

ASSESSING ECOLOGICAL RISKS AND BENEFITS OF GENETICALLY MODIFIED CROPS

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Abstract: Genetically modified (GM) crops and biotechnology are providing new opportunities for increasing crop productivity and tackling agriculture problems, such as diseases, pests and weeds, abiotic stress and nutritional limitations of staple food crops. As GM crops are being adopted in various locations with different ecosystems, a scientifically based understanding of the environmental effects of cultivations of GM crops would assist decision makers worldwide in ensuring environmental safety and sustainability. In this paper are discussed some of the most important problems related to the GM crops into the environment such as: plant protection, hybridisation, ecological effects of HRCs, gene flow, biodiversity, stress, ecological risks (ERA), effects on the soil ecosystem etc.

Key words: GM crops, biotechnology, environment, plant protection, HTG, biodiversity.

Introduction

Through the plant selection history, new gene combinations have regularly been included. Integrations of technologies contributed most to the genetic improvement in yield, adaptation to the environment (Dale, 2002; Stewart, 2004; Wesseler, 2005; Garcia and Altieri, 2005), resistance toward parasites and pests, as well as regularly demanded quality improvement by industrial food producers and consumers. Molecular biology investigations and genetic engineering can have undesirable influence on the environment (Conner et al., 2003), human health and economical level of increasing poverty (Figure 1). In the following period more attention has to be paid to the commercially and economically justified use of GM

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crops in agricultural food production (Bošković et al., 2001; Bošković et al., 2006; Bošković and Isajev, 2007; Prijić et al., 2008). The link between science and politics should be important for the common assessment of adoption and widening of GM crops.

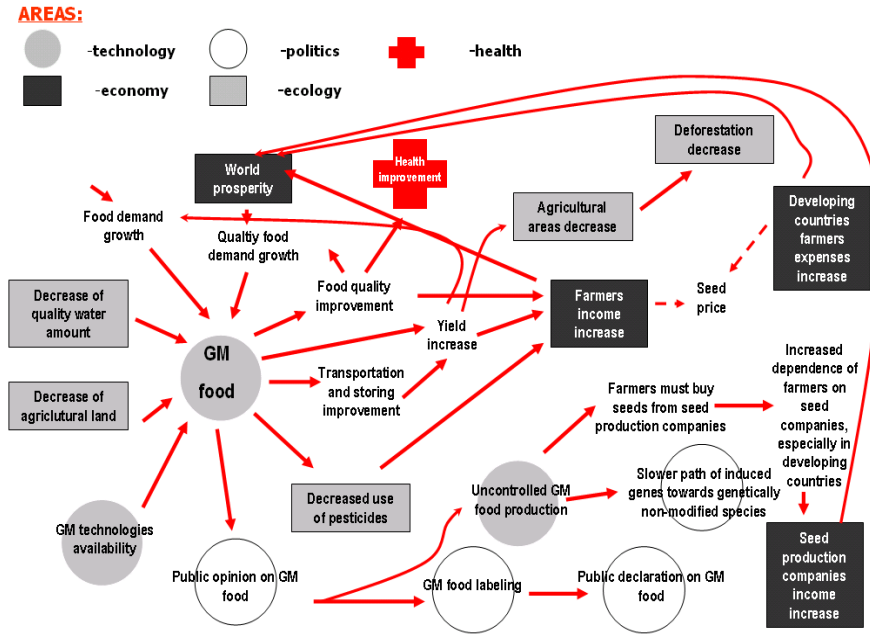


Figure 1. Possible effects of GM food (Bošković et al., 2004).

Horizontal gene flow

Horizontal gene flow (HTG) is the transfer of the genetic material between cells or genomes that belong to different species, and these are processes that differ from the common reproduction (Richardson and Palmer, 2007; Pontiroli et al., 2009). In basic reproduction processes genes are transferred vertically from parents to offspring. Bacteria are known to participate in gene exchange between different species in nature. It is performed in three manners: during conjugation when genetic material passes between opposite cells, by transduction in which genetic material is transferred from one cell of infective viruses into another and by transformation in which genetic material is taken over directly from the cell and its environment (Daniell, 2002). For successful HTG foreign genetic material must become part of the cell genome, or to be maintained stable in the recipient cell of the other form (Bock, 2009).

There are many potential pathways for HTG in plants and animals. Last investigations in gene therapy indicate potentially high importance of transformation for mammal cells, including humans. Direct transformation is not so significant for plant cells that have protective cell walls. However, soil bacteria that belong to the genus *Agrobacterium* are able to transfer T (tumor) segment of its induced tumor (Ti) plasmid into plant cells in the conjugation process. This Ti-DNA is widely used as a resource of gene transfer in plant genetic engineering. Foreign genetic material from insects and arthropods with strong mutagenic reactions can also be built into plant and animal cells (Mitreva et al., 2009). Additionally, bacterial pathogens that penetrate into plant and animal cells can take over foreign genetic material and carry it over in cells as vectors, probably to any kind of organisms on the planet.

Recording of horizontal transgenic DNA transfer

Transgenic DNA is probably more widening, as it was found for the widening of the HTG. There are molecular data that prove structural stability of transgenic DNA, with regard to its location, point of penetration into genome and gene arrangement into following generations. In fact transgenic can be stabilised in successive generations or lost as a whole. Gene for tolerance toward herbicides incorporated into *Arabidopsis* with vector can be 30 times more oriented to avoid vector, and it widens as well as the identical gene obtained by mutagenesis. Obtained results suggest that it can happen with the secondary horizontal gene flow over insects that visit plants for pollen and nectar, and that pollen can transfer transgenic DNA to bacteria into the bee larvae gut (Snow et al., 2004).

It has been experimentally confirmed that secondary horizontal transgenic and gene resistance markers transfer to antibiotics in genetically modified plants in soil bacteria and fungi is possible. Successful kanamycin resistance gene markers to the soil bacteria *Acinetobacter* were achieved by use of extracted total DNA from homogenised plant leaf from the list of transgenic plants: *Solanum tuberosum* (potato), *Nicotiana tabacum* (tobacco), *Beta vulgaris* (sugar beet), *Brassica napus* (canola) and *Lyopersicum esculentum* (tomato). It has been evaluated that about 2500 copies of kanamycin resistance genes are enough for a successful transformation of bacteria, regardless if there are 6 millions of folded strands of the present plant DNA.

Above all, genetic material taken from dead and living cells resists all outer conditions, it does not dissolve nor devastate as it has been previously assumed. This indicates the claim that sand, humus acid parts and plant debris enable infections with more microorganisms in soil. Bacteria transformation in the soil from absorbed DNA into sandy clay has been confirmed by experiments on microorganisms.

Since 1993 researchers in Germany have started a serial of experiments for acceptance of the rhizomania resistant transgenic sugar beet plants that contained gene marker for resistance to kanamycin, stability of transgenic DNA and horizontal gene flow of transgenic DNA into the soil bacteria.

Thus, horizontal gene flow represents a leading phenomenon that occupied significant place in the evolution of species, and it is still today (Knispel et al., 2008). This suggests that natural horizontal gene flow represents a regulated process, limited by specific obstacles and mechanisms that reject and inactivate foreign genetic material. Genetic engineering created great variability of artificial construction for overcoming barriers among all kinds of organisms and overwhelming all genomes.

Plant Protection and GM crops (GMCs)

Main considerations of GMCs use for plant protection are possibilities of incorporation of resistance in protection from insects, viruses, with stress to the main problem of long-term resistance (Bošković et al., 2000). Pest plant protection by genetic modification is use of Bt toxins, that has been successfully used as a spray for years; in different plant species (tomato, tobacco, cotton, etc.). GM plants provide great possibility of benefits to the environment by reduced pesticide use, development of pest resistance. However, these advantages can be quickly denied: these are possible strategies of reduction in exposure of pests to transgenic products, thus lowering resistance level and applying restricted transgene action (Bouchard et al., 2003; Nunes et al., 2006).

Application of genetic modification in control of fungal and bacterial plant pathogens has also been developed (Bošković and Bošković, 2001). As in case of pests the main problem is transient resistance and complex of interactive relations of pathogens and hosts. This resistance has been attempted to be improved by use of GM plants. In addition to this, strategies for multiple resistance, i.e. pyramiding resistance genes toward differing virulence of plant parasites have also been needed to be searched for (Bošković et al., 2004; Bošković et al., 2008a, b, c; Bošković and Bošković, 2009).

Tolerance and plant resistance to herbicides (HRC)

Herbicide tolerance can be achieved through increase of protective mechanism, by reduction of herbicide uptake, by degradation or reduction of susceptibility. Herbicide tolerance genes are widely used as markers in transgene plants selection (Knispel et al., 2008). If genes are of different tolerance to herbicides, developed or incorporated into the identical plant species, they could

stipulate creation of weeds with multiple resistance genes (Dewar et al., 2003). Hybridisation of plants resistant to herbicides (HRC) with populations of wild relatives makes these plants complicated for control, especially if they possess resistance to widely used herbicides (Altieri, 2000). Transgene plant resistance to herbicides makes chemical control easier, above all because it includes compounds that are active in very wide spectrum of weed species (Konstantinović and Bošković, 2001).

Non-cultivated populations of transgenic plants and gene flow

In some cases of cultivated crops, i.e. rye, difference between non-cultivated and natural population is unclear, whereas in case of the other species settlement is not extensive and there has probably been no harmful influence for non-cultivated plant species (Anderson and Carmen de Vicente, 2010). Possibilities of gene flow from trial field with GM plants through pollen will depend upon sexual compatibility between GM crops and their wild relatives, and possibilities for pollination and obtaining of seed (Pretty, 2001; Poppy and Wilkinson, 2005).

Frequency of this occurrence will be influenced by important spatial isolation between GM crops and suitable recipient that depend upon method of pollination, wind or insects, isolation in time, i.e. flowering season. The experiments have been carried out in order to determine rates of cross pollination between potato and non-GM potato planted in different spatial distance from each other.

These results have been well harmonized with each other, and both show that transgene movement outside GM trial field has been neglected at distance less than 10 m, and low rates of cross pollination that is usually present in potato have also been harmonized.

On the other hand, in canola seed the compatible inbreeding is present. It can produce huge seed quantities and it is pollinated by wind and insects. Pollination at huge distance happens probably due to the insects; air born pollen can be found 30-50 m away of canola plants, but it is reduced by distance. Experiment of field trial type that uses GM or non-GM plants can provide useful data in regard to necessary isolation distances that are used in order to avoid release of transgene. However, trials on natural populations suggest that in fact the situation could be more complex, and under-classifications of a local population can strongly influence the transgene incorporation into wild populations (Dale, 2002). Interpretation of the results has been also complex, and emphasis is on significance of calculation of changes in rates with distance of GM trial field, rather than absolute percentage of GM seed on the given distance from the field. Further work on spreading genes in populations can be necessary during assessment of the potential transgene dispersal. World group for wheat identified three crops that

have sexually compatible weed relatives for which it is probable that they will be subject to gene transfer in agricultural systems. Breeding by pollination or production of fertile hybrid varies from case to case. If chosen characteristics have positive advantage, introgression of new characteristics into existing weed population is still possible. Risk of environmental damage is then dependable upon weed habitat. These studies suggest that in assessed complexes of weed-crops in which habitats of weed relatives have been restricted to agricultural systems there are no possibilities for this new trait to endanger natural ecosystems (Creswell et al., 2002; Lu and Snow, 2005).

Hybridisation

Hybridisation between transgenic or conventional plant species and sexually compatible relatives occurs in many crops and produces new forms of weeds in obtained populations. In numerous papers this hybridisation has a detailed description and it can be expected that transgenes will transfer even over great spatial and significant obstacles of genetic incompatibilities (Perry, 2002). In some systems, an accidental transfer of transgenes by hybridisations seems unavoidable. However, in other cases it is not clear if hybridisation is proportionally limiting phase in transfer of transgenes. It is the assumption that hybridisation can even be proportionally limiting in some circumstances, i.e. when hybridisation occurs over significant obstacles of incompatibility. Aspects of weed ecology that can influence hybridisation levels in these situations include weed cropping systems and effects of spatial and timely distribution of weeds in several phases.

Selection system between weeds in field agro ecosystems of crops is mixed system of fertilisation in which inbreeding and cross fertilisation (outbreeding) occur, although the other reproductive system has also been known. Therefore, the widely distributed systems of weed selection enable hybridisation, but such fertilisations must happen during a significant level of inbreeding. Weed density can have counter effect on the hybridisation levels, when plant serves as female parent. In this case, high densities can favour hybridisation with advantage of achievement of great local weed pollen densities, and homogenous weed density can reduce plant hybridisation.

Impact of GM plants on biodiversity

One of the restrictions for introduction of GM plants into the environment is the influence of these plants, and even their devastation of biodiversity (Abud et al, 2007; Ferry and Gatehouse, 2009). Fear for loss of biodiversity is important base for withstanding of several influenced scientific groups from the world for

environmental protection that are against genetic modifications and GM plants. Influence of GM plants on biodiversity is complex and complicated problem (Figure 2). Scientific discussions and studies have been directed toward delimitation if GM crops influence the biodiversity and what qualitative and quantitative differences are from commercial crops. Biodiversity is very important for survival, regulation and maintenance of global planet conditions that give aesthetic, scientific, cultural and other values. Global value of the world biodiversity is assessed on about 33 trillions \$ annually (Constanza et al, 1997). In regard to multidimensional complexity of biodiversity concept, taking into account significance of technological development of GM plants, further studies that will even more clarify this interdependence are needed (Khachatourians et al., 2002). In broader sense it will be social-economical and political context of genetic modification application that will determine if hitherto risks or potential advantages of GM plants to biodiversity can become reality (Snow et al., 2005).

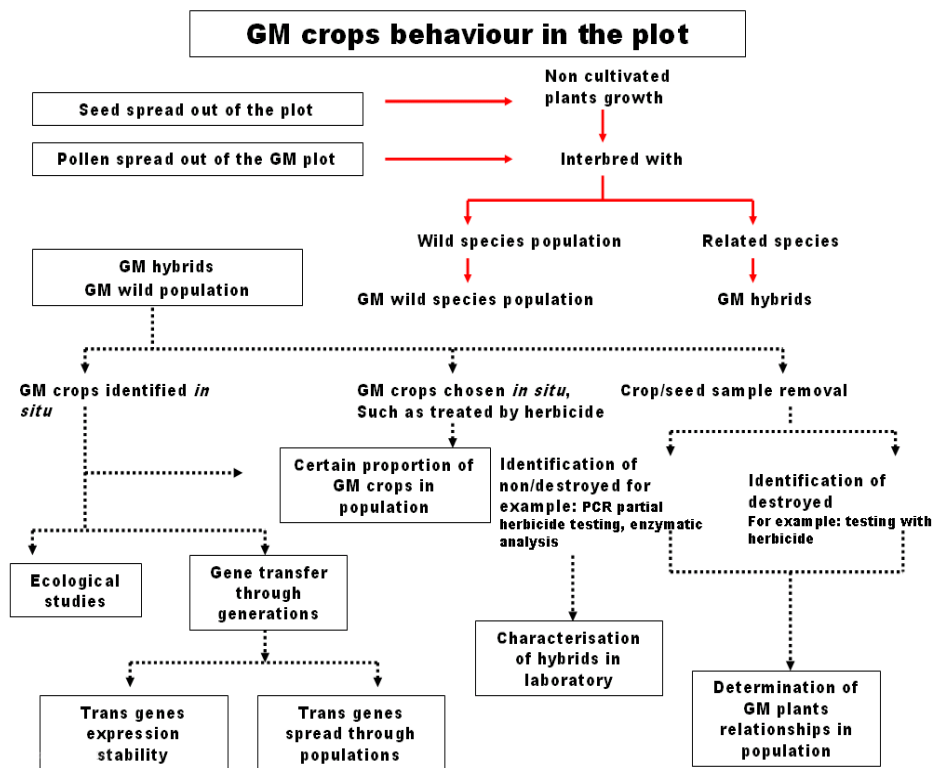


Figure 2. GM crops behaviour in the plot.

Monitoring

Genetic engineering development of several crops carrying useful traits has become a reality (Nunes et al., 2006; Faria et al., 2006; Clive, 2008, 2009), (Figure 3, Table 1). Ecological monitoring of GM crops in complex ecosystems is needed even after commercialisation (Bošković et al., 2003). This complexity varies from year to year and indicates indirect biotic effects. As laboratory and field experiments can not sufficiently repeat all interactions that occur in one ecosystem, the only way for evaluation of the full level of ecological effects of GM plants is monitoring in natural ecosystems. Some of these effects cannot be predicted in advance, so that ecological monitoring will be needed to reveal and differentiate existing ecological influences (Altieri, 2000; Dale, 2002).

Table 1. Global area of biotech crops in 2008: by country (million hectares) (www.earthtrends.wri.org).

Rank	Country	Area (million hectares)	Biotech crops
1*	USA	62.5	Soya bean, maize, cotton, canola, squash, papaya, alfalfa, sugar beet
2*	Argentina	21.0	Soya bean, maize, cotton
3*	Brazil	15.8	Soya bean, maize, cotton
4*	India	7.6	Cotton
5*	Canada	7.6	Canola, maize, soya bean, sugar beet
6*	China	3.8	Cotton, tomato, poplar, petunia, papaya, sweet pepper
7*	Paraguay	2.7	Soya bean
8*	South Africa	1.8	Maize, soya bean, cotton
9*	Uruguay	0.7	Soya bean, maize
10*	Bolivia	0.6	Soya bean
11*	Philippines	0.4	Maize
12*	Australia	0.2	Cotton, canola, carnation
13*	Mexico	0.1	Cotton, soya bean
14*	Spain	0.1	Maize
15	Chile	<0.1	Maize, soya bean, canola
16	Colombia	<0.1	Cotton, carnation
17	Honduras	<0.1	Maize
18	Burkina Faso	<0.1	Cotton
19	Czech Republic	<0.1	Maize
20	Romania	<0.1	Maize
21	Portugal	<0.1	Maize
22	Germany	<0.1	Maize
23	Poland	<0.1	Maize
24	Slovakia	<0.1	Maize
25	Egypt	<0.1	Maize

*14 biotech mega-countries 50,000 hectares, or more, of biotech crops. Source: Clive, 2008.

Monitoring of the environment is very expensive, and information for activities should be used in the frame of a clear system of the adaptive management. This management includes repeated cycles, posted rules of designed programs, use, evaluation and estimation of the monitoring in whole (Snow et al., 2004).

More significant problem for monitoring of GM plants is that systems of adaptive management have not been developed specially for this purpose. Monitoring of new GM plants will need to be accessed by broader groups of scientists including those from agriculture, forestry, ecology of water areas, entomology, pathology, etc. In the future, scientists and technological advancement will continue to widen possibilities for artificial design and construction of plant organisms. Genomics and bioinformatics influence easier identification of significant genes whose potential can be transferred among plant species. Ecologists will significantly contribute to the wider public dispute so that society and environment can prevent risks and contribute to the advantages from these innovations.

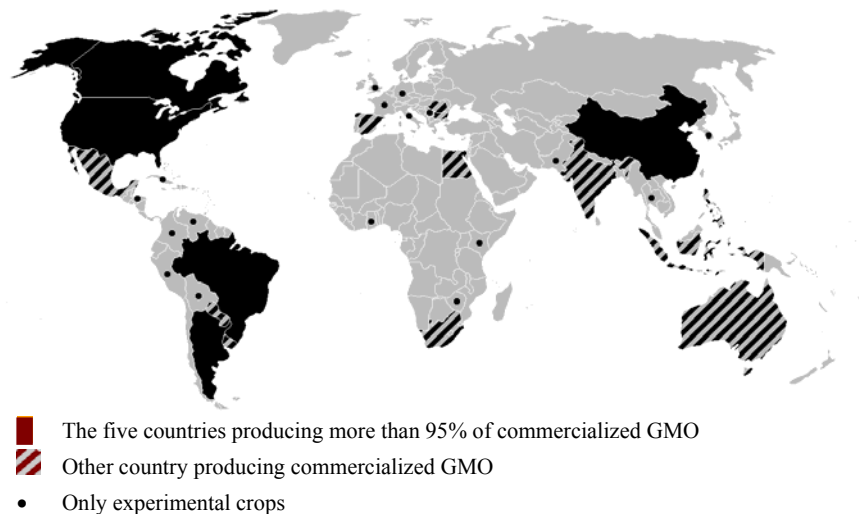


Figure 3. World map GMO production in 2005 (<http://commons.wikimedia.org>).

Conclusion

Application of merely classic breeding techniques in recombination of new genes in cultivated plant species is timely demanding process for breeders. Transgenic technologies overcome problems in breeding related to existence of sexual incapability between distant species and genus and provide convenient

conditions for use of wild relatives as gene pools for different kinds of resistance. It is important to remark that genetic modifications, as well as all other new scientific technologies bring certain risks in use, and especially their behaviour and influence on the environment.

Identification of application of the foreign modified plant material and study of risk evaluation in regard to the environment must be more intensive.

For this information is needed from many disciplines such as weed science, genetics, conventional and molecular selection, molecular biology, plant pathology, entomology, population biology, ecology and others. Scientific knowledge about explanation of risks in decision making is needed, and this, above all, depends upon total knowledge of the scientists from all above named disciplines.

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PROCENA EKOLOŠKIH RIZIKA I DOBITI OD GENETIČKI
MODIFIKOVANIH USEVA

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R e z i m e

Genetički modifikovani (GMCs) usevi i biotehnologija stvaraju nove mogućnosti za povećanje produktivnosti useva i rešavanje problema koji se javljaju u poljoprivredi, kao što su bolesti, štetočine, korovi, abiotički stresovi i hranidbena ograničenja u biljnoj proizvodnji. S obzirom da su GM usevi već prošireni na različitim lokalitetima i ekosistemima neophodno je bolje razumevanje i naučno dokazivanje uticaja GM useva na životnu sredinu kako bi se pomoglo u njenom očuvanju. U radu se razmatraju neki najvažniji problemi vezani za GM useve, njihov uticaj na kvalitet životne sredine, kao što su zaštita biljaka, hibridizacija, ekološki efekti otpornosti na herbicide (HRCs), horizontalni prenos gena (HTG), protok gena, biodiverzitet, stres, procena ekoloških rizika (ERA), uticaj na zemljišni ekosistem itd.

Ključne reči: GM usevi, biotehnologija, životna sredina, zaštita biljaka, HTG, biodiverzitet.

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