

Transgenic crops—why gene flow matters

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Several key challenges face researchers attempting rigorous empirical assessment of gene flow from genetically modified (GM) crops to related commercial crops, weeds, and wild relatives. A workshop held recently at Ohio State University (Columbus, OH)* brought together plant population ecologists, evolutionary biologists, weed ecologists, crop scientists, and molecular biologists to discuss progress in the field and appropriate methods for studying questions related to gene flow, with an emphasis on crops and related species in North America. Clearly, there is a paucity of interdisciplinary research on the ecological and agronomic effects of gene flow, and increased public investment in this type of research is sorely needed.

Gene flow from crops to wild or weedy relatives is often cited as a potential risk in the commercialization of transgenic crops¹⁻⁴. Although crops and weeds have exchanged genes for centuries, genetic engineering raises additional concerns because it not only enables introduction into ecosystems of genes that confer novel fitness-related traits, but also allows novel genes to be introduced into many diverse types of crops, each with its own specific potential to outcross. Most cultivated plants mate with one or more wild relatives in some portion of their geographic range, and many crops are known to naturalize and persist as feral weed populations^{5,6}. This means that newly introduced genes could potentially disperse into nearby populations, bringing along new phenotypic traits such as resistance to insects, diseases, herbicides, or harsh growing conditions. Enhanced understanding of this process—and, more importantly, of the impact of crop gene introgression into populations growing on roadsides, field margins, or uncultivated areas—is needed as GM crops continue to be adopted.

Most government agencies that regulate GM plants ask for information about gene flow and its consequences, but it's often difficult to find peer-reviewed publications with relevant data. To some extent, the problem can be traced to a lack of funding (and interest) from government programs that sponsor competitive agricultural research grants. Also, GM crop research is

relatively new, and the pace of commercialization has outstripped the rate at which multiyear, multisite field studies have been carried out and published (one of the only long-term projects of this kind did not include GM crops that were likely to pose ecological risks⁷, making it irrelevant to the issues at hand). To complicate matters further, few biotechnology companies are willing to fund independent risk assessment research or provide precommercial transgenic cultivars for study.

Discussions at the Ohio meeting clarified several issues that should help direct future research⁸. First, a gene is a gene, and our limited experience from environmental studies confirms that transgenes disperse and become incorporated into the genomes of other species in the same manner as other crop genes.

Second, gene flow can be surprisingly widespread. New cases of crop-to-wild gene flow are still being discovered (such as wheat to jointed goatgrass), and crop alleles can persist in weed populations for decades. It is now evident that certain crops (such as oilseed rape) can pass genes to a wild relative even when those genes are carried on unshared (nonhomologous) chromosomes. Some commercially important grass species can hybridize with nearby congeners and then switch to asexual seed production (apomixis), allowing crop genes to spread widely, even when F1 hybrids are sterile.

Third, certain crop types will require new approaches to risk assessment. For trees and other long-lived species, for instance, gene flow is best studied by a combination of empirical studies and simulation models because multigeneration field studies are not feasible.

Fourth, a range of possible fitness costs and benefits have been associated with particular GM traits. Under some conditions, single or multiple transgenes will not have any detectable effect on the survival or reproduction of wild or weedy species. If there are effects, they may be difficult to detect unless weed populations are released from strongly limiting factors (such as drought stress, salinity, or herbivores). Data presented at the meeting indicated that in wild sunflowers at least, a *Bacillus thuringiensis* (*Bt*) gene for lepidopteran resistance can result in an unexpected large boost in seed production.

Fifth, when novel genes spread to free-living plant populations, they have the potential

to create or exacerbate weed problems by providing novel traits that allow these plants to compete better, produce more seeds, and become more abundant.

Showing that a GM trait can enhance a plant's evolutionary fitness prompts several questions. What is the effect on population size and dispersal dynamics of the weed? What is the effect on genetic diversity of wild relatives, above and beyond the "genetic swamping" that already occurs as a result of gene flow from some conventionally bred crops? And what is the likelihood that weeds carrying GM traits could have negative effects on non-target species, trophic interactions, or the diversity of ecological communities?

For most questions about the ecological and agronomic consequences of gene flow, our ability to quantify and predict these outcomes is still rudimentary. It is much easier to rule out unwanted scenarios for certain low-risk crop plants, such as soybean in the United States, than to demonstrate that higher-risk crops such as *Bt* sunflower pose serious environmental risks. When there is good scientific evidence to support the potential of gene flow to exacerbate weed problems or threaten biodiversity, a prudent solution is to delay commercialization.

It is currently impossible to prevent gene flow between sexually compatible species in the same area. Pollen and seeds disperse too easily and too far to make containment practical. This makes the need for environmental studies all the more urgent. Clearly, industry and science can no longer afford to neglect this area of research. Until such studies are carried out, it is unwise to presume that gene flow doesn't matter.

* *The Scientific Methods Workshop on Ecological and Agronomic Consequences of Gene Flow from Transgenic Crops to Wild Relatives, March 5-6, Ohio State University, Columbus, OH.*

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