APPLICATION OF GENETIC ENGINEERING TECHNOLOGY IN AGRICULTURE AND ENVIRONMENTAL IMPACT

[1]Jelena Bošković[1], [2]Radivoj Prodanović[2]

Abstract

Application technologies are considered genetic engineering in agriculture with the introduction of genetically modified crops (GMCs) are constantly creating new opportunities to increase crop production and to solve problems in agriculture, such as diseases, pests, weeds, abiotic stresses and nutritional limitations. These are formed, and the plants having new properties that enable their use in pharmaceutical manufacturing. As the GM crops introductions to various locations characterized by a variety of ecosystems, types of agriculture, biodiversity and agriculturally practice, it is necessary to scientific understanding of the effects of growing GM crops on the environment, which will provide security and environmental sustainability. The most important research she focused on the invasiveness of the GM crops, vertical and horizontal gene transfer, the impact on biological diversity and on other products. These tests are very complex multi, inter and transdisciplinary. This article discusses some of the most important problems related to the application of the technology of genetic engineering in agriculture and the introduction of GM crops into the environment, such as plant protection, ecological effects of horizontal gene transfer, biodiversity, stress, the effects of land etc.

Key words:*genetically modified crops (GMCs), environment, plant protection, HRCs, HTG, gene flow.*

Introduction

Through the plant selection history new gene combinations have regularly been included; artificial manipulation of chromosome number, development

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[1] Jelena Bošković, Ph.D, Full Professor, University Business Academy In Novi Sad, Faculty of Economy and Engineering management, Cvecarska Street no. 2, 21 000 NoviSad, Serbia, E-mail: jboskovic@fimek.edu.rs

[2] Radivoj Prodanović,PhD,Assistant Professor, University Business Academy in Novi Sad, Faculty of Economy and Engineering management, Cvecarska Street no. 2, 21 000 Novi Sad, Serbia, E-mail: rprodanovic@fimek.edu.rs

of additions and substitutions, lines with specific chromosomes, chemical and radioactive treatments for induction of mutations and chromosomal rearrangements, cell, tissue and embryo culture, *in vitro* fertilization and protoplast fusion in order to enable finding of interspecies species and genus hybridization. Integrations of these technologies contributed the most to the genetic improvement in yield, adaptation to the environment (Dale, 2002; Garcia and Altieri, 2005), resistance toward parasites and pests, as well as regularly demanded quality improvement by industrial food producers and consumers. Development of molecular biology investigations and genetic engineering, the efficient modification of crops has been enabled. These technologies can have undesirable influence to the environment (Conner *et al*., 2003), human health and economical level of increasing poverty. In the following period more attention is to be paid to the commercially and economically justified use of GM crops in agricultural food production (Drobnjavić*et al.,* 2018). Link of science and politic should be important for the common assessment of adoption and widening of GM crops. In majority of countries there are still significant disagreements in regard to the extent of the measure in which areas such as sustainability, globalization, ethic and sociological – economical approaches should have as part of GM crops use risk evaluation.

Horizontal gene flow

Horizontal gene flow (HTG) is transfer of the genetic material between cells or genomes that belong to different species, and these are processes that differ from the common reproduction. 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 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 Horizontal gene flow foreign genetic material must become part of the cell genome, or to be maintained stable in the recipient cell of the other form. In certain cases, foreign genetic material that enters the cell, especially if it belongs to the other species, will be removed before it builds (incorporates) in into the genome. Under specific ecological conditions that are scientifically still not clarified, foreign genet material avoids to be removed and builds in into the genome.

Horizontal gene flow is well known in bacteria, but last years this occurrence is recognized in higher plants and animal. In its base this process comprises whole biosphere, and bacteria and viruses are intermediary in gene flow, gene pool, replication and recombination (Conner *et al*., 2003; Snow *et al*., 2004).

There are many potential pathways for horizontal gene flow in plants and animals. As there are many viruses that infect plants and animals, it is expected for transduction to be the most frequent. Last investigations in gene therapy indicate potential high importance of transformation for mammal cells, including humans. Direct transformation is not as 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-DNK is widely used as resource of gene transfer in plant genetic engineering. Foreign genetic material from insects and arthropods with strong mutagenic reactions can also be built in into plant and animal cells. 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. The most significant barriers for horizontal gene flow are employed after penetration of the foreign genetic material into the cell.

However, viruses and the other genetic parasites, such as plasmids and transposons, have special genetic signals and probably possible structure that enables them to avoid annihilation. Viruses posses genetic material that is protected in the protein coat. They discard their protein coat for penetration into the cell enabling thus creation of many more copies or direct pass into the cell genome. Plasmids are *free fractions* usually round in shape so that genetic material can finally be maintained in the cell separately from the cell genome. Transposones (*jumping genes*) are blocks of genetic material that have possibility to insert in to the genome or out of it, with or without their replication in the process, kept in plasmids for the further reproduction. Genes of these genetic parasites such as viruses, plasmids and transposones have significantly higher possibility to be successfully transferred into the cell and genome. In such a manner these genetic parasites function as vectors for Horizontal gene flow, and it is also clear that gene transfer is regulated by inner characteristics of the organism, and it is especially linked to the specific ecological conditions.

Recording of horizontal transgenic DNA transfer

It is believed that once incorporated transgenic DNA into transgenic or modified organism becomes as stable as the organisms that possess also DNA. However, there exist direct, as well indirect recording against this assumption. Transgenic DNA is probably more widening, as it was found for the widening of the Horizontal gene flow. There exist molecular data that prove structural stability of transgenic DNA, in regard its location, point of penetration into genome and gene arrangement into following generations. In fact transgenes can be stabilized in successive generations or lost in whole. Gen for tolerance toward herbicides incorporated into *Arabidopsis* with vector can be 30 times more oriented to avoid vector, and it widens 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 transgene and gene resistance markers transfer to antibiotics in genetically modified plants in soil bacteria and fungi is possible. Transfer to fungi was achieved simply by co-cultivation, for transfer to bacteria was accomplished by reisolation of transgene DNA or whole DNK of transgene plant. Successful kanamycin resistance gene markers to the soil bacteria *Acinetobacter* was achieved by use of extracted total DNA from homogenized plant leaf from the list of transgenic plants: *Solanum tuberozum* (potato), *Nicotiana tabacum* (tobacco), *Beta vulgaris* (sugar beet), *Brasica napus* (canola) and *Lyopersicum esculentum* (tomato). It has been evaluated that about 2500 copies of kanamycin resistance genes are enough for successful transformation of a bacteria, regardless if there exist 6 millions of folded strands) of the present plant DNA.

However, natural conditions in the environment are widely unknown and unpredictable, and researches of certain scientists on synergetic effects could not bee neglected in this case. Free transgenic DNA would be free in rhizosphere around plant root, and it is also significant critical point of the environment. The other scientists have found horizontal resistance gene flowtoward kanamycin from transgenic DNK to *Acinobacter*, and positive results have been obtained by use of homogenized 100µ of plant leaf.

Biotechnology industry insists that existence of horizontal gene flow in laboratory conditions does not mean that it is naturally occurring. However, there are already researches that confirm that it can occur in nature. Above all, genetic material taken from dead and living cells resists in all outer conditions, it does not dissolve nor devastate as it has been previously assumed. This indicates to the claim that sand, humus acid parts and plant debris enables 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 acceptation of the rhyzomania resistant transgenic sugar beat plants in diwls (Trkulja et al., 2016), 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 leading phenomenon that occupied significant place in the evolution of species, and it is still today. All this suggest that natural Horizontal gene flow represents 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 of barriers between all kinds of organisms and overwhelming by all genomes.

Plant Protection and GMCs

Main considerations of GM crops (GMCs) use for plant protection are possibilities of incorporation of resistance in protection from insects, fungal and bacterial pathogens, viruses, with stress to the main problem of long-term resistance (Boskovic et al., 2000). Pest plant protection by genetic modification is use of Bt toxins from *Bacillus thuringiensis* , that has been successfully used as spray during many years; that has been introduced in more plant species such as: tomato, tobacco, cotton, etc. It has been proved that pea lecithin protects against insect attack in transgenic potato and tobacco. Tripsin inhibiting protein of fodder pea has also been used. 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 apply restricted transgene action (Bouchard et al., 2003).

It has been proved that use of transgenic resistance to viruses through indirect protection of cap-proteins is possible, and it can be used as a method for the wide spectrum of viruses and hosts, e.g. expression of TMV cap-proteins for tobacco mosaic virus of potato and tomato resistant to PVX and PVY (Daniell, 2002)

Application of genetic modification in control of fungal and bacterial plant pathogens has also been developed. As in the 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, there is a need to develop multiple resistance strategies (i.e. *pyramiding resistance genes*) towards different virulence levels of plant parasites (Danieell, 2002; Bouchard et al., 2003; Bošković and Bošković, 2009; Trkulja et al., 2015, 2016; Drobnjaković et al., 2018).

Tolerance and plant resistance to herbicides (HRC)

Great efforts have been directed also toward increase of crop tolerance toward herbicides, and it has been tested world wide. 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. 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). Hybridization 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 to very wide spectrum of weed species.

Non-cultivated populations of transgenic plants and gene flow

Possibility of transgenic plant introduction will be highly dependent upon their adaptive capability to the new environment. For many crops it is known that they form temporary non-cultivated populations, and these are species such as canola, lucerne, radish, carrot, rye, clover, sugar beet, chicory, beet, cabbage, of which some are native, whereas the others have probably been introduced for cultivation. 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 probably has been no harmful influence for non-cultivated plant species. 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).

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.

In contrast, in canola seed the compatible inbreeding is present, it can produce huge seed quantities, it is pollinated by wind and insects. Pollination at huge distance happen 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 use 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 to 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. However, gene flow can depend not only from crops, but also from variety, location and season (Marshall et al., 2003). Experiments on gene flow in populations of wild radish suggest that size of donor and recipient population play significant role in gene flow. In that way would huge pollen sources, such as great spectrum of GM genes introduction have significant influence to small wild population of compatible plants. They also note that there are noticeable variations in evaluations of gene flow, probably due to local-positional and pollinator effect. The other researches have fund similar effects in *Cucurbita* populations and in rye. Further work on spreading genes in populations can be necessary during assessment of the potential transgene dispersal. Such assessments become especially actual in searching out of possibilities for transgene transfer from cultivated crops to their wild relatives. World group for wheat identified three crops that have sexually compatible weed relatives for which it is probable that 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 than dependable upon weed habitat. These studies suggest that in assessed complexes weed-crops in which habitats of weed relatives have been restricted to agricultural systems exist no possibility for this new trait to endanger natural ecosystems (Creswellet al., 2002; Lu et al., 2005).

Hybridization

Weed ecology and evolutionary biology are of high importance in assessment of perspective of accidental flow of resistant transgene to harmful organisms in population of agricultural weeds (Bošković et al., 2011). Model for accidental transgene flow has three phases that lead to forming of widely distributed weed populations that carry transgene. Hybridization between weed and transgenic crop is the first phase. The second one is occurrence of the introgression process and adaptation in which evolutionary mechanisms improve inadaptable traits in hybrid products of earlyl generation. Consequence of this is that weeds transfer resistance transgene to harmful organisms, and due to that have normally high adaptation level for certain agro ecosystems. Finally, process of dispersion and dissemination of these neo-new weeds in nature, together with local adaptation of various conditions is important during transition of sufficiently wide area.

Weed ecology and evolutionary biology aspects are important for interactive action of the three above described phases. There lack real scientific data on weed ecology. Last decades scientists that study weeds focus on herbicide weed control. In these predominant studies ecological ones have been neglected and especially theoretical description (Altieri, 2000; Conner et al., 2003).

Hybridization 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 hybridization has detailed description and it can bee expected that transgenes will transfer even over great spatial and significant obstacles of genetic incompatabilities. In some systems accidental transfer of transgenes by hybridizations seems unavoidable. However, in other cases it is not clear if hybridization is proportionally limiting phase in transfer of transgenes. It is the assumption that hybridization can even be proportionally limiting in some circumstances, i.e. when hybridization occurs over significant obstacles of incompatibility. Aspects of weed ecology that can influence to hybridization 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 fertilization in which occur inbreeding and cross fertilization (outbreeding), although the other reproductive system have also been known. Therefore, the widely distributed systems of weed selection enable hybridization, but such fertilizations must happen during significant level of inbreeding.

For selection systems and other aspects of genetic systems and reproductive ecology, that influence to the hybridization levels it is known to vary within and between weed populations. For instance, *Datura stramonium* populations in the Northern Carolina have flowers that open to pollinators and exhibit approximately 10% outbreeding level. Contrary, certain populations are exclusively self pollinating, with flowers that do not open to the pollinators. In some cases this variation refers to adaptation of selection system after great expansion (Cresswell et al,. 2002): however pollinator attitude can vary even geographically. These aspects of reproduction therefore should not be considered as permanent characteristics in the frame of weed species.

Spatial weed distribution can strongly influence hybridization weed-plant species. First, many weeds have uneven distribution in fields, and in some papers it is described that uneven distribution in some species has certain level of temporary stability (Perry et al., 2003). Uneven distribution can be caused by edaphic factors or by persistent effects of high seed production. In the frame of a field, uneven weed distribution can reduce hybridization weed-crop. Occurrence of weeds in plant population of adequate density, with small proportion of single weeds at the ends of these plant populations is limits populations proportionally to hybridization. More homogeneous and uneven distribution can significantly favor to considerably higher levels of cross fertilization. In locally isolated individuals can be present higher quantities of crop pollen due to changes in movement of pollinators as function of local density. Weed density can have contra effect to the hybridization levels, when plant serves as female parent. In this case, high densities can favor hybridization with advantage of achievement of great local weed pollen densities, and homogenous weed density can reduce plant hybridization.

Introgression and adaptation

The evolutionary process that follows after hybridization will probably influence many ecological weed properties in agro systems of cultivated plants. First, nature of these systems seems to prevalent at weeds only some more expressed factors for regulation of population. This, in comparison with the majority of annual plant populations that are short living and inhabit other kinds of ecosystems can favor to transgene introgression, even if hybrids and starting backcrossed generation have low level of adaptive features in comparison to weeds that do not carry transgenes (Fagan et al., 2003).

Weed populations are frequently occurring small and sometimes temporary; therefore, effects of selection, migration and random genetic changes will have influence to the evolution of introgression. Finally, seed ecology is primary for weed survival and because of these effects of transgenes for other genes of plant species and seed ecology will probably show strong selective effects to these genes. Introgression of genes that improve adaptation of weeds to these predominant selective factors can significantly increase the average adaptability of weed population. Exchanges between adaptations to different limiting factors that result from introgression of a single gene can also be minimal. The best example is evolution of herbicide resistance in weeds. Occurrence of herbicide resistance often significantly increases the average survival and level of weed population growth. Herbicide resistant mutation can have high absolute adaptability, despite basic functional damages that are caused by pleiotrophic effects of resistance mutations. This example illustrates how selection can favor mutant that exceed limiting factors. The other line of evidences for this point of view rises from multiple examples of increased distribution and density of weeds that resulted from field trials over hybridization (Perry et al., 2003). Finally, many cases of the basic increase in distribution and density of certain weeds follow moderate changes in cropping systems, providing the additional proof that many weed communities are regulated with several strong factors.

If it is correct, this assumption suggest that adaptation of weeds that carry randomly transferred transgenes after hybridization is greatly made easier by biological uniformity of the actual ecosystems of field crops. Weeds can demand relatively narrow evolutionary movement, as it is break of linkages toward undesirable characteristics of plant species in accordance with adaptation to wide area. One criterion for assessment of transgene spread into weed population is that survival of the hybrid weed-crop that carries transgene should be higher than adaptability of non-hybrid weeds. This criterion can be much easier met in temporary ecosystems of field crops than in majority of others. Therefore, transfer of transgenes can be fast process. Even hybrids with very low adaptability and early back crossings can survive in agro systems in adequate densities. There exist possibility for introgression and adaptation that make their survival easier. These assumptions can be applied on accidental transfer of transgenes that influence to the tolerance to abiotic factors. However, for weed populations in wider areas it is possible to be restricted by one biotic factor to which adaptation would give basic increase in survival (Snow et al., 2004).

The other characteristics of weed ecology that probably influences to adaptation of the crop-weed hybrid is frequency of occurrence of low efficient population size and high levels of self-fertilization, especially in the process of colonization. Small population sizes cause random changes in genetic composition. These mechanisms can act at genetic base produced by hybridization; producing a row of genetically differentiated small populations from genetically different back crossed weed populations.

This implies that adaptation in weed populations that contain random transgenes probably will be influenced by selection and random genetic change. Presence of both factors enable occurrence of evolutionary processes that do not occur when selection is dominant evolutionary mechanism. Specifically, adaptive effects of transgene combinations, other crop genes and weed genes can be more adaptable in expression with mutual action of random genetic exchanges in regard to the selection that acts alone (Conner et al., 2003). These mechanisms can be especially strong when weed populations have high levels of weakening and repeated colonization, forming thus ecological and genetic metapopulations. Although, it is still not clear if weeds in agriculture have metapopulative structure, occurrence of such structures, in combination with small sized population and altering selection pressures creates convenient conditions for equilibrium processes. However, effect of these processes can itself be unpredictable due to geographic variations in population structure in some weed species due to the cropping system, local adaptation after colonization, time span from colonization and hybridization with relative categories (Dale, 2002).

Molecular and biochemical data on homology levels between kinds of crops and their wild relatives world wide indicate to gene introgression from crops into populations of wild relatives. Introgression can occur in various plant species, including maize, melon, carrot, sugar beet and rye. Possibility of transgene introgression into wild populations, during time period in some species and in some geographic areas would be very high. Hybrids between crops and their wild relatives most probably occurred with crops that are of low adaptation and cropped in the frame of the same region from which they originate. Minimal divergence and maximum exposure from the other relatives should be ensured. Level of transgene introgression into wild species from crops is influenced by factors such as overlapping of flowering period with wild species, and capability of hybrid to back cross with wild relatives in population. From this emanate that gene that possibility of gene transfer is especially significant in tropic areas, for many important crop plant species evolutionary originates from these areas.

Spatial seed dispersion and weed colonization

Efficient spatial dispersion of seed is considered a primary feature of weeds (Kudsk and Streibig, 2003) and it is expected that weed ecology influences the fate of the accidentally transferred spread transgenes in a number of ways. On the field scale, simulation modeling indicates that high levels of weed seed dispersal generally greatly increase the population of weeds. For most weeds in field crops dispersion is determined by the interaction of characteristics of weeds and human activities, such as contaminated seeds of cultivated plants, equipment, water for irrigation and seed transmission. When human activities become the main vectors of the spread of weed seed, those dispersions are difficult to characterize, because of the geographical variations of the processing system. As a result, the maximum spreading distances are not known in most cases. On a wider scale, many cases of rapid expansion of the sub-continental weed species are known. Weed species were found to become abundant over large areas west USA, due to the changes in farming methods that improve their abundance, such as *Aegilops cylindrica*, sexually compatible weed in wheat. Weeds resistant to herbicides spread over hundreds of kilometers of road shoulders in less than a decade. These observations suggest that weed populations of road shoulders of other non-field habitats may be important for the spatial spread of weeds, recognizing the importance of weed ecology in agricultural areas and the accidental spread of the transgenes (Altieri, 2000). Herbicide resistant crops can be agronomically harmful if the resistant species germinates before the sown plants germinate, or if the herbicide resistant plant occurs as a weed on another field (Tyystjarvi, 2009). Weeds can have significantly higher adaptability over large spatial areas of the transferred transgene. In theory, the resulting spatial homogeneity of a suitable habitat (Perry, 2002; Conner et al., 2003) and the absence of the need for local adaptation accelerates rapid expansion of the colonizing organisms. Therefore, the ecology of weed spread and population regulation in agro-ecosystems and agricultural areas seems to enable large and rapid expansion of the adapted weeds. The weed properties that affect their spreading (e.g. seed size, shape, similarity to crop seeds, etc.) should be considered adaptive characteristics that are probably the result of a strong selection. The effects of crop genes and ecological expansion can adversely affect the adaptation of hybrids. The weed spread may have an evolutionary role. In small basic population it can cause adaptive process, which does not occur in large populations. In the increasing balancing process, the spread of weeds has an important role in evolution, moving into small populations in other areas and affecting changes in other populations. The weed ecology in cultivation systems can facilitate the random transgene transition, allowing the survival of weed-crop hybrids that are not adjusted, compared to wild-type weeds, in a series of adaptability components. This probably happens when the hybrids and next generation back cross, carrying the appropriate transgene adaptive value. Ecology of seed, the expansion of some basic characteristics responsible for the weed adaptability and the level of population growth are not widely accepted parameters. Effects arising from transgenic and other crop genes will greatly influence the adaptation of weed-crop hybrids and back cross generations. Most of the main weed species show intensive spatial and temporal variations in reproduction, ecology and seed spread on several scales. This variation has both genetic and environmental causes. The populations of agricultural weeds are widespread in agricultural regions, including many populations that appear out of farmland. Specific ecology of these populations may affect all phases of the random transgene transfer.

Monitoring

Ecological monitoring of GM crops in complex ecosystems is needed even after commercialization. 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 can not be predicted in advance, so that ecological monitoring will be needed to reveal and differentiate existing ecological influences (Dale, 2002).

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. For management of evolution of resistance toward pathogens and pests, resistance frequency should be monitored in the field; however, additional studies are needed for making of monitoring standards and determination of adequate management with the aim of easier clarification of the problem (Boskovic et al., 2004). Monitoring of new GM plants will need to bee 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 to easier identification of commercially significant genes that potential can be transferred among plant species. Ecologists will significantly more contribute to the wider public dispute on the way in which society and environment can prevent risks and contribute to the advantages from these innovations.

Conclusion

Application of merely classic breeding techniques in recombination of new genes in cultivated plant species is timely demanding process for breeders. Transgene technologies enable breeders to use genes from the wide spectrum of the living world and to combine them in the frame of one plant genotype. This overcomes problems in breeding related to existence of sexual incompability between distant species and genus and provides 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 behavior and influence to the environment.

Studies in the field of genetic manipulations are significant from the aspect of understanding of this technology, manner of identification of application of the foreign modified plant material and study of risk evaluation in regard to the environment and must be more intensive.

For this are needed information from many disciplines such as weed science, genetics, conventional and molecular selection, molecular biology, plant pathology, entomology, population biology, ecology and others. Scientific knowledge on 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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