects should be put into quantitative relation to long term monitoring data under field conditions with non-Bt maize, where more pesticides are used. The differences in the results between the field studies of Zwahlen and Head might stem from differing regional climate parameters, but also from differing experimental conditions.

There is a vast body of knowledge also on the use of Bt toxin as a bio pesticide: (Glare & O'Callaghan, 2000).

Conclusions ↺

Agricultural practices adversely affect in-field biodiversity in a number of obvious ways. Most of these adverse effects can be effectively or partially mitigated through judicious use of available technologies and crop management strategies. For example, GM crops can replace agricultural practices that would otherwise depress and disrupt species biodiversity, and can encourage or complement other practices that enhance biodiversity. Existing agricultural policies and other political factors also strongly affect the decisions made by farmers. That said, the potential exists to directly or indirectly reward farmers for making environmental improvements to their land (Mellor, 1995; UNDP, 2001) through the appropriate use of GM crops, but also through the adoption of many other farmers practices with environmental benefits, such as the selective use of mixed cropping (Zhu et al., 2000a; Zhu et al., 2000b) or organic or integrated farm management strategies. There is basically no scientifically plausible reason to keep GM crop and organic/integrated farmer practices strictly apart.

Natural biodiversity ↺

General impacts of modern intensive agriculture

As discussed in Section 1, experts generally agree that the factor most responsible for decreases in natural biodiversity, both locally and globally, is habitat destruction and fragmentation as land with native communities is cleared for agricultural or other use. Farming is the biggest threat to natural biodiversity. The past 35 years have brought a 1.68-fold increase in the amount of irrigated cropland and a 1.1-fold increase in cultivated land (Tilman, 1999; Tilman et al., 2002). This problem is most severe in developing countries with a large amount of subsistence agriculture. Even looking within different agricultural systems, the degree of fragmentation increases with the intensity of agricultural management. For example, (Belanger & Grenier, 2002) showed that fragmentation increased along a gradient from traditional dairy agriculture to more intensive cash crop agriculture in the St. Lawrence Valley of Quebec, Canada.

Pesticide use ↺

Pesticide use, and particularly insecticide use, has significant off-site effects on biodiversity. Aerial drift and movement in water can expose natural communities to potentially toxic amounts of pesticides. These effects will be most severe on communities adjacent to agricultural lands. (Boutin & Jobin, 1998) found the species composition in habitats adjacent to agricultural habitats to be adversely affected by intensive agriculture, as measured by tillage practices and pesticide and fertilizer use. These non-crop habitats adjacent to cropped land are critical for the maintenance of plant species diversity, for the conservation of beneficial pollinating and predatory insects, and as essential habitat for birds and other organisms (Mineau & McLaughlin, 1996; Nentwig, 1999). However, we should not forget that it is mankind in the center of activities, and some insecticides having been banned a long time for good reasons in countries which can afford to substitute DDT, there are still situations in poor countries where DDT has to be sprayed on order to fight malaria. And DDT did not only harm in long term effects the environment, but it was also beneficial in avoiding millions of deaths due to malaria disease. (Tren & Bate, 2001)

Tillage and fertilizer use ↺

more about tillage ↺

The impacts of tillage on biodiversity in agricultural fields were described earlier, the disruption of in-field communities and reduction of soil quality being the most obvious. However, the impacts of tillage on natural habitats are even greater. Soil erosion due to tillage leads to high levels of fertilizers and pesticides being carried off agricultural fields into waterways. Remember that the past 35 years have seen a 6.87-fold increase in nitrogen fertilization and a 3.48-fold increase in phosphorus fertilization within intensive agricultural systems (Tilman, 1999; Tilman et al., 2002). As they move into aquatic systems, these chemicals can have direct toxic effects on natural communities, while the fertilizers cause eutrophication. Eutrophication leads, in turn, to direct losses in biodiversity, pest outbreaks, and changes in the structure of natural communities. In addition, because erosion leads to various forms of nitrogen and fertilizer dust being redistributed aerially, natural terrestrial ecosystems also are being eutrophicated. (Hayati & Proctor, 1991; Woo & Zedler, 2002) Many of these problems can be reduced or avoided by reducing tillage practices. In North America and Europe, high-yield farming and conservation tillage have reduced soil erosion by 65-98% (Buffett, 1996). However, subsistence farming in developing countries is causing substantial soil erosion and habitat loss, and is a significant threat to natural biodiversity.

Genetically modified crops ↺

GM crops have the ability to benefit natural biodiversity in a number of ways. *First*, GM crops have the demonstrated potential to increase yields and decrease variability in yields (Gianessi et al., 2002) thereby reducing the need to put additional land into agricultural production. By slowing the rate at which natural habitats are destroyed, GM crops and other technologies that increase agricultural productivity can help to preserve natural biodiversity. *Second*, insect resistant crops reduce the use of broad-spectrum insecticides that would otherwise have direct and indirect effects on natural communities dwelling near agricultural fields. The insecticidal proteins expressed in Bt crops are both highly specific and contained within plant, minimizing the possibility of any off-site effects due to spray drift. *Third*, herbicide tolerant crops facilitate a reduction in tillage, thereby reducing soil erosion, eutrophication and contamination of aquatic communities (see earlier discussion of the impacts of tillage and the following chapters on the impact of GM crops on genetic diversity).

Conclusions ↺

The greatest threat to natural biodiversity comes from habitat loss, much of which is driven by agricultural demand. Increasing the productivity of land currently in production is necessary to slow this process. Other agricultural practices also can negatively impact natural communities through various off-site effects, including movement of fertilizers into aquatic systems and pesticidal drift. Reducing tillage and decreasing the use of pesticides can mitigate some of these impacts. GM crops can be a partial solution to several of these problems; GM crops enhance productivity, minimize off-site effects, and (in the case of herbicide tolerant crops) facilitate reductions in tillage. It has to be reiterated here again, that GM crops can go well with other farming practices, as long as the specific usage prescribed is not neglected. Basically, GM crops can also be installed within organic and integrated farming strategies, they might help to develop new knowledge-based agricultural practices in the future.

Impacts on Genetic Diversity ↺

Crop genetic diversity

General impacts of modern intensive agriculture

As observed earlier, conventional agriculture is characterized by the use of highly productive varieties generated through breeding programs, and low crop species diversity. Because the number of varieties of any given crop maintained by breeding programs necessarily will be limited, this focus has led to a steady loss of genetic diversity in crop species and the permanent loss of many varieties over the last 100 years. This issue has been the motivation for the establishment of genetic archives for many important crop species.

Genetically modified crops ↺

Biotechnology represents a tool for enhancing genetic diversity in crop species through the introduction of novel genes. This statement does not aim at the single transgene inserted, but is based on the fact that beneficial characters can now be inserted in a whole variety of crops which have been left aside, since traditional breeding methods would be limited for various reasons.

However, with the introduction of GM crops, concern has been expressed that overall genetic diversity within crop species will decrease because breeding programs will concentrate on a smaller number of high value cultivars. A number of studies have specifically focused upon this subject and they have concluded that the introduction of transgenic cultivars in agriculture has not significantly affected levels of genetic diversity within crop species. For example, (Sneller, 2003) looked at the genetic structure of the elite soybean population in North America, using coefficient of parentage (CP) analysis. The introduction of herbicide tolerant cultivars with the Roundup Ready ® trait was shown to have had little effect on soybean genetic diversity because of the widespread use of the trait in many breeding programs. Only 1% of the variation in CP among lines was related to differences between conventional and herbicide tolerant lines, while 19% of the variation among northern lines and 14% of the variation among southern lines was related to differences among the lines from different companies and breeding programs. Similarly, when (Bowman et al., 2003), examined genetic uniformity among cotton varieties in the United States, they found that genetic uniformity had not changed significantly with the introduction of transgenic cotton cultivars. In fact, when they compared the years before and after transgenic cultivars were introduced, they observed that both the percentage of the crop planted to a small number of cultivars and the percentage planted to the most popular cultivar had declined. Thus genetic *uniformity* actually decreased by 28% over the period of introduction of transgenic cultivars. In the light of those data theoretical concepts of (Gepts & Papa, 2003) that GM crops should be held responsible for a biodiversity decline within crops are not very convincing. It remains to be said that the continued use of locally adapted traits gained in traditional breeding should play an important role, more important than today (Swaminathan, 1998).

Conclusions ↺

Preservation of the genetic diversity present in crop species is an important need being addressed by various public and private programs. In this respect, biotechnology can be a valuable tool for introducing novel (alien or non-alien) genes. Furthermore, the development and introduction of GM crop varieties does not represent any greater risk to crop genetic diversity than the breeding programs associated with conventional agriculture. After all, the overall performance of a plant and the quality and quantity of its product is the result of thousands of genes and the genetic background is almost always more important than a single transgene.

Natural genetic diversity ↺

General impacts of modern intensive agriculture on natural biodiversity

There is no doubt that the intensification of agriculture had a marked impact on the natural genetic diversity: A dramatic reduction to five or six major crops (wheat, maize, rice, cotton, beet, alfalfa) worldwide caused a monotone agricultural practice with all its adverse effects.

Conventional agriculture has adversely impacted the genetic diversity and population structure of many wild plant and animal species, with severe implications for the conservation of many species and ecosystems. The greatest impact has come through direct loss of natural habitats. As land is put into agricultural production and natural habitats are destroyed, the habitat available to any particular species will become limited and more fragmented. This, in turn, it will reduce the effective population size of many species, potentially reducing genetic diversity to critical levels and causing inbreeding that can have additional adverse effects on the fitness of populations.

Putting land into agricultural production and fragmenting the available natural habitat also can limit gene flow among populations of a species. Where individuals of an animal species are unable to move through agricultural fields, populations will become more isolated, further reducing effective population sizes and threatening the viability of these populations. (Hanski, 2002)

Agricultural strategies all have the goal to produce food, and most claim to do this in a sustainable way. What is the connection between biodiversity and sustainability? It is assumed that there is (up to a certain degree) a positive connection between agricultural and natural productivity, we have hints that pest problems can be reduced through better management of biodiversity: Some weeds are also important hosts of beneficial insects which reduce the populations of pest insects. (Nentwig, 1999). On the other hand, toxic weeds seeds create problems to the harvested grain. (Beck et al., 1999).

Impacts of GM crops on genetic diversity ↺

Claims, that in the long run herbicide-tolerant crops could be harmful to the biodiversity of a whole landscape including bird fauna have been questioned.

> (Johnson, 2000) "The irony is that biotechnology may hold the key to less damaging forms of agriculture, yet it appears that it is currently being used by some parts of the industry in some countries to produce the opposite effect. We are challenging the industry to change direction in R&D, toward producing crops that contribute to more sustainable forms of agriculture, demonstrating real and tangible benefits for the environment. I believe this needs to be done wherever the products of biotechnology are intended to be used, whether in industrial or developing countries."

Recent results (Elmegaard & Pedersen, 2001; Strandberg & Pedersen, 2002) contradict the above cited statements by Johnson: The results reveal that the implementation of Roundup Ready ® fodder beets may increase biodiversity in beet fields. In general, the weed flora and arthropod fauna in Roundup Ready plots contained more individuals and species than the Tillage plots in June. These results cannot be generalized, they might be different from crop to crop and from region to region, and also they might heavily depend on the application mode and the kind of herbicide.

Organic agriculture tends to enhance biodiversity on the field at the cost of yield, but energy input during the production process is also lower (Mäder et al., 2002), (Stokstad, 2002), (Zoebl et al., 2002), (Goklany, 2002). Despite of persisting scepticism against new agricultural strategies (organic or biotech), there is a lot of potential to discover in making food production still more ecological. It remains to be shown how widespread organic farming in large areas can effectively control pests. Still, the vision is justified to develop new GM crops, better adapted to the local ecological conditions, thus reducing fertilizer use, pesticide use and enhancing biodiversity directly through more crop diversity and indirectly through enhancing biodiversity in the fields.

The following chapters are written in the style of a scientific controversy, and the most important publications are cited. It should illustrate the present day debate about GM crops and their impact on biodiversity.

The Debate about GM Crops and Biodiversity, Selected Case Histories ↺

The scientific controversy about GM crops I: ↺

Gene flow between crops and to wild relatives

Planting of crop species in close proximity to wild, sexually-compatible relatives will permit gene flow between the crop and wild relative. Typically this process will have little direct effect on the genetic diversity of the wild relative because of the limited ability of most crop species to outcross over significant distances. However, even though the amount of gene flow will usually be low, it is possible that this process could lead to the transfer of genes that code for traits with significant impacts on fitness of the recipient plants, or in rare cases to the loss of alleles that are adjacent to the transgene chromosomal regions, if selective sweep or background selection might occur (Gepts & Papa, 2003) But it is very important to note that those effects can also be seen in traditional breeding. Unexpected effects are often encountered in any breeding process and is traditionally overcome by long years of testing the crops for the quality of genomic expression.

This out crossing is normally not adversely affecting the wild species because traits associated with decreased fitness will be rapidly selected out of the recipient population. However, if fitness is greatly increased, then weedy characteristics of the wild relative could be enhanced. Such an effect could cause indirect negative effects on natural plant communities and the animals dependent upon them.

There is a plethora of studies and summaries of research results, which all demonstrate that no or only very limited effects on the environment have been detected in relation to out crossing. (Den Nijs et al., 2004, in press) Basically, we have the same phenomena as with non transgenic crops. There are possible scenarios imaginable, where an escaped transgene could permanently initiate a selective advantage, but so far this has not occurred. It is also difficult to imagine such a scenario, since agricultural traits have transgenes inserted, which are useful only in the artificial environment of intensive agriculture. Reviews are available as reports from the European Community: (Eastham & Sweet, 2002). The conclusions do not give simple recipes for safety distances, and in addition they cannot reveal a single case of a negative ecological impact of a documented case of transgene flow.

"The possible implications of hybridization and introgression between crops and wild plant species are so far unclear because it is difficult to predict how the genetically engineered genes will be expressed in a related wild species. The fitness of wild plant species containing introgressed genes from a GM crop will depend on many factors involving both the genes introgressed and the recipient ecosystem. While it is important to determine frequencies of hybridization between crops and wild relatives, it is more important to determine whether genes will be introgressed into wild populations and establish at levels which will have a significant ecological impact." (Eastham & Sweet, 2002)

The important study is done in the best reductionistic tradition, relying 100% on measurements of escaped transgenes in the field, which automatically means that only short term results can be interpreted – with all its limitations (bias on weather conditions, local and regional topographic conditions etc.)

Recently, a new study (Stewart C.N. et al., 2003) revealed that in a case of transgene flow in oilseed rape the metabolic costs of the transgene are obviously so high that the new transgenic wild relative is less fit in subsequent corn fields after crop rotation: Wheat had decreased yield and biomass when grown in the presence of any Brassica competitor, but fared best when competed against BC2F2 Bulk transgenic feral B. rapa populations. The latter decreased wheat yield by 25%, while nontransgenic B. rapa, nontransgenic BC2F2 and transgenic B. napus reduced wheat yield by 47%; a significant difference. These results have led the authors to pose a genetic load hypothesis: selection for a transgene in introgressed weeds will be accompanied by crop genes in linkage disequilibrium, decreasing the competitive nature of an erstwhile highly fit weed by the genetic pollution of crop genes.

A comprehensive review has recently been given by (Messeguer, 2003) with a balanced view, warning of unfounded generalizations. Negative generalizations are also not supported by facts (Ellstrand, 1992), the author reflects on the possibility to do better in agro ecology of the future, since the transgenes and other molecular markers offer a much more precise picture of the dynamics. A method to assess long-term potential gene flow is given by (Frietema, 1996) and by (Ammann et al., 1996) and (Ammann et al., 2000b; Louwaars et al., 2002), making use of the excellent 'databases' of herbaria, collections of vast amounts of crops, their wild relatives and their well-documented (and often over-represented hybrids. With the help of morphometric analysis and subsequent field excursions with testing molecular markers in hybrid zones, with experimental hybridization, it is possible to give a reliable overview of potential gene flow in a given region. There are published studies for beet and sunflower that compare introgression of genes from cultivars between sympatric and allopatric populations (Bartsch et al., 1999; Linder et al., 1998) . Although crop-specific marker were found in sympatric wild populations, no loss of genetic diversity was observed. Another aspect is described by (Keller et al., 2000): Genetic introgression from distant provenances reduces fitness in local weed populations, an interesting result, but it should not be generalized prematurely.

Where transgenic cultivars are grown near wild relatives, the transgenic event may be transferred to the wild relative. At least with currently commercialized GM crops, no significant impact on the wild species is expected because the traits involved should not affect the fitness of individuals of the wild species (Bartsch & Schuphan, 2002). The long-term experiment with four GM crops in England and a given set of transgenes suggest that competitiveness of the wild relatives outside the field prevents survival of the GM crops after a few years: (Crawley, 1999; Crawley et al., 2001; Crawley et al., 1993).

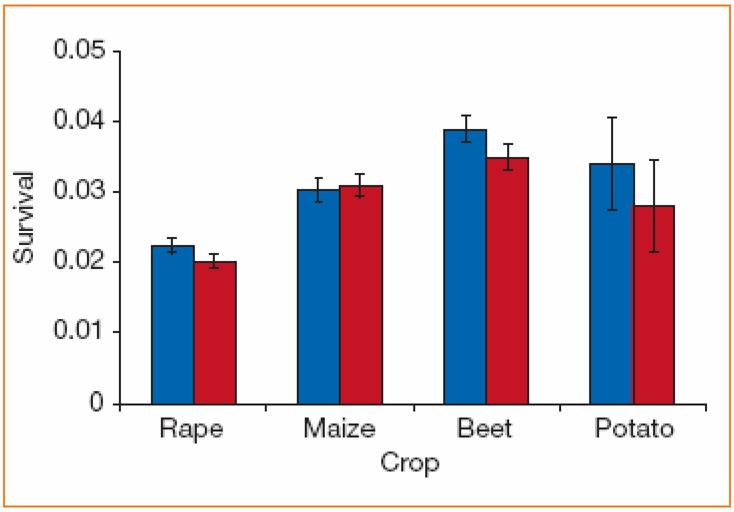


Figure 31: The performance of conventional (blue) and transgenic (red) crops in natural habitats. Survival is the fraction of seeds sown (or tubers planted in the case of potato) that produce mature plants at the end of the first growing season. Error bars, 1 s.e. Data are averaged over habitats and replicates within habitat. In no case did populations of either conventional or transgenic plants increase, and transgenic plants never persisted significantly longer than conventional plants. All populations of maize, rape and sugar beet were extinct at all sites within 4 years of sowing. Potato still survives at one site, 10 years after planting, but the survivors are all conventional. (Crawley et al., 2001)

The scientific controversy about GM crops II ↺

The case history about the Mexican corn gene flow

The paper "Transgenic DNA introgressed into traditional maize landraces in Oaxaca, Mexico (Quist & Chapela, 2001), rose a worldwide debate about its results and abuse of science for political rather than for scientific discussions, despite early publications on the same matter, which did not raise concerns (Martínez-Soriano & Leal-Klevezas, 2000). Some of the rebuttals of the paper were published: (Aldhous, 2002; Berne Debate, 2002; Christou, 2002; Hodgson, 2002; Kaplinsky, 2002a; Kaplinsky, 2002b; Mann, 2002; Martínez-Soriano & Leal-Klevezas, 2000; Metz, 2001; Metz & Futterer, 2002; Metz, 2002; Pauli, 2002; Quist & Chapela, 2002; Salleh, 2002; Suarez et al., 2002; Wager et al., 2002; Worthy et al., 2002). Nature's editor Philip Campbell reacted with an editorial note in the issue of April 4, 2002 (Campbell, 2002). This editorial note does not correct or retract the publication but admits: "Nature has concluded that the evidence available is not sufficient to justify the publication of the original paper."

The initial publication and the scientific debate stimulated an amazing degree of anxiety among the opponents; they accused wrongly all those who questioned the results of Quist/Chapela as being 'notorious pro GE-scientists' who denigrated the possibility of transgene flow in Mexico. Here is a sample of such unfounded allegations taken from AgBioView, circulated on Debate, a listserv which is run by the author since 1998: (Berne Debate, 2002; Prakash, 2002). The whole discussion does, astonishingly enough, not take notice of the manifold scientific data of gene flow, although one has to admit that those data are up to now not published in peer reviewed papers, and the references are somehow difficult to find: (Kato, 1997; Kermicle, 1997), the url is still active.

http://www.cimmyt.org/ABC/Geneflow/geneflow_pdf_Engl/contents.htm.

Despite the factual and scientifically proven gene flow from modern traits towards teosinte and maize landraces there is evidence of stability among the landraces and their wild relatives and no negative processes were detected.

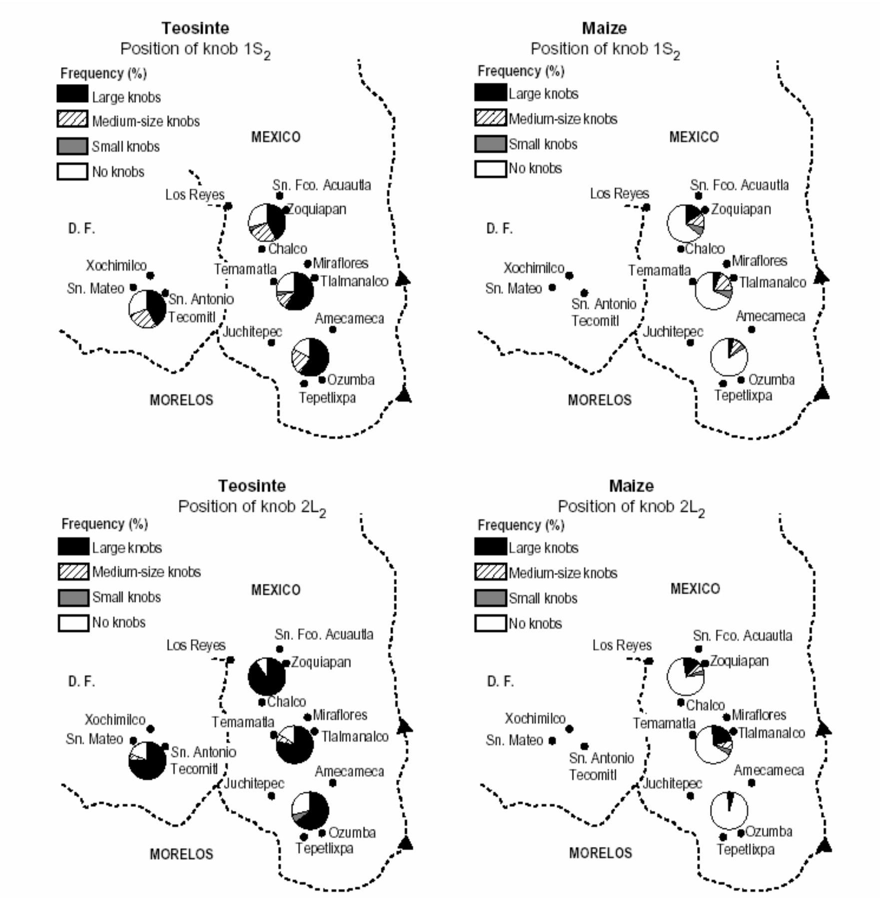


Figure 32: Frequency distribution of knobs at positions 1S2 and 2L1 in Chalco-Amecameca teosinte and maize. Extensive analysis of chromosome morphology with Mexican maize and its wild relative Teosint(l)e hints to a stable diversity of the landraces and teosintes, despite the fact of heavy gene flow for decades from modern traits to landraces and teosintes going on. (Kato, 1997)

Today, the fact is confirmed that transgene flow also has happened in Mexico, and the Mexican Government is still working on sorting out the complex details about the origin of the transgenes and their introgression into the landraces, which obviously went on for years including various events. In fact, hybrid corn has been cultivated in the vicinity of landraces and teosinte for more than 50 years without any documented damage to landraces and teosinte. A reliable summary has been given by (Alvares-Morales, 1999) and more comprehensively recently: (Wisniewski et al., 2002). It should be noted that Mexican land races are not threatened through gene flow but because of the falling prizes of corn products due to imports from the North (Dejanvry et al., 1995).

Figure 33: Maize – Teosinte hybrid complex in farmers field near the airport of Mexico City, September 2003, photo K.Ammann

Figure 34: Teosinte inflorescence: Maize field near Airport of Mexico City, September 2003, Photo K.Ammann

Figure 35: Teosinte: Female inflorescence, details. Maize field near airport of Mexico City, September 2003, photo K.Ammann

The case of herbicide tolerance in wild species induced by hybridisation with herbicide-tolerant transgenic crops

(Madsen, 1994) tested the competitive ability and growth behaviour of a hybrid between sea beet (*Beta maritima*) and transgenic sugar beet (*Beta vulgaris*) with a glyphosate resistance. She tested in a field experiment whether the hybrid had a higher biomass and a higher competitive ability than the non-transgenic parental types. The hybrid did not produce more biomass than sugar beet and the competitive ability of the hybrid did not exceed the expected level of a non-transgenic hybrid between sugar beet and sea beet. In the general discussion of herbicide resistance evolving herbicide resistant weeds, Madsen concludes that during herbicide applications, selection pressure from e.g. glyphosate is posed on the population privileging herbicide resistant types what should be prevented by crop- and herbicide-rotation. This fits well with the case study of *Brachypodium* by (Gressel, 1994) where certain herbicide types developed mutational resistance of a weed which was problematic only during herbicide application: 6 years after the application stop the resistant grass mutants have been totally outcompeted.

The first author came to positive conclusions some years later: (Madsen & Sandoe, 2001)

> “Risk assessment studies of herbicide resistant sugar beet have revealed no risks to human health or the environment. Indeed it appears that commercial growth of this crop might secure benefits such as decreased herbicide use and increased biodiversity.”

These findings are supported by (Bartsch et al., 2003) who found no difference between transgenic glyphosinate-tolerant and non-transgenic individuals *of Beta vulgaris* and *Beta maritima* x *Beta vulgaris* hybrids in field experiments between 1993 and 2000, if the complementary herbicide was not used.

Considerations for the release of herbicide tolerant crops have been published by (Bainton, 1993). The author concludes that,

> “although there are no grounds for major concern, the Ministry of Agriculture, Fisheries and Food of the United Kingdom should remain alert to adverse developments and be ready to investigate any matters to which the Advisory Committee on Releases to the Environment draws attention.”

Regarding (semi)natural habitats, (Crawley et al., 1993) and (Timmons et al., 1996) acclaim that a herbicide resistance outside the arable land does not provide an advantage to a wild relative, because there is no selection pressure in favour of herbicide resistance in natural habitats. For more details see (Carpenter et al., 2002). (Sukopp & Sukopp, 1993) add that there are other odds against a rapid spread of crops in natural habitats: Long term observation of traditional weeds of agricultural systems show that these species are often nicely confined to areas strongly influenced by man. Massive application of herbicides has led to the development of numerous herbicide resistant weeds up to now. (Andreasen & Jensen, 1994). Herbicide resistant weeds usually disappear after stopping the application of the corresponding herbicide.

Enhanced weediness in transgenic crops?

For a more analytic debate about weediness and transgenic crops, separating the most important factors influencing weediness, see (Ammann et al., 1996, 2000c). It should also be noted, that weediness of any plant species, rare or abundant, can be influenced strongly by soil biota:

(Callaway et al., 2004) claim that many mechanisms are involved in the expansion of exotic plant species. Their results provide comparative biogeographical experiments testing mechanisms for invasive success, and show that a switch from negative plant–soil microbial feedback in native habitats to positive plant–soil feedbacks in invaded habitats may contribute to the expansion of some of the world's worst invaders like Centaurea maculosa.

In their often cited PROSAMO field study (Crawley, 2001) showed that the analysed transgenic varieties of oilseed rape were slightly less competitive than traditional ones. Considering population biology, the analyses can be criticized in the way that only mean values are discussed. (Weber, 1995) demands in her critical, but purely theoretical discussion of that risk problems accessible to empirical verification should actually be approached empirically. This has been done extensively in the meanwhile, as summarized by (Sweet et al., 1999):

> Detection of herbicide tolerance in seed of male sterile oilseed rape plants at distances of up to 400m show that there is potential for oilseed rape pollen to be dispersed by wind and remain viable over considerable distances.
>
> Numbers of volunteers recorded at National List sites were low and it is evident from these results that GM herbicide tolerant oilseed rape does not appear to increase problems of volunteer management in following crops. A proportion of seeds sampled from GM plots were hybrids expressing tolerance to both glufosinate and glyphosate but there was no indication that these multiple tolerant hybrid plants were more difficult to control in following crops than conventional or single tolerant rape varieties.
>
> The numbers of glufosinate tolerant compared to non-GM volunteer plants found both in following crops and in field margins were low at the Plant Genetic Systems Cambridgeshire site. Previous work looking at the survival and persistence of GM rape lines reflects the situation reported here (Booth, 1996; Crawley et al., 1993; Crawley, 1993; Sweet, 1997) Incidence of GM herbicide tolerant rape plants in these volunteer populations suggest that weediness and invasiveness is not enhanced by this specific genetic modification.

(Sukopp & Sukopp, 1994) p. 67 stated that:

After three years running time the following results can be seen: (Crawley et al., 1993) Transgenic and non-transgenic crops (oilseed rape, potatoes, maize) have the same competitiveness outside agro systems. They hardly can persist more than one generation. In no case sexual reproduction has been observed.

Since there are only a few long term monitoring studies on transgenic crops existing which concentrate on weediness in all aspects, scenarios must for the moment remain speculative, see concepts cited in (Ammann et al., 1999) There are more details about potential weediness and GM crops discussed in (Ammann et al., 2000c).

A balanced discussion on the fate of exotic species in agricultural habitats is given in (Meiners et al., 2002)

“Agricultural practices may also influence the future impacts of exotics. The frequent plowing associated with row crop agriculture prevents the accumulation of exotic perennial cover. When these sites are abandoned, both natives and exotics start invading at the same time, resulting in a plant community that does not show significant effects of exotic species. In contrast, agricultural practices with repeated biomass removals such as hay fields, meadows and grazing result in perennial exotic communities that resist invasion by other species (Mack 1989). These effects may persist for 15 yr or more. One-time plowing was not sufficient to reduce the impacts of these species on community development in these sites. It is important to note that it is not the invasion of an exotic plant, per se, that reduces species richness but the dominance of a patch by exotic species that may result in reduced species richness. Species richness of natives and exotics are positively associated, showing no effects of exotic invasion on native species richness.

However, when exotic plants make up a large proportion of the total cover of a plot, we observed reductions in community richness (Meiners et al., 2001). Therefore, managers should focus control efforts on species that have the potential to dominate local plant communities.”

According to (Fredshavn, 1994; Fredshavn J.R., 1995; Fredshavn, 1992; Fredshavn & Poulsen, 1994) the environmental consequence of releasing transgenic plants to unconfined conditions depends on the changes in survival rate, growth behaviour and hybridisation possibilities caused by the transformation.

The survival rate depends on the growth conditions: soil type, water and nutrient supply and plant cover. Crucial for invasion of natural habitats is the establishment period immediately after the seed has germinated („the equivalent of child mortality“). Later the competitiveness of the plant determines the success as an invader. Fundamental changes in growth behaviour may allow the plant to invade new habitats not formerly occupied by the non-transformed genotype, but more likely, the growth behaviour is only slightly modified, and the transformed plant is limited to the same habitats as the non transformed genotypes.

Such phenomena concerning sensitive developmental phases should be considered when planning a long term monitoring system.

From the literature, (Madsen, 1994) concludes that there is no evidence that herbicide tolerant crop plants should become weeds, unless they already possess the traits for weediness, and if only one herbicide is used consecutively in several crop rotations for a longer period of time.

Long before transgenic herbicide tolerant crops have been a concern, (Rauber, 1977) pointed to the possibility of negative consequences: The following scenario developed by Rauber is still valid today.

“New developments are made possible with the availability of modern herbicides: Their impact lacunas produce ecological niches for resistant populations. A possible future problem is that new weeds could emerge from hybrids from crops and their wild relatives (cultivated and wild oat) and also from the crops themselves (sugar beet and weedy beet). In spite of or because enhanced precision physiological and ecological selectivity of future herbicides, it will be more and more difficult to fight these new tolerant varieties. They will have the same genome as the cultivar, except for at least one allele causing weediness. Possibly there will be some future annual weeds, developing as a perfect mimicry to crops, in this way reaching back to prehistoric times where weeds and crops where still very close and connected through a full range of intermediate forms in fields and seed mixtures.”

However there are scenarios which could hint to gene flow causing more fitness in certain wild relatives of transgenic crops: (Alexander et al., 2001) and (Snow, 2003): In a field experiment crossing cultivated and wild sunflowers, the resulting hybrids that contained the Bt transgene had 50 percent more seeds than control hybrids. It is not known whether the crossing experiments also included the true null-hypothesis: crossing non-transgenic cultivars with the wild relatives. Other results of sunflower experiments under different conditions with other transgenes demonstrate no selective advantage of a transgene that confers resistance to white mold: (Rieseberg & Burke, 2001), (Burke & Rieseberg, 2003). Again this is a hint that we need to study case by case, transgene by transgene, and again: this is certainly a valid statement for many traditional new breeds of crops as well. But concern should be measured with the long term agricultural reality: Hybrids between cultivated and wild sunflowers involving gene flow with many other advantageous genes may have arisen for decades. However, no weedy hybrids have been observed which cause problems.

Beside the insertion of various herbicide resistance genes into the beet genome, the transformation of beet to give resistance to the soil-born virus, beet yellow vein necrosis virus, which causes a serious disease called rhizomania, has been targeted extensively (Bartsch & Schuphan, 2002). In particular, rhizomania-resistant genotypes were examined for sugar beet as well as for sugar beet – Swiss chard hybrids. The beet`s ecological performance was compared under various environmental conditions with regard to parameters such as competitiveness, winter hardiness and seed production. No difference was found in seedling performance even under virus infestation. The competitive performance of beet was tested against *Chenopodium album*, a common weed in sugar beet fields and young fallow. Field experiments carried out between 1993-2001 demonstrated that transgenic sugar beets often grew better than virus-susceptible beets, but only when the virus was present. The difference between susceptible and resistant beets declined as more competing weeds were placed nearby. No differences were observed in most cases if the virus was absent, but occasionally potential costs of resistance were reported for some transgenic events in sugar beet (Bartsch & Schuphan, 2002). Some of the experiments focused on over-wintering of transgenic and non-transgenic sugar beet at different locations in Europe representing mild to cold winters in the years 1994-1999. No survival differences were found even under virus infestation conditions. In conclusion, this experiments addressed primarily the ecological consequences of gene flow in a hybrid environment, since crop - variety hybrids were used as a model for crop – wild crosses in the experiments. By complementary use or transgenic and near-isogenic genotypes, direct comparisons were made in experiments, so that any difference measured was caused by the transgenic event. For all cases examined, increased fitness effects were not found based on transgenic rhizomania-resistance genes (Bartsch et al., 2003).

The scientific controversy about GM crops V: Herbicide Tolerant Crops:

The British Farm Scale Experiment 2003 on herbicide application management ↺

Highly publicised even before it started, the results of the 3 years experiment on three genetically modified herbicide-tolerant (GMHT) crops over more than 200 fields in Great Britain have lately had a great impact in the press and the public. (Brooks et al., 2003; Champion et al., 2003; Firbank, 2003; Firbank et al., 2003; Haughton et al., 2003; Hawes et al., 2003; Heard et al., 2003a; Heard et al., 2003b; Perry et al., 2003; Roy et al., 2003; Squire et al., 2003; Zeki, 2003). See also the critical assessment by (Freckleton et al., 2003). The well intended experiments yield lots of data related to herbizide and crop management differences – rigorously collected and duly peer reviewed.

The results can be summarized as follows:

Differences in biodiversity between crops exceed differences between GMHT and conventional crops (Brooks et al., 2003; Haughton et al., 2003; Hawes et al., 2003; Heard et al., 2003a; Heard et al., 2003b; Roy et al., 2003). Higher early season weed numbers and biomass in all three GMHT crops (Heard et al., 2003b). Higher weed mortality in GMHT sugar beet and canola resulting in lower late-season biomass and seed rain of weeds in those crops, but lower weed mortality in GM maize (Heard et al., 2003b). More detritivores (collembola) in all three GMHT crops as a result of higher weed detritus (Brooks et al., 2003; Haughton et al., 2003). Lower numbers of bees, butterflies, and Heteroptera in GMHT sugar beet and canola as a result of reduced weed populations; generally higher numbers of invertebrates in GM maize (Brooks et al., 2003; Haughton et al., 2003). Lower herbicide inputs in GMHT crops (Champion et al., 2003). It has been argued that GM maize is performing better, because it has been treated with the broad band herbizide atrazine, but (Perry et al., 2004) showed with a more detailed analysis of data from the trials that this is not the case: Even GM maize treated with non-atrazine herbizides performed still a bit better than non-GM-maize regarding biodiversity, see Fig. 36.

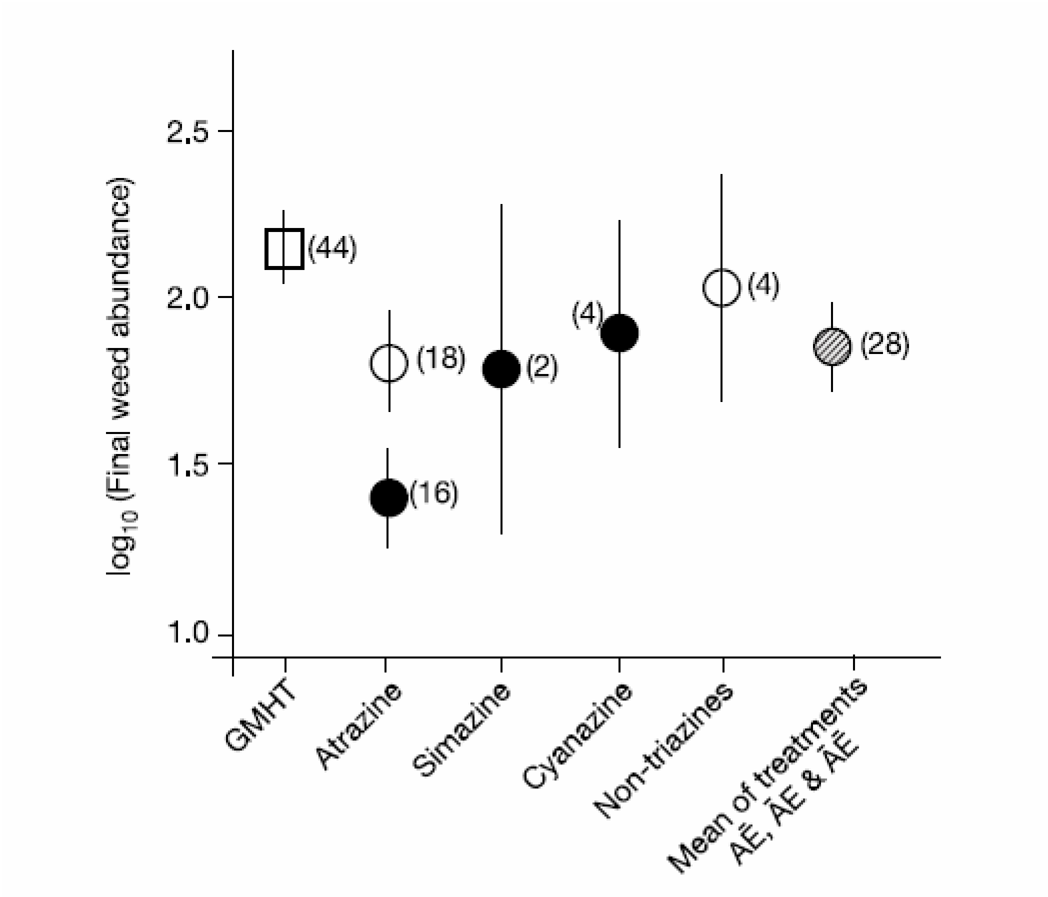


Figure 36: Mean abundance of total pre-harvest weeds and herbicide use. Consistent treatment effects from Table 2, illustrated here by mean abundance of total pre-harvest weeds in FSE fodder-maize per GMHT (square symbol) or conventional (round symbols half-fields, and treated either with pre-emergence herbicide plus possible postemergence application(s) (filled symbols, E) or with post-emergence herbicide only (open symbols, E). Hatched symbol represents the mean o the three conventional regimes AE , AE and AE: that is, all those other than atrazine applied pre-emergence. Numbers in brackets denote N, the number of half-fields. Bar represents 95% confidence interval for each mean.

This is the fig. from (Perry et al., 2004) explaining, why GM maize (the crop with best biodiversity performance in the trials) is still better performing than the non-GM maize treated with non-atrazine herbicides. Benefits for biodiversity with herbicide tolerant GM maize are obvious.

The GMHT crops have been planted in Great Britain for the first time and farmers actually have not been experienced enough to apply advanced techniques such as no tillage, which would have then given full advantage of the method. It is quite logical and has never been contested by anybody that the application of a broad band herbicide such as Roundup Ready would be very efficient in killing weeds, and as a consequence the biodiversity within the fields is reduced with all its followups, which have been studied in detail. The farm scale studies actually could be summed up in a simple message: no weeds → no insects and → no weed seed. In turn, no insects and no weed seed → no bird food. No bird food → no birds. But it is not that simple: First of all, we have again to realize that we are not dealing with natural habitats and even the sky larch is an artificial product of agriculture, as much as we all love the song of these unique birds. If that is so, then we will have all chances to manage better, since we are dealing with highly dynamic ecosystems. With only little change we will be able to get more biodiversity back to the fields by applying the appropriate methods. The Farm Scale experiments fail to take into account that management methods have changed in the US with the advent of GM crops. It is not appropriate to compare in a seemingly scientific way the two so different systems in fields divided into half. Experimental outlays in field research need to take into account the full potential of management in modern farming such as no tillage. Even seen as a true management experiment it is not done in a true farm scale manner: it fails to compare to yield and other input-output data, to residue analysis of conventional herbizides within the non-GM crop fields. It would have been possible to apply standard methods used in integrated pestizide management systems such as the Cornell Environmental Impact Formula (Kovach et al., 2003; Levitan, 2000; Levitan et al., 1995). Here just one example is cited (out of the overall comments of one of the author groups of the Farm Scale Experiments: (Squire et al., 2003)):

> „When, in the USA, large areas of crops were replaced by GMHT varieties, the profile of agrochemical inputs on the farm changed, the proportion of the land that was tilled before sowing sometime decreased, less chemicals were lost in leachates and run-off from the field, and, as glyphosate and glufosinateammonium are relatively short lived and of low toxicity to animals, the change in profile was considered to lessen the wider impact of farming (Carpenter et al., 2002; Phipps & Park, 2002) The chain of impacts was not the same for all crop species, and generalizations are difficult (Carpenter et al., 2002; Fernandez-Cornejo & McBride, 2002) "

If all those data would be available and a better adapted management would have been applied, results would not look so bleak for the Roundup Ready technology – this has been shown for economic data in Romania: Economically it is indeed rewarding to use the Roundup Ready technology. (Brookes, 2003). As a whole, the author is optimistic, that with the flexibility and simplicity of the herbicide tolerant crop method it will be easier to make progress (which has its limits there, where farmers do not like too much weed components in the harvest, since there are a number of problematic toxicity cases known connected to certain species in weeds (Damron & Jacob, 2003; Damron, 1998). With the incentive of the economic advantage farmers will agree more easily to do something extra for agricultural biodiversity in order to enhance conservation in arable fields. See also the chapters on (no-) tillage and pesticide use: (Mineau & McLaughlin, 1996; Nentwig, 1999). It will be rewarding to see the data of the Farm Scale experiments to be explored by more researchers – a laudable move by the Farm Scale research coordinators – especially if statisticians have a closer look at variation, dynamics and individual treatments. Some of those treatments could well reveal key data on how to enhance successfully biodiversity in the fields with GMHT crops. It is quite obvious, that in a first round researchers have concentrated on the first big question of comparing the two technologies as a whole and also with sound statistics of average values – average values which could have been achieved with less 'statistical overkill', and which of course bury the subtle details from which we could learn more. Having a closer look at variation related to the individual management methods would most probably also have the potential of projection into future strategies. As a whole, we encounter the same phenomenon often seen in scientific controversies on complex ecological issues: It is easy to loose sight and to pick out in a reductionistic manner data which fit to your own view, it is more difficult to keep an open mind and to analyze agricultural issues on biotechnology and biodiversity within a truly holistic approach. Chassy et al. comment that the really important questions have not been asked yet: (Andow, 2003; Chassy et al., 2003).

The scientific controversy about GM crops VI ↺

Summary of GM crop benefits related to biodiversity

At first sight and mindful of the recent English farm scale experiments (Firbank, 2003), GM crops are always related to negative effects on biodiversity, but it is not that simple as critics of the farm scale experiments reveal: (Chassy et al., 2003). The fate of biodiversity depends heavily on the herbicide management and varies from crop to crop. Fighting off weeds within the harvested crop is a necessity, and it is done with less labour and energy input with broad band herbicides in combination with herbicide tolerant crops – consequently, farmers will be encouraged to follow up strategies to enhance off-field biodiversity of the margins with a clear beneficial effect as proposed by (Nentwig, 1999).

There are clearcut biodiversity benefits shown in a field trial with Bt potatoes: (Reed et al., 2001):

See figure 30 next page.

Also, it has been shown that no-tillage strategies are easier put in place with herbicide tolerant crops and demonstrate considerable positive effects on the soil biodiversity (Elmegaard & Pedersen, 2001; Fawcett et al., 1994; Fawcett & Towery, 2002; Strandberg & Pedersen, 2002; Trewawas, 2003), see Fig. 20 from Elmegaard et al., and the comments on conservation tillage with the Fig. 8-12 from Fawcett et al. All those figures demonstrate the advantages of conservation tillage related to soil life and thus soil fertility overall.

Non-target insects are certainly better off in Bt crop fields, as has been demonstrated repeatingly, in this report in previous chapteres, see the figures 16, 17-19, 22, 29. Follow the keyword index on benefits.

Many other accounts and prospects of benefits have been described by (Kershen, 2002) on animals and manure, (Carpenter et al., 2002; Carpenter, 2001; Carpenter-Boggs et al., 2003; Dale, 2002; Gianessi et al., 2002; Gianessi & Carpenter, 2000; Hin et al., 2001; Phipps & Park, 2002) on environmental aspects in general. It is clear, that the reduction of pesticide use and the shift from environmentally problematic herbicides to degradable and environmentally more benign herbicides will on the long term also have beneficial impact on biodiversity. Reports such as (Benbrook, 2003) stating that GM crops have a negative balance in pesticide use (i.e. require in average more pesticides and herbicides) are based on selective use of statistics: It is the lower environmental toxicity related to GM crop growing which decides over the fate of biodiversity. (Parrott, 2004)

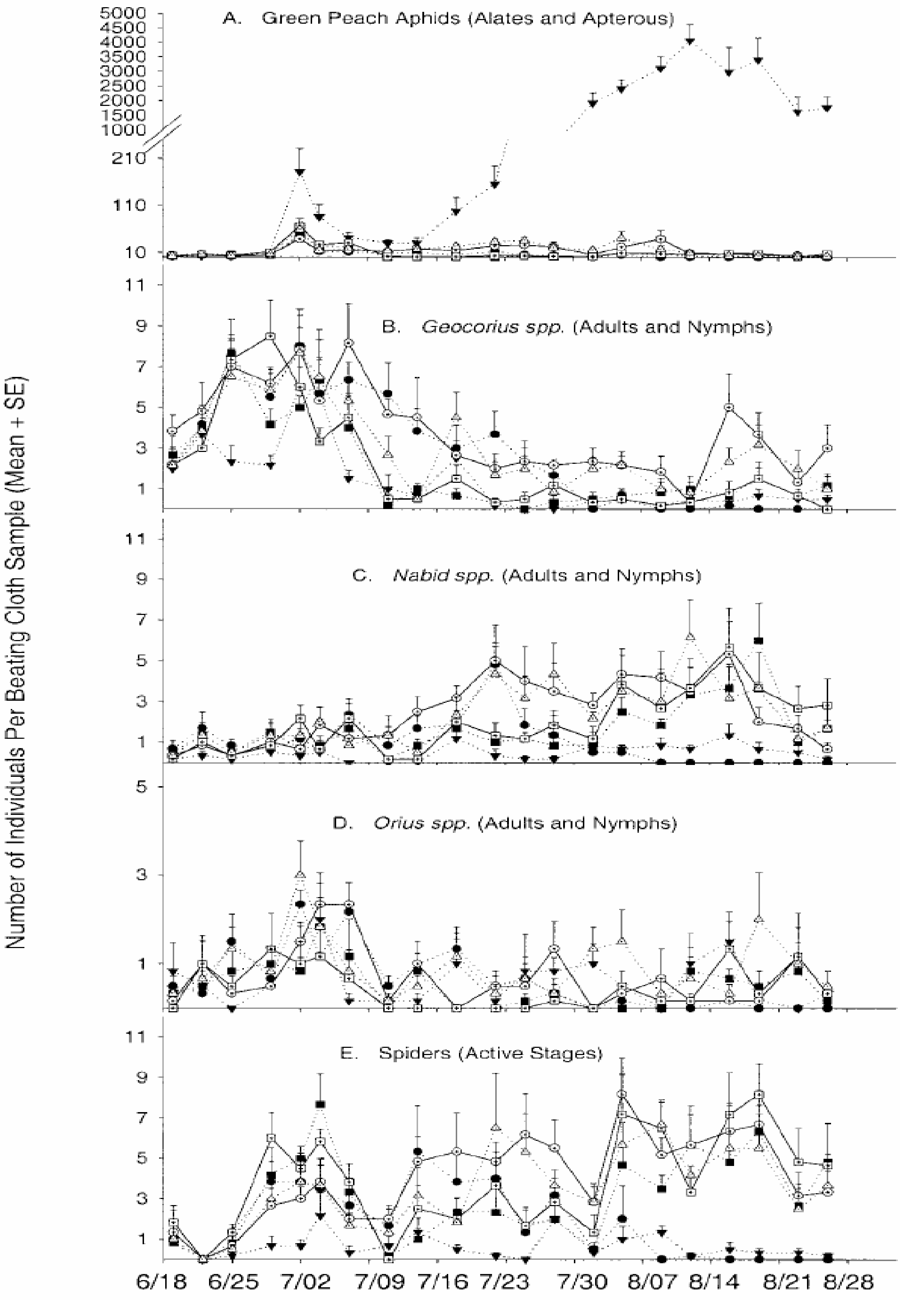
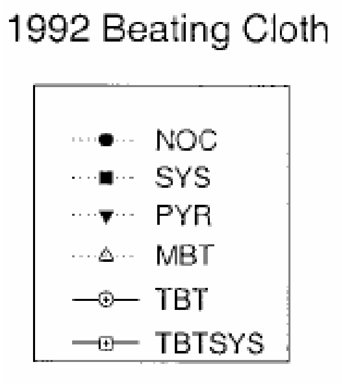

A. Green Peach Aphids (Alates and Apterous)
B. Geocorius spp. (Adults and Nymphs)
C. Nabid spp. (Adults and Nymphs)
D. Orius spp. (Adults and Nymphs)
E. Spiders (Active Stages)
Number of Individuals Per Beating Cloth Sample (Mean + SE)
6/18 6/25 7/02 7/09 7/16 7/23 7/30 8/07 8/14 8/21 8/28

Figure 37: Population dynamics of green peach aphids and major predators in different treatment plots sampled with beating cloths in 1992 field trial. Treatment description: NOC = conventional potato with no control measures; SYS = conventional potato with systemic insecticide treatments; PYR = conventional potato with pyrethroid treatments; MBT = conventional potato with microbial Bt sprays; TBT = transgenic Bt potato alone; TBTSYS = transgenic Bt potato with systemic insecticide treatments. (Reed et al., 2001)



The scientific controversy about GM crops VII: Generalities ↺

Interpreting science and the example of non-target insects in fields of transgenic and non-transgenic crops

Some basic remarks need to be made at the end of this chapter about some recent controversies: The background of many of the controversies are some more important misunderstandings about agricultural ecology (Ammann, 2004)

A fundamental, and unresolved issue for answering these questions is what data most effectively should be used to assess environmental impacts. This needs further investigation. As for now, some preliminary remarks must be enough: For a deeper understanding, we must delve into the distinctions between natural and agricultural habitats, the first of which is that agriculture is a human invention, with its purpose founded in serving human needs.

There is a widespread trend, even among learned ecologists, to treat agricultural systems the same way as natural ecosystems when planning, modelling or interpreting ecological field experiments. Although some of the same methods can be applied by comparing natural and agricultural sites, data interpretation must take care of some fundamental differences:

- Dramatically and artificially reduced biodiversity in agricultural sites (Altieri, 1991; Hutton & Giller, 2003; McLaughlin & Mineau, 1995; Pyke & Archer, 1991)
- Crops and many weeds are the result of man ingenuity.: Most agricultural weeds are not “wild species”. derived from millennia of selective adaptation. A good example is the widespread weed Galeopsis tetrahit see (Ammann et al., 2000a; Müntzing, 1930)
- Soils are often subjected to heavy tilling, significantly affecting soil microbial life Crop rotation is important in controlling levels of pests, but there is no close counterpart to this activity in nature.

- Commonly accepted inputs, such as fertilizers, herbicides, and other pesticides, effect environmental disturbance, which never occur at this level in natural habitats.

For these reasons it is not appropriate to apply the same ecosystem and biodiversity standards for comparison to both cases, although it is always important to compare them with the same scientific methods. Importantly, the risk conclusions are in many cases very different. Whereas a disturbance factor in the case of a natural system as alpine grassland can well affect the species composition over decades (Hegg et al., 1992), while agricultural environments are subjected to regular disturbances causing transient impacts that are measure primarily in terms of yields of output. We have to realize that there is no automatic symmetry in conclusions regarding the same phenomenon for both types of sites. Instead of applying the same interpretation standards, we should also differentiate in risk assessment.

Agricultural systems are highly artificial and certainly show a much higher dynamics through manifold farmer activities such as tilling, sowing monocultures, harvesting, crop rotation, to name the ones having the most dramatic impact on biodiversity.. This is why reports such as the one of Ecostrat, commissioned by Greenpeace (Hilbeck et al., 2000) are factually correct, but written as if standards of natural habitats could be taken as the scale on how safety standards should be applied to the new crops. For instance, the sequence and pace of disturbance and crop regime make the types of long-term assessments requested by Ecostrat near impossible to control experimentally and yield useful information for regulators. This does not mean that academics do not play an important role in examining basic ecological questions and expanding knowledge. It merely means that, in cases like agriculture, it would be imprudent to wait for these types of long-term experiments before launching any new, potentially beneficial technology such as GM. It is also interesting that, in the hindsight it is now clear that the trends have been interpreted correctly. (National-Research-Council, 1989; Sears et al., 2001a).

There are more reasons to pay more respect to agricultural dynamics and related long-term experience. There is a plethora of gene flow studies published to date, and it is very likely that more will be coming (Eastham & Sweet, 2002). As a botanist, I am compelled to remind the scientific community of the experience and hybridization data to be found in plant collections such as herbaria (Ammann et al., 2000b). An equally valuable source of practical information comes from the long term experience of seed producers, who have a strong economic interest to keep the seed lines genetically well defined for agricultural purposes. (OECD, 2003).

Finally, the challenge for regulators is to make decisions on real products in real environments within a realistic timeframe. They must include in their evaluation experience from agriculture based on traditional methods and crops. It is important to give thorough consideration to baseline comparisons between the traditional and GM crops and agricultural methods of all kinds. (Babendreier et al., 2003c)

However, this also has to be said: the Ecostrat report concentrates (see publication date!) on the early phase of US regulation, where field experiments were done for the sole purpose of getting approvals as swiftly as possible - but some of those early experiments lack indeed sound statistics and do not deal enough with the intricate ecological web of life in the production fields. In the hindsight it is clear that the trends have been interpreted correctly. Today, de Greefs rebuttal of the report is justified in the light of new field research:

(de Greef, 2000) „The environmental impact of Bt maize, including the impact on non-target insects, is part of this safety assessment and of ongoing work. The overwhelming body of scientific evidence supports the view that non-target insect populations are not at risk from Bt maize."

"compared to crops treated with conventional chemical pesticides, the transgenic crops have no detrimental effect on a substantial number of individuals in beneficial insect populations."

"The US Environmental Protection Agency (EPA) has recently released a Fact Sheet on Novartis Bt maize. In it, it outlines the evaluation done on Bt maize, including studies done on ecological effects and effects on non-target beneficial organisms. It includes a formal review of studies done by Hilbeck, one of the authors of the EcoStrat report, on the effects of Bt maize on the green lacewing, a beneficial insect. The EPA concludes, "the results of these studies do not support the conclusion that the Bt toxin was directly responsible for the observed differences in lacewing mortalities." Furthermore, they conclude "compared to crops treated with conventional chemical pesticides, the transgenic crops have no detrimental effect on a substantial number of individuals in beneficial insect populations."

Another typical case of questionable interpretation of scientific data is the report on the Chinese Bt cotton issued by Greenpeace: Again the problems are approached with the same wrong optics of mixing up natural and agricultural habitats. The report concludes wrongly, that Bt cotton in China has revealed to be a risky culture with lots of negative environmental impact (Xue, 2002), the rebuttal: (Gathmann & Bartsch, 2002), including several replies, also the one of Dr. Wu, who, as an author of the original study, has been misinterpreted by Greenpeace (He is a member of the National GMO Biosafety Committee). According to Dr. Wu, his results "strongly oppose the major conclusions in Greenpeace's report and do not support their views." Dr. Wu specifies in this reply results of Chinese Bt-research from 1997 to 2001, which show efficient pest-control and reduced chemical insecticide use by Bt- cotton. Just one example of the questionable perspective: The Greenpeace editors interpreting Wu's work seem not to be aware of the fact, that if pest insects are effectively controlled, their parasites also show a dramatic decline, which cannot per se be interpreted as a negative impact (Rufener Al Mazyad & Ammann, 2002). Finally, in this context it is worthwhile to mention the difference between basic ecological research done in the lab with forced feeding experiments - they reveal valuable insights in the food web and the basic toxicology related to certain transgenes (Hansen et al., 2001; Hilbeck, 2001). Those results need to be confirmed under real time and real locality conditions, as Sears has indicated (Sears et al., 2001a):

"Previous reports ((Hansen & Obrycki, 2000; Losey, 1999) indicating the hazard of *Bt* corn pollen to monarch butterfly are inadequate to assess risk, because assigning risk can be accomplished only when the likelihood of toxic response can be properly expressed and the likelihood of exposure is estimated through appropriate observations. We have used a comprehensive set of new data and a formalized approach to risk assessment that integrates aspects of exposure to characterize the risk posed to monarch from *Bt* corn pollen. Characterization of acute toxic effects alone indicates that the potential for hazard to monarchs is currently restricted to event 176 hybrids, which express Cry1Ab protein in pollen at a level sufficient to show measurable effects. Event 176 hybrids have always had a minor presence in the corn market and current plantings, which comprise, 2% of corn acres, are rapidly declining."

Other events either express negligible Cry1Ab protein in corn pollen (Mon810 and Bt11) or express Cry protein of significantly less toxicity to monarch (Dbt418, Cbh351, and Tc1507 expressing Cry1Ac, Cry9c, and Cry1F proteins, respectively). Chronic exposure to *Bt* pollen over the entire larval growth of monarchs has not been documented in these studies and may reveal sensitivity to Cry proteins not accounted for here. Monarch populations share their habitat with corn ecosystems to a degree previously undocumented (Oberhauser et al., 2001). Despite this, the portion of the monarch population that is potentially exposed to toxic levels of *Bt* corn pollen is negligible and declining as planting of event 176 hybrids is phased out through 2003. Because the effects portion of the risk probability equations described above (*P*t) is such a small value for the dominant corn hybrids currently planted, the sensitivity of the model to factors describing ecological exposure (*P*e) and for risk (*R*) will remain low. Evidence supporting this risk conclusion has been collected.

Evidence supporting this risk conclusion has been collected over a wide geographic area and under a variety of conditions in both laboratory and field settings (Hellmich et al., 2001; Oberhauser et al., 2001; Pleasants, 2001). Findings from studies done in multiple locations were consistent, even though methods differed from one study to another. This approach to risk characterization is consistent with accepted risk assessment procedures and shares many similarities with previous assessments over a wide range of situations describing potential risk associated with a described hazard. It is imperative that future conclusions concerning the environmental or nontarget impacts of transgenic crops be based on appropriate methods of investigation and sound risk-assessment procedures.

For more details about the case of the Monarch larvae see Chapter 'Genetically modified (GM) crops' ↺. Even though, field results have the potential to show great variation, which is shown as an example with Bt maize pollen deposition on leaves under field condition (Byrne et al., 2003).

What really counts in growing GM crops, is the actual impact under field conditions, and this impact has been shown to be negligible. For more details about non-target insects see the above introductory chapter on GM crops.

The US Environmental Protection Agency has concluded, that Bt crops pose no significant risk to the environment or to human health (Mendelsohn et al., 2003). And recently (Fox, 2003) circulated the news that surprisingly no Bt resistance has been found up to now in Bt crops.

A final remark should be made on the biocontrol of the European corn borer with Trichogramma, just to remind the reader that, if we want to be critical about Bt crops, we should apply here the same scientific rigeur. This has been done by (Bigler et al., 2002) and (Babendreier et al., 2003a, b; Babendreier et al., 2003c). Although the authors can denominate a certain risk that Trichogramma under field condition is also changing unexpectedly its host from the European corn borer to non-target insects such as various species of butterflies, they consider the risk under field conditions as low.

Conclusions of the Report as a Whole: ↺

Habitat loss and fragmentation represent the greatest threats to natural genetic diversity. Practices that increase the productivity of existing agricultural lands will help to limit these effects. (UNDP, 2001). GM crops can be useful in this respect. Preservation of the genetic diversity present in crop species is an important need being addressed by various public and private programs. In this respect, biotechnology can be a valuable tool for introducing novel genes or valuable genes from old cultivars. Furthermore, the development and introduction of GM crop varieties does not represent any greater risk to crop genetic diversity than the breeding programs associated with conventional agriculture. The view, early published by the (National-Research-Council, 1989), that “GM crops offer more precision in lab and field testing than conventional ones” has not been disproven to date.

The study concentrates on the impact of agricultural biotechnology on biodiversity, but in several chapters it becomes clear that biotechnology with its doubtless great potential can only play part of the game, and we need in future to dig into many other agricultural strategies to produce more and better food. Designing the best future solutions for food production certainly needs open minds and there is no doubt that we also should learn from traditional agriculture and recent trends like integrated and organic farming.

There are some caveats to be made in the above statements:

The positive outcome of the impact analysis of the report is restricted to the present day transgenes such as herbicide tolerance and Bt insect resistance. The future transgenes need to be scrutinized thoroughly case by case and transgene by transgene, and any transgenes producing pharmaceutical substances need of course special care in risk assessment.

Philosophically, a caveat should be entered about the discussion of all scientific results: Let’s cite Karl Popper (Popper, 1972) who wrote extensively about critical issues in the science world: He accuses those scientists who believe in a rather naïve way in facts alone:

> “For they say that only those things exist which can be observed. They do not realize that *all observation involves interpretation in the light of theories,* and that what they call 'observable' is what is observable in the light of pretty old-fashioned and primitive theories. Though I am all for common sense, I am also for enlarging the realm of common sense by learning from science. At any rate, *it is not science but dubious philosophy (or outdated science) which leads to idealism, phenomenalism, positivism; or to materialism and behaviourism,* or to any other of anti-pluralism.”

According to Karl Popper, falsifiability is the crucial feature of scientific hypotheses - and beliefs which can never be tested on the basis of empirical evidence are dogmatic.

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