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Transgenic Crops and Their Impact on Biodiversity

Worldwide an increasing share of agricultural land is being sown with transgenic seeds. Advocates of genetic engineering tout the potential of this technology to fight hunger, produce healthier food, secure higher yields, supply more biofuel and reduce pesticide use. Up to now, most of these promises have not been fulfilled. Instead, genetic engineering technology has accelerated the industrialization of agriculture – with some alarming consequences for agricultural biodiversity.

Johannes Kotschi

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Genetic engineering (GE) of crops is heralded as key technology to intensify agriculture in order to eliminate hunger, increase income and improve biofuel supply. Agricultural diversity, on the other hand, can be considered a global resource base for food and bio-energy, a resource that may be vital in responding to unknown future needs, such as adaptation to climate change (Kotschi 2007). Although both are important issues in agriculture, little attention has been given to their interrelationship. The main question is: How does GE technology impact on biodiversity? Is it beneficial, neutral or detrimental? This article reviews scientific evidence on biological and economic changes from the use of genetically engineered, or “transgenic” crops, and investigates their impact on biodiversity. The short article cannot be comprehensive. However, it highlights the most important features and illustrates them presenting a few examples. Since the majority of plant genetic resources is located in tropical and sub-tropical regions and is largely preserved by small farmers, it focuses on smallholder agriculture in developing countries.

The Distribution of Transgenic Crops

The estimated global distribution of transgenic crops is presented in table 1 (James 2006). This information is published annually by the *International Service for the Acquisition of Agri-biotech Applications (ISAAA)*, a biotechnology-promoting network. No other sources are available, and some researchers consider the

figures to be inflated (Ashton 2003, Robinson 2004, Zarzer 2006, López Villar et al. 2007). Nevertheless, they may give an indication of the distribution of genetically modified organisms (GMO) by crops and by countries.

Four crops account for 95 percent of all transgenic varieties planted: soybean, maize, cotton and canola. Most are grown for industrial purposes or as animal feed. Approximately 40 percent of the acreage under transgenic crops is in developing countries, and this share is concentrated in only six countries: Argentina, Brazil, China, India, Paraguay and South Africa (table 1).

A third feature also deserves consideration. Until now, only two genetically induced traits have gained commercial importance: herbicide tolerance (HT) and pest resistance through insertion of a gene from *Bacillus thuringiensis* (Bt).

Do Transgenic Crops Contaminate Genetic Resources?

After a transgenic plant is released from the greenhouse to the field, it cross-pollinates with other varieties and sometimes even with wild relatives. The case of Mexican maize (see box) is a well-known example. This pollination, followed by “introgression” of transgenes, is irreversible and difficult to limit regionally.¹ Pollen can spread much further than expected. For instance, Watrud et al. (2004) measured distances of up to 21 kilometers for pollen of transgenic grass (*Agrostis stolonifera*). Greater distances

Contact: Dr. Johannes Kotschi | Johannes Acker 6 |
35041 Marburg | Germany | Tel.: +49 6420 822870 |
E-Mail: kotschi@agrecol.de

¹ *Cross pollination*: pollination between different varieties or strains of a plant species; *introgression*: DNA from one plant is stably incorporated into the genome of another plant and can be inherited to the following generations.

were assumed but not quantified. This makes the coexistence of transgenic crops with non-transgenic crops very difficult.

Another question remains controversial. Is the introgression of transgenes a threat to genetic diversity, or an enrichment? According to the International Maize and Wheat Improvement Center (CIMMYT 2002) and referring to the Mexican problem, landraces of maize may change as they frequently do through cross pollination with other (new) varieties. Through this, they do not disappear and in fact, with the transgenes, they can become even more diverse. On the other hand, all Centers of the Consultative Group on International Agricultural Research (CGIAR) are advised by FAO (2007a) to do everything possible to avoid unintentional transgenic introgression into their *ex-situ* gene bank collections. Obviously this is an unsolved policy issue within CGIAR.

Distinguished molecular biologists have raised their voices to explain the risk of genetic engineering (Gould 1993, Strohmman 1997). They argue that the regulation of living organisms and their traits is much more complex than supposed by the present paradigm of genetics. When the *Human Genome Project* revealed that *Homo sapiens* does not have a significantly greater number of genes than a simple plant or an earthworm, a renowned biologist at Harvard University wrote: “The collapse of the doctrine of one gene – one direction from basic codes to elaborate total-ity, marks the failure of (genetic) reductionism for the complex system we call biology” (Gould 2001). Meanwhile, the globally operating research project *Encyclopedia of DNA Elements (ENCODE)* has provided evidence that not only is the tiny fraction of the DNA consisting of those genes that are translated into proteins important for cell function and evolution, but also the vast amount of what has previously been termed “junk DNA”. These parts of the DNA so far had no value for GE scientists and were thus regarded as unnecessary for the understanding of organisms and for GMO risk assessment. The *ENCODE* project stated that, “al-

TABLE 1: Estimated global distribution of transgenic crops by crops and by countries. Source: James (2006).

| global distribution of transgenic crops | million ha | % |
|---|--------------|--------------|
| by crops | | |
| soybean | 60.0 | 58.8 |
| maize | 20.1 | 19.7 |
| cotton | 12.1 | 11.9 |
| canola | 5.0 | 4.9 |
| other | 4.8 | 4.7 |
| by selected countries | | |
| Argentina | 18.0 | 17.6 |
| Brazil | 11.5 | 11.3 |
| China | 3.5 | 3.4 |
| India | 3.8 | 3.7 |
| Paraguay | 2.0 | 2.0 |
| South Africa | 1.4 | 1.4 |
| Canada | 6.1 | 6.0 |
| United States | 54.6 | 53.5 |
| other | 1.1 | 1.1 |
| total world | 102.0 | 100.0 |

BOX: The Case of Transgenic Maize in Mexico

Around 10 000 years ago, maize was discovered and domesticated in the Oaxaca region of Mexico. Since then, an abundant diversity of landraces has been developed; hundreds of local subvarieties represent a unique genetic diversity of maize, maintained largely by smallholders and “on-farm”. Today Mexico probably has the richest maize gene pool in the world: “Farmers and crop breeders worldwide depend on the genetic diversity stored for all of humanity in the local maize races developed over 9 000 years by indigenous people and peasant farmers in Mesoamerica” (Rosset 2002).

With the commercial use of transgenic maize varieties in North America, the government of Mexico issued a moratorium on genetically modified (GM) maize in 1998, but did not take further action to control or define conditions for maize imports (e.g. labelling of genetically modified organisms). Transgenic maize entered the country in various ways. Large North American food imports of non-segregated varieties that contained 30 percent or more GM maize made up the major share.

In 2001 evidence was produced that GM varieties had introgressed into the genome of landraces of maize in southern Mexico (Quist and Chapela 2001), a finding that was later confirmed by other research teams (CEC 2004).

though we have good models for how protein-coding regions evolve, our present understanding about the evolution of other functional genomic regions is poorly developed. Experimental studies that augment what we learn from evolutionary analyses are key for solidifying our insights regarding genome function” (ENCODE 2007, Sample 2007). It can be assumed that these findings are not restricted to the human genome but also apply to animals and plants.

In addition, unexpected phenomena and unintentional changes of GE organisms query the paradigm of genetic determinism. For example, “Roundup Ready” (RR) soybeans – soybeans resistant to the herbicide Glyphosate – have up to 20 percent higher lignin content. Therefore, it is assumed that the new gene influences lignin metabolism. The change in lignin content has a negative influence on heat tolerance, which in turn results in lower yields of transgenic soybeans under heat stress (Gertz et al. 1999). Many more unintended effects have been reported (Liebman and Brummer 2000, Haslberger 2003). Genetic regulation is obviously more complex and dynamic than commonly assumed. It goes beyond single genes and is implemented by a network. Secondly, its traits appear to be dynamic as they change over time. The term “epigenetic” has been established for this phenomenon, and a growing number of molecular biologists are demanding a paradigm shift from genetics to epigenetics (see figure, p. 38).

This has far reaching implications for the impact of transgenes: They may create fundamental disturbances in the overall physiology of a living organism, and sometimes with a substantial time lag (Wilson et al. 2006). If this holds true, genetically engineered crops contain unknown risks and the unintentional introgression of transgenes must be considered a genetic contamination of plant genetic resources.

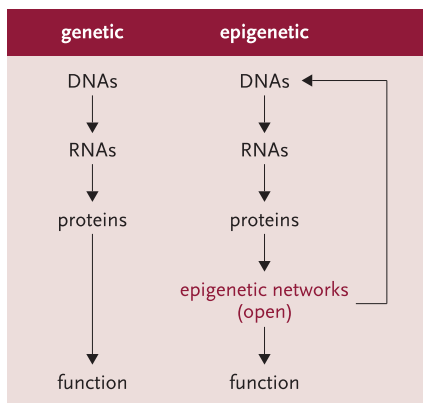


FIGURE: Genetic and epigenetic theories of information processing (Strohman 1997). According to epigenetic theory, cell functions are regulated not only by DNA and in a one-way process but by an open network of cell components and with a feedback cycle. In addition, acquired functions can be stored in other cell components except DNA and inherited.

Does Herbicide Tolerance Affect Biodiversity?

In the mid-1990s transgenic soybean varieties were introduced in Argentina. RR soybeans allow fully mechanized production. With herbicidal weed control, no-till techniques were applied more often, cropping became easier, production risks were reduced and moderate yield increases achieved. But the main reason for adoption was that less agricultural skill is required. “Farming without farmers” became possible and large acreages could be managed by only one person.

In Argentina, a country with an already high share of industrial soybean production, the RR technology accelerated the ongoing drastic changes to land use and farming systems. Within ten years (1994/95 to 2003/04), the acreage under soybeans has increased from six to 14 million hectares, the share of transgenic soybeans from zero to 99 percent. In addition, the government of Argentina aims to increase the soybean acreage by another four million hectares until 2010 (Lopez 2003). As a result, the diversity of landscapes and farming systems has been reduced significantly (table 2). “The rapid shift of land to soybean production eroded two traditional sources of strength in the Argentinian agricultural sector – the coupling of livestock and crop production on the same farm, and second, adherence to diversified rotations needed in order to break pest and disease cycles and sustain soil productivity. (...) Farmers are increasingly growing a single crop, soybeans” (Benbrook 2005).

According to national statistics, food production has fallen significantly. For rice and potatoes a reduction of 40 percent and 38 percent respectively has been recorded (Domínguez and Sabatino 2003), even higher losses have been observed for vegetables, and a similar trend has been observed for animal products such as milk, eggs and meat (Jacobson 2005). This socio-economic change has a strong impact on biodiversity: The mixed farming systems of smallholders are gradually disappearing, and they are being replaced by large monocropped fields.

Furthermore, there is growing concern that the herbicide Glyphosate has a negative impact on soil microbial communities. In the United States it was found that the intensive use of Glyphosate led to increased levels of the pathogen soil borne fungus

Fusarium (Means and Kremer 2007) and had an adverse impact on soybean root development and nitrogen fixation (King et al. 2001, Zablotowicz and Reddy 2007).

Does Bt Technology Reduce the Negative Impact of Cropping on Biodiversity?

The incorporation of bacterial DNA from *Bacillus thuringiensis* (Bt) into agricultural crops promised to reduce pesticide application and alleviate damage to the fauna of agro-ecosystems. Many studies from the early years of using Bt crops – cotton in particular – stated that pesticide use was substantially reduced, costs of production decreased and net incomes were improved (e. g., Qaim and Zilberman 2003, Traxler et al. 2003). A reduced negative impact on insect biodiversity (compared to conventional production) was observed in farm scale field trials by Cattaneo et al. (2006).

Meanwhile the picture has changed. For instance, in a study of 481 farms in five provinces of China, researchers from Cornell University found that such benefits of Bt cotton had completely disappeared. “A majority of Bt cotton farmers cited the fact that they must spray 15 to 20 times more than previously to kill secondary pests, Mirids, which did not require any pesticide in the early years.” Further, farmers spent the same amount on pesticides as non-Bt growers and about two to three times more on seeds (Wang et al. 2006). A similar finding is reported from the Makhatini Flats, the leading Bt cotton area in South Africa (Hofs et al. 2006), and the authors state that Bt cotton has not generated sufficient income to achieve a significant and sustainable socio-economic improvement. Finally, a much more comprehensive evaluation of 47 peer reviewed articles on the economic impact of Bt cotton on farms in developing countries concludes: “... the overall balance sheet, though promising, is mixed. Economic returns are highly variable over years, farm type and geographical location” (Smale et al. 2006).

In summary, it can be concluded that the incorporation of the Bt gene into crops does not reduce pesticide use in the long term, and there is an increasing number of cases which show more intensive pesticide use. Another issue of concern is the impact of Bt toxins on beneficial insects and soil microorganisms, but the results achieved so far are not yet conclusive. At best, the impact of Bt in cotton on biodiversity is neutral compared to conventional cropping systems.

TABLE 2: Land use changes in Argentina: Land newly planted with soybeans (1996 to 2004). Source: Benbrook (2005).

| land use before soybean production | % of total area newly under soybean |
|--|-------------------------------------|
| major crops: wheat, sorghum, maize, sunflower | 25 |
| other crops: rice, cotton, oats and beans etc. | 7 |
| pasture and forage production | 27 |
| forest and savannah | 41 |

Changes in Seed Supply and Access to Breeding Material

Monopolized seed supply and growing corporate control over genetic resources probably have the greatest impact on biodiversity. Within the past 25 years an unparalleled concentration of the seed sector has taken place and a worrying shift from the public to the private domain can be observed (GRAIN 2007). “Based on 2006 revenues, the top 10 seed corporations account for 55 % of the commercial seed market” (ETC 2007). As far as transgenic crops are concerned, only one company – Monsanto – provides seed for approximately 90 percent of the total area under transgenic crops, with the right to claim licensing fees on every single hectare and for every cropping cycle. This quasi monopoly creates dependency among farmers. At the same time it leads to genetic uniformity of cropping systems as reported, for instance, from the United States: “For many farmers across the country it has become difficult if not impossible, to find high quality, conventional varieties of corn, soy and cotton seed. Making matters worse, the direction of land grant university research has been shifting away from producing conventional seed varieties

and toward biotech applications. Research on conventional crops is now minimal and patents have replaced public ownership of these new varieties” (CFS 2004).

Needless to say, the monopolization of the seed sector is not caused by biotechnology. But biotechnology has accelerated and reinforced this process. One main reason is that the breeding costs for GE crops are extremely high; the necessary investment can only be borne by larger companies. These companies are increasingly required to take advantage of economies of scale, which implies that they are interested in distributing a standardized variety or a whole cropping technology as widely as possible.

A second aspect is no less worrying: the increasing control of genetic resources by a few companies through patents on genes. In the past, genetic material for breeding purposes has been in the public domain. Today, it is becoming increasingly inaccessible without the permission of patent holders. By granting or withholding their permission, they have a strong influence on breeding programmes and strategies. During the past 25 years a shift of fund allocation towards GE breeding has been observed in the private and the public sector, whereas “... all over the world, conventional plant breeding has fallen on hard times, and is seen

Small farmers in Mexico cultivate and preserve a large variety of Maize landraces, probably the largest maize gene pool in the world. Cross pollination with genetically modified seeds poses an unknown risk to the overall physiology of traditional landraces and to the maize gene pool in general.





Genetic engineering has accelerated the industrialization of agriculture and may lead to a contamination of genetic resources by transgenes. The picture shows a variety of local vegetable seeds presented by a group of smallholders in India.

as the unfashionable older cousin of genetic engineering” (Knight 2003). Today, the concentration in the seed sector can be considered the most serious factor responsible for the reduced genetic diversity of agricultural crops.

Conclusions and the Way Forward

As a main conclusion it can be stated that transgenic crops have accelerated the industrialization of agriculture and have thus amplified the negative impact of farming on biodiversity. In addition, biodiversity is now exposed to a new and unpredictable threat: the contamination of genetic resources by transgenes.

The question in this respect is whether such biodiversity “sacrifices” are necessary to address future needs. So far most of the promises of GE protagonists – to reduce global hunger, for instance – have not been fulfilled. Neither drought resistance, nor salt tolerance, nor yield increase for food crops has become a reality from genetically engineered breeding. Most of the progress in plant breeding has been achieved by conventional methods (Meyer 2007).

Another question is whether existing transgenic crops have the ability to perform better than non-GE crops. Scientific comparisons often show a bias when selecting an appropriate reference system. GE cropping technologies are usually compared with outdated technologies. The sector of cotton production may illustrate this. Pesticide savings and yield increases through Bt cotton are measured in comparison with conventional cropping systems. This reference system will automatically give Bt cotton an advantage. The task should be to compare GE cropping systems with other innovative breeding and production technologies that have emerged within the past 20 years, parallel to the GE cropping technology. Two such innovations can be considered success stories in cotton production. One is *Integrated Pest*

Management (IPM) (Russel and Kranthi 2006 a and b), and the other is Organic Agriculture (Eyhorn et al. 2007, Williamson et al. 2005, Blaise 2006, Lanting et al. 2005). Both *IPM* and Organic Agriculture are economically competitive and environmentally friendlier; they work with reduced or no synthetic pesticide input, and they enhance biodiversity (FAO 2002).

Marker assisted selection (MAS) is the third innovation that merits attention (Bernardo and Yu 2007, FAO 2007b). Gene markers are used to identify desired traits more easily, a method that can already be adopted in the seedling stage of a plant. *MAS* speeds up the selection process enormously, and allows wild relatives to be included more easily. It has upgraded classical breeding and is intensively used by almost every major seed breeding company.

The performance and competitiveness of GE technology must always be appraised in comparison with the best technologies at hand and, in addition, be based on thorough risk assessment of GE organisms. In general, we must bear in mind that biodiversity is an indispensable resource. Agricultural intensification must not proceed at its expense but must be harmonized with biodiversity conservation. Ecological innovations as described above offer a reasonable chance of achieving this.

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Johannes Kotschi



Born 1949 in Düsseldorf, Germany. Dipl.-Ing. agr. in Agronomy and Soil Science from the Technical University Munich. Doctorate in Agricultural Ecology and Organic Agriculture from the Justus Liebig University Gießen in 1980. For more than 20 years independent advisor to national, international and civil society organisations in rural development with a focus on natural resources management and Organic Agriculture. Co-founder of AGRECOL – Association for AgriCulture and Ecology.