Potential Risk of Genetically Modified Plants in Korean Ecosystem: a Proposal for Unintended Effects on Korean Wild Species

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ABSTRACTS: Introgression from genetically modified plants (GMPs) may be dependent on the genetic similarity to wild relative plants. In Korea, many wild plant species are botanically related to the cultivated plants that have a potential to be genetically transformed. The controversy for hazards of GMPs is continuing because the studies on gene flow or introgression are little. Based on the systematic criteria, we have surveyed Korean wild plant species that showed the similarity to cultivating crops. The consideration for feasibility of genetic pollution (introgression of transgene) is necessary for the successful accomplishment in the practical use of GMPs. Although the detrimental effects of GMPs on wild relatives have not been clearly verified, Korean wild plant species related to crop plant (potential GMP) have to be investigated with respect to the introgression. Korean flora consists of ca. 5,500 species. Among them, 1,448 species are classified as weed species (966 native, 325 naturalized, and 167 escaped ones), which is vulnerable to GMPs in term of introgression. We suggested the principal Korean wild plants related to major crops that might be affected by GMPs via introgression. The investigated species herein are selected based on the morphological and phenological relationship. It is necessary to verify the genetic relationship between cultivated plants and wild relatives using more precise molecular techniques, which provide the information of likelihood for the introgression of transgene.

Keywords: genetically modified plants, GMPs, Korean flora, ecological risk, gene flow, introgression

G enetic engineering has created the new types of bacteria, fungi, and animals as well as plants. The genetically modified plants (GMPs) improve the quantity and quality of agricultural products. However, the release of GMPs into natural ecosystem can cause such serious problems as unintended hybridization with natural wild relatives (Dale, 1994; Darmency, 1994; Bartsch & Pohl-Orf, 1996) and gene transfer from plant to microbial kingdom (Nielson *et al.*, 1997). The artificially transferred genes into crop species to improve

the agronomic traits are various from biotic and abiotic resistance genes to quality-related genes (Law, 1995). Although the engineered genes are tested under the controlled environment, the unexpected genetic transformation can occur. Moreover, the safeness of GMPs is still in debate (Kessler et al., 1992; Käppeli & Auberson, 1998; Ruibal-Mendieta & Lints, 1998). Because natural ecosystem is different from the experimental conditions, unintended effects can be broken out. The typical example of the release of GMPs is an introgression of transgene into wild species (Kessler et al., 1992; Raybould & Gray, 1994; Picard-Nizou et al., 1997). The introgression of transgene can sometimes occur serious problems since the preferred target traits are resistant genes that confer a higher competitiveness for GMPs (Dale, 1994; OECD, 2000). These genes can change the ecological niche of recipients and escaped plants (volunteer) from cultivating fields. Moreover, a number of reports for natural hybridization support the potential risk of introgression (Darmency, 1994; Mikkelsen et al., 1996; Ellstrand et al, 1999).

Levin & Kerster (1974) classified the gene flow as two different types, potential gene flow and actual gene flow. Potential gene flow is the movement of seed and pollen. Actual gene flow is the amount of succession in fertilization (pollen) and establishment (seed). The frequencies of fertilization and establishment are dependent on the genetic similarity and environmental conditions, respectively. The detection of gene flow can be directly conducted with the observation of seed and pollen movement. Also it indirectly can be evaluated via determining genetic relationship between taxa.

The potential hazard of GMPs can be also derived from the imported crop products that are harvested from genetically modified plants. For instance, the loss of imported grain in the course of transportation (from harbor to milling or feeding plants) can cause spontaneous seed shedding (personal observation of B. H. Kang). This escape is another type of gene flow that has not yet reported all over the world. However, there is no regulation to prevent such escape, which causes a disturbance in endemic plant ecosystem.

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Due to the potential hazards of GMPs to ecosystem, many countries try to confine the experiments with GMPs (Ruibal-Mendieta & Lints, 1998; Torgersen *et al.*, 1998). In recent, the risk assessment of GMPs is carried out with ecological approach. If the wild relatives are the endangered species or dominant weeds, the gene flow from GMPs should be catastrophic.

A remarkable success in the development of transgenic plants can be found in herbicide resistant crops. The herbicide resistant cultivars, however, have a potential danger to ecosystem. The herbicide resistance is a most frequent and preferred target for genetic transformation, since most herbicide resistant developed so far is controlled by single gene (qualitative trait) (James 1998). The herbicide resistance sometimes stemmed from a marker gene (e.g. bar gene for glufosinate ammonium) can be released into ecosystem without deliberation of its unintended effects. Weeds cause a serious problem in agricultural production, and decrease the farmers' income. The continuous use of herbicide to control the weeds has led to the occurrence of herbicide resistant weed species that consequently increase the herbicide application rate to reduce the weed population with economic threshold. The group to be affected by gene flow is weed due to their abundance in agricultural lands and similarity to crop plant. Generally, dominant weeds are phenologically similar to cultivated plant. The weed flora in Korea consists of 1,448 species including 966 native species, 325 naturalized species, and 167 escaped species (Kang, 1999). Besides weed species, several wild species have been noticed as the possible recipient of pollen from cultivated plant due to their close relationship with crop and their abundance in natural ecosystem (Ellstrand et al., 1999).

However, the investigation of wild flora is necessary to predict the genetic pollution from GMPs or artificially bred plants. Unfortunately, we have no information on the current condition of wild taxa and their genetic relationship to cultivated plants. In this paper, we surveyed Korean wild plant species that shown the similarity to cultivated crops.

THE POTENTIAL HAZARDS OF GMPs WITH RESPECT TO WILD SPECIES

The feature of Korean flora resulted from both *in site* surveys and botanical literatures (Ellstrand *et al.*, 1999; Kang & Shim, 1997; Lee, 1982; Shim & Kang, 2000; Umberto Quattrocchi, 2000) was different from foreign countries. Due to the poor information based on genetic analyses for the relationships between cultivating crops and wild relatives, the researches should commence with morphological, systemat-

Table 1. Major crop species in Korea on the basis of acreage (FAOSTAT database, FAO, 2000).

(1AOS1A1 database, 1AO, 2000).				
Crop	Crop Scientific name	Area	Production	
Сюр		(100 ha)	(100 ton)	
Apple	Malus domestica	31	490	
Barley	Hordeum vulgare	85	330	
Dry bean	Phaseolus vulgaris	22	24	
Buckwheat	Fagopyrum esculentum	3.9	3.9	
Chinese cabbage	eBrassica campestris var.	50	755	
· ·	pekinensis			
Carrot	Daucus carota var. sativa	5.7	165	
Chestnut	Castanea crenata	43	120	
Citrus	Citrus unshiu	27	608	
Grape	Vitis vinifera	5.6	407	
Red pepper	Capsicum annuum	81	307	
Cucumber	Cucumis sativus	10	408	
Eggplant	Solanum melongena	9.5	16	
Garlic	Allium sativum	42	384	
Ginger	Zingiber officinale	3.0	5.6	
Groundnut	Arachis hypogaea	7.5	14	
Kiwi fruit	Actinidia delicosa	0.5	3.0	
Lettuce	Lactuca sativa	6.6	162	
Corn	Zea mays	20	82	
Millet	Panicum miliaceum	2.9	3.0	
Onion + shallot	Allium cepa+Allium	23	512	
	fistulosum			
Peach	Prunus persica	13	157	
Pear	Pyrus pyrifolia var. culta	26	259	
Plum	Prunus salicina	4.1	43	
Potato	Solanum tuberosum	23	561	
Pumpkin	Cucurbita moschata	10	203	
Rapeseed	Brassic campestris subsp.	1.0	1.2	
	napus var. oleifera			
Rice	Oryza sativa	1,059	7.3	
Sesame	Sesamum indicum	49	24	
Sorghum	Sorghum vulgare	1.2	1.6	
Soybean	Glycine max	98	145	
Spinach	Spinacia oleracea	8.4	129	
Strawberry	Fragaria ananassa	6.4	154	
Sweet potato	Ipomoea batatas var. edulis	16	339	
Tea	Thea sinensis	1.1	1.5	
Tobacco	Nicotiana tabacum	24	65	
Tomato	Lycopersicon esculentum	3.9	188	
Walnut	Juglan sinensis	0.6	1.3	
Watermelon	Citrullus lanatus	1.3	37	
Wheat	Triticum aestivum	1.0	5.0	

ical, and ecological data.

The classification of plant species by systematics may reflects not only the possibility of the exchange of genetic materials, an introgression but also the adaptability or fitness of plant species under a special environment. Although the taxonomical relatedness is sometimes not fit to the genetic relatedness, the deduced results can reflect appropriate relationships between related species.

Based on the current status of cultivation area of major crops (Table 1) and representative GMPs (Table 2), the

Table 2. Representative genetically modified crop species already commercialized (OECD product database, OECD, 2000).

Crop Trait Chicory Male sterility Herbicide resistance Carnation Modified flower color Increased base life Corn Insect Resistance Herbicide resistance Male sterility Cotton Herbicide resistance Insect resistance Insect resistance Flax Herbicide (soil residue) resistance Oilseed rape Altered oil composition Herbicide resistance Male sterility Papaya Virus resistance Potato Insect resistance Virus resistance Virus resistance Male sterility Rice Herbicide resistance Soybean Herbicide resistance Altered oil composition Squash Virus resistance Sugar beet Herbicide resistance Tomato Altered ripening Delayed ripening Insect resistance	commercialized (OECD product database, OECD, 2000).		
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Sugar beet Herbicide resistance Tomato Altered ripening Delayed ripening		*	
Tomato Altered ripening Delayed ripening	Squash	Virus resistance	
Delayed ripening	Sugar beet	Herbicide resistance	
	Tomato		
Incact resistance			
		Insect resistance	
Tobacco Herbicide resistance	Tobacco	Herbicide resistance	

major crop species and their wild relatives that have to be noticed in Korea are presented (Table 3).

Wild soybean (Glycine soja)

The wild species of soybean can be easily found in Korea. *Glycine soja*, known as an ancestor of soybean has been found frequently not only in natural ecosystem but also agroecosystem. *Glycine soja* is a climbing plant and its purple flower is similar to *G. max* in morphology. Maughan *et al.* (1996) reported that there is the higher genetic similarity between wild and cultivated *Glycine* based on AFLPs. Kwon (1972) carried out the artificial hybridization between taxa. He reported the segregation pattern of progeny and the potential natural cross between taxa. As a wild ancestor of cultivated plants, *Glycine soja* has been investigated and exploited for providing genetic materials.

Weedy rice (Oryza sativa, red rice)

Rice is the most important food crop in Korea (Table 1). Rice plant has lower outcrossing rate due to their covered (closed) caryopsis and poor attractiveness to pollinators. Nevertheless, there are an artificial hybridization, success in gene flow, and introgression between cultivated rice and red rice (Chu & Oka, 1970; Langevin *et al.*, 1990). Among wild rice species, red rice (*Oryza sativa*, weedy rice) is an only wild *Oryza* species occurring in Korea. In recent, the change in cultural method for rice from transplanting to direct-seeding increases the occurrence of weedy rice. The escape of cultivated rice from the fields to wild and subsequent long-term alteration may cause difference in genetic constitution

Table 3. Major crop species and their wild relatives in Korea.

Cultivated species	Wild relatives	
Malus domestica	Malus baccata, Malus baccata for. jackii, Malus baccata for. minor, Malus baccata var. genuina, Malus baccata var. mandshurica, Malus baccata var. mandshurica for. jackii, Malus baccata var. mandshurica for. minor, Malus baccata var. praecox, Malus mandshurica, Malus micromalus, Malus sieboldii	
Hordeum vulgare	-	
Phaseolus vulgaris	Phaseolus nipponensis	
Fagopyrum esculentum	•	
Brassica campestris var. pekiner	nsis Brassica juncea	
Daucus carota ssp. sativus	Daucus littoralis var. koreana	
Citrus unshiu	Poncirus trifoliata	
Vitis vinifera	Vitis amurensis, Vitis amurensis for. glabrescens, Vitis amurensis for. glabrescens, Vitis amurensis var. ciliata, Vitis amurensis var. coignetii, Vitis amurensis var. lanigera, Vitis austrokoreana, Vitis ficifolia, Vitis ficifolia for. glabrata, Vitis ficifolia for. glabrata, Vitis ficifolia var. glabrata, Vitis ficifolia var. sinuata, Vitis ficifolia var. thunbergii, Vitis flexuosa, Vitis flexuosa var. choii, Vitis flexuosa var. rufo-tomentosa, Vitis kaempferi var. glabrescens	
Capsicum annuum	-	
Cucumis sativus	-	
Solanum melongena	Solanum americanum, Solanum carolinense, Solanum japonense, Solanum japonense, Solanum laciniatum, Solanum lyratum, Solanum lyratum for. xanthocarpum, Solanum megacarpum, Solanum nigrum, Solanum var. humile, Solanum nipponense, Solanum sarachoides	

Table 3. Continued.

Cultivated species	Wild relatives	
Allium sativum	Allium anisopodium, Allium anisopodium var. zimmermannianum, Allium chinense, Allium condensatun Allium cyaneum, Allium cyaneum for. stenodon, Allium cyaneum var. deltoides, Allium deltoide-fistulosun Allium grayi, Allium jaluanum, Allium japonica, Allium komarovianum, Allium macrostemon, Allium maimowiczii, Allium monanthum, Allium nipponicum, Allium ochotense, Allium ouensanense, Allium sacci liferum, Allium schoenoprasmum var. orientale, Allium senescens, Allium splendens, Allium taqueta Allium thunbergii, Allium victorialis, Allium victorialis for. variegatum	
Zingiber officinale	-	
Arachis hypogaea	-	
Actinidia delicosa	Actinidia arguta, Actinidia arguta var. platyphylla, Actinidia arguta var. rufinervis, Actinidia kolomikta, Actinidia polygama, Actinidia rufa	
Lactuca sativa	Lactuca bungeana, Lactuca chilidoniifolia, Lactuca debilis, Lactuca denticulata for. tairensai, Lactuca denticulata var. typica, Lactuca dracoglossa, Lactuca hallaisanensis, Lactuca indica, Lactuca indica fo indivisa, Lactuca raddeana, Lactuca raddeana, Lactuca scariola, Lactuca sibirica, Lactuca triangulata	
Zea mays	-	
Panicum miliaceum	Panicum bisulcatum, Panicum capillare, Panicum capillare var. occidentale, Panicum dichotomiflo rum, Panicum dichotomiflorum, Panicum italicum	
Allium cepa	See wild relatives of Allium sativum	
Allium fistulosum	See wild relatives of Allium sativum	
Prunus persica	Prunus avium, Prunus buergeriana, Prunus cerasus, Prunus choreiana, Prunus davidiana, Prunu densifolia, Prunus donarium, Prunus glandulosa, Prunus ishidoyana, Prunus itosakura, Prunu jamasakura, Prunus japonica, Prunus koraiensis, Prunus leveilleana, Prunus linearipetalus, Prunu maackii, Prunus mandshurica, Prunus maximowiczii, Prunus meyeri, Prunus mume, Prunus padus Prunus pendula, Prunus quelpaertensis, Prunus robusta, Prunus sachalinensis, Prunus salicina, Prunus sargentii, Prunus serrulata, Prunus sibirica, Prunus takesimensis, Prunus tomentosa, Prunus triloba, Prunus verecunda, Prunus yedoensis	
Pyrus pyrifolia vat. culta	Pyrus acidula var. spontanea, Pyrus calleryana, Pyrus calleryana var. fauriei, Pyrus communis, Pyru fauriei, Pyrus hakunensis, Pyrus macropuncta, Pyrus macrostipes, Pyrus maximowicziana, Pyru montana, Pyrus nankaiensis, Pyrus pseudo-calleryana, Pyrus pseudo-uipongensis, Pyrus pyrifolic Pyrus seoulensis, Pyrus serotina var. culta, Pyrus uematsuana, Pyrus uipongensis, Pyrus ussuriensi. Pyrus uyematsuana, Pyrus vilis	
Prunus salicina	See wild relatives of <i>Prunus persica</i>	
Solanum tuberosum	See wild relatives of <i>Solanum melongena</i>	
Cucurbita moschata		
Brassic campestris subsp. napus var. oleifera	See wild relatives of Brassica campestris var. pekinensis	
Oryza sativa	Oryza sativa (weedy rice)	
Sesamum indicum	-	
Sorghum vulgare	Sorghum halepens, Sorgnum nitidum var. majus	
Glycine max	Glycine soja, Glycine max (wild soybean), Amphicarpaea trisperma	
Spinacia oleracea	•	
Fragaria ananassa	Fragaria nipponica, Fragaria orientalis	
Helianthus annuus	Helianthus annuus (wild), Helianthus tuberosus (wild)	
Ipomoea batatas var. edulis	Ipomoea coccinea, Ipomoea hederacea, Ipomoea hederacea var. integriuscula, Ipomoea hederace var. integriuscula, Ipomoea lacunosa, Ipomoea lacunosa, Ipomoea nil, Ipomoea purga, Ipomoea purea, Ipomoea triloba	
Thea sinensis	Thea sinensis (wild tea)	
Nicotiana tabacum	-	
Lycopersicon esculentum	-	
Juglan sinensis	Juglans ailanthifolia, Juglans cordiformis, Juglans mandshurica, Juglans mandshurica for. steno carpa, Juglans mandshurica for. stenocarpa, Juglans mandshurica var. sieboldiana	
Citrullus lanatus	-	
Triticum aestivum	-	

⁻ No known related species in Korea.

between taxa. Suh *et al.* (1997) classified weedy rice by morphology and molecular marker pattern, and identified genetic variation within weedy rice collections. The ecological and morphological characteristics of weedy rice can be differentiated from cultivated rice by higher dormancy, more tillers, longer culms, susceptibility to seed shattering, pubescent leaves, and red pigmentation in seed coat (Cohn & Hughes, 1981; Diarra *et al.*, 1985; Noldin *et al.*, 1999). However, little has been known about the cross-ability of cultivated and weedy rice, which is necessary to estimate the frequency of introgression.

Wild Brassica species (Brassica juncea)

Many species in the genus Brassica are known as interfertile (Kerlan et al., 1993; J ϕ rgensen et al., 1996; J ϕ rgensen, 1999). The genus Brassica is one of the popular species that have used as a material for genetic transformation (OECD, 2000). In Korea, Brassica juncea (Indian mustard) is classified as weed because it frequently occurs in non-cultivating fields by escaping from cultivated lands (Park, 1994). Although the acreage of oil seed rape cultivation in Korea has been decreased in recent, the occurrence of wild mustard (Brassica juncea) and already-settled wild species was increased (personal observation).

Wild Sorghum (Sorghum halepense)

There are no wild relatives to sorghum in Korea. However, *Sorghum halepense*, naturalized plant species immigrated from abroad, becomes a dominant weed in southern part of Korea (Park, 1994). *Sorghum halepense* (johnsongrass) is perennial weed, which is able to spontaneously hybrid with cultivated sorghum (Arriola & Ellstrand, 1996). In spite of rarity in Korea, gene flow into *S. halepense* has potential hazard because of its harmful potential such as vigorous growth and longevity in fields (Holm *et al.*, 1991).

Wild carrot (Daucus littoralis var. koreana)

Cultivated carrot (*Daucus carota* ssp. *sativus*) has wild relatives, which are classified as weed species. In Korea, only one species has been known as wild carrot, *Daucus littoralis* var. *koreana* that grows in the proximity of seashore. The occurrence of *Daucus carota* ssp. *carota*, a prominent weed species in the world, has not been reported in Korea. Several results suggested that the natural gene flow between cultivated and wild *Daucus* species is possible (Wijnheijmer *et al.* 1989; Shim & Jørgensen. 2000). Shim & Jørgensen (2000) reported the genetic relationship between cultivated and wild carrot. Although there are some reproductive barriers (e.g. protan-

dry), the introgression via spontaneous hybridization between cultivated and wild carrot was proposed.

Wild Lactuca (wild relative of lettuce)

Lettuce is one of the most popular vegetables in Korea. Genus Lactuca includes a number of wild species such as Lactuca indica, Lactuca scariola, Lactuca bungeana, Lactuca chilidoniifolia, and Lactuca debilis. In Korea, we can find many wild Lactuca species not only near cultivating lands but also in disturbed areas. In agricultural fields, the emergence of Lactuca species resistant to sulfonylurea herbicide was already observed (Mallory-Smith et al., 1990). It is caused by a consequence of natural evolution under a selection pressure imposed by herbicide. Although the probability of gene flow from cultivated to wild relatives in Lactuca species is relatively low (Raybould & Gray, 1993), the occurrence of herbicide tolerant wild Lactuca suggests that the gene flow from herbicide resistant GMPs may cause the disturbance in ecosystem.

Wild sunflower (Helianthus annuus)

Sunflower is not a major crop, but has been cultivated for fodder of birds or oil in some area in Korea. The escaped sunflowers are classified as a weed in Korea. Arias & Rieseberg (1994) reported that natural hybridization that is the consequence of gene flow occurred at substantial rates with the distances up to 1000 m from cultivated sunflower. Since the cultivating area of sunflower is vast over the world, the potential risk should be considered.

Wild relatives of millet (Panicum miliaceum)

Millet was a major food in Korean ancient times. According to the changes in preference for food, acreage of millet cultivation has been dramatically reduced. Two dominant wild *Panicum* in Korea are *Panicum bisulcatum* and *Panicum dichotomiflorum*. The former is native species and the latter is naturalized (exotic) one from abroad (Park, 1994). However, there is no report for the hybridization between cultivated *Panicum* and wild relatives.

Wild relatives of Allium crops

Genus *Allium* belonging to Liliaceae includes a number of vegetables such as onion, chive, shallot, and garlic. Wild *Allium* species are ubiquitous in Korea (Table 3). They have used as vegetables and traditional medicine. Interspecific hybridization within genus *Allium* has been elucidated (Peterka *et al.*, 1997). The natural introgression can occur

due to the abundance or diversity of *Allium* species in nature (Table 3).

Wild relatives of sweet potato

The flowering of sweet potato (*Ipomoea batatas*) is rare under the natural condition. Therefore, vegetative propagation is common in practice. The breeding of this species, however, is sometimes carried out by the artificial pollination, which uses intact flower induced by grafting the sweet potato scion on the stock of wild morninglory (*Ipomoea nil*, *Ipomoea hederacea*, *Ipomoea purpurea*). Considering the compatibility of vegetative tissue, the hybridization via pollen is possible.

Wild Solanums species

The major species belonging to genus *Solanum* in Korea are eggplant and potatoes. Wild *Solanum* species are shown in Table 3. *Solanum nigrum* is most abundant in agricultural and disturbed areas. The hybridization between cultivated and wild *Solanum* species has been reported (Raybould & Gray, 1993; Rogers & Parkes, 1995).

Avena fatua (wild oat)

Oat (Avena sativa) has been cultivated as forage crop in the southern part of Korea. The wild relative, Avena fatua, can be easily observed over the temperate regions. The high similarities in morphology and phenology suggest that the natural hybridization should not be neglected.

Wild Lolium species

Lolium species, Lolium perenne, Lolium multiflorum, and Lolium rigidum, are used for forage and sward. In Korea, wild Lolium plants are escaped from pasture or grassland. Although the Lolium species are not native in Korea, their adaptability is relatively high compared with other introduced species (Park, 1994). Thus they become dominant species in ecosystem. The genetic constituent of wild Lolium plants is identical to cultivated Lolium species since they are the escaped plants. Because the genetic transformation of Lolium species has been reported (Ye et al., 1997; Dalton et al., 1999), the genetically modified Lolium species should be found in Korea near future.

CONCLUSION

The ecological risks of GMPs are various depending on the traits of transgenes in GMPs. However, there is a consensus that the evaluation and prediction of GMPs have to precede the commercialization of GMPs. The unintended targets or recipients of GMPs are wild relative plants that constitute natural or agricultural ecosystem. Up to day the studies on the possibility of gene flow or introgression of transgene into wild relatives are rare because the spontaneous gene flow between crops and wild relatives has not been noticed. By the peer at Korean ecosystem, we could find some species that can be affected by GMPs. It is important to consider that the feral plant species is not economically important but they are essential and inevitable components of our ecosystem.

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