Gene Flow from Transgenic Crops to Wild Relatives: What Have We Learned, What Do We Know, What Do We Need to Know?

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ABSTRACT

I present a brief history of the science of crop to wild gene flow and a glimpse into its future. Scientists have long recognized that crops can spontaneously mate with their wild relatives. However, for reasons probably associated with the cultures of basic vs. applied science, study of that process was largely neglected. The realization that transgenes could end up unintended in wild plants generated a closer examination of the process of crop-to-wild gene flow and its consequences. I expect that this field will continue to grow, with increased emphasis on using transgenic crops themselves as experimental organisms. However, a sister phenomenon, crop-to-crop transgene flow, and its consequences, may prove to be a more urgent emerging issue to be addressed by specialists in transgene flow.

INTRODUCTION

You would think that spontaneous gene flow from crops into wild populations would be an ideal research topic for basic and applied plant evolutionists, ecologists, and population geneticists. Crops are among the best studied plant species; their genetics and ecology have been studied for centuries. Since many wild relatives of crops are important weeds and/or important sources of germplasm, they are also better studied than your average plant species. The various research questions associated with the process are obvious: What are the factors that influence hybridization between evolutionarily distinct lineages? What is relative hybrid fitness in the field? Do different immigrant alleles introgress at different rates? What are ecological impacts of immigrant alleles at the level of the population, community, or ecosystem? Do any of these immigrant alleles contribute to weediness, invasiveness, niche shifts, or increased extinction risks? Have wild populations collected "heirloom" alleles from past varieties?

Then why did it take the advent of transgenic crops to put the spotlight on a field that had attracted the attention of no more than a handful of plant evolutionists? The key is the phrase "basic and applied". There has been a chasm between "basic plant biology" whose tradition comes from the "ivory tower" field of botany and "applied plant biology" whose tradition comes from the "practical" agricultural fields of agronomy and horticulture. The cultures of the two fields marked their territories; splitting plants into (1) those that have a direct impact on human affairs, the useful and noxious ones, and (2) those with no practical significance, such as *Arabidopsis*. The cultures also generated a bit of disdain for scientists working in the other field. Since spontaneous hybridization involves plants from each of the two groups, it doesn't fit well into either category. While it is surprising that any work at all was done on crop to wild gene flow given these cultural barriers, it might not be surprising that the handful of scientists who published in this area prior to the advent of transgenics are among the brightest lights of their fields: examples include Edgar Anderson, Herbert Baker, Spencer Barrett, J. M. J. De Wet, Jack Harlan, and Charlie Heiser.

Let's take a brief look at the development of the field, the principles that have emerged, and the most important research questions that remain unanswered.

PAST

The fact that cultivated plants naturally mate with their wild relatives has been recognized for a long time (De Candolle 1886). In fact, decades ago Edgar Anderson (1949) described what he called "superweeds", especially noxious plants resulting from the hybridization between domesticated plants and their wild relatives. For most of the 20th century, what research was done on the topic concerned itself largely with two areas, (1) the introgression of domesticated alleles into weed populations resulting in increased crop mimicry (e.g., Barrett 1983) and (2) the spontaneous introgression of wild alleles into crop landraces that might serve as a substrate for crop improvement (e.g., Jarvis and Hodgkin 1993). A few scientists took a broader view, writing papers suggesting that domesticated plants, their associated weeds, and wild relatives form actively evolving complexes of plants, joined through both shared ancestry and occasional hybridization (e.g.,De Wet and Harlan 1975, Small 1984), similar to the what "basic" plant evolutionists call a "syngameon" (Grant 1981).

Despite these contributions, the prevailing view of both basic and applied plant scientists at the time of the creation of the first transgenic plants was that spontaneous hybridization between domesticated plants and their wild relatives was rare and idiosyncratic. Most likely, this attitude among basic plant scientists was part of a broader backlash to decades of enthusiasm for identifying natural hybrids and describing their evolutionary impact, only to have genetic analysis topple some of the "classical" examples, and the attitude among applied plant scientists probably resulted from the frustrations some breeders encountered in attempts to make wide crosses. This now-outdated view has persisted in some quarters. For example, Martina McGloughlin (2000), Director of Biotechnology at the University of California at Davis, recently wrote in a guest editorial for the *Washington Post*, "Breeders have found that, with rare exceptions, the crops do not successfully cross-breed with other plants in the environment, especially plants in crop-growing regions."

PRESENT

Given that common view, it is surprising that much thought was given to what might happen if transgenes found their way into natural populations. Interestingly, among the first to address the issue were two Calgene scientists (Goodman and Newell 1985) who wrote, "The sexual transfer of genes to weedy species to create a more persistent weed is probably the greatest environmental risk of planting a new variety of crop species". For reasons that are still somewhat unclear to me, of all the environmental concerns voiced about crop biotechnology, those associated with transgene flow into the populations of wild relatives have received the most attention. Indeed, almost every general treatment of the environmental impacts of plant biotechnology gives some consideration to the topic (e.g., Colwell et al. 1985, Hails 2000, Keeler and Turner 1990, Marvier 2001, McHughen 2000, National Academy of Sciences 1989, 2000, 2002, Rissler and Mellon 1996, Scientists' Working Group on Biosafety 1998, Snow and Moran-Palma 1997, Tiedje et al. 1987, Traynor and Westwood 1999, Van Aken 1999, Wolfenbarger and Phifer 2000).

The renewed focus on gene flow has had important consequences. Gene flow is a primary concern for regulatory oversight of transgenic plants in the United States and other countries. It is a consideration for regulatory decisions made about transgenic plants grown under notification and permit as well as those being considered for deregulation (USDA-APHIS 1997). In addition, renewed research effort has been focused on the topic.

Much of the effort has been to address the question of whether domesticated plants are capable of spontaneously mating with wild relatives under field conditions. Indeed, there is now substantial evidence that at least 44 cultivated plants mate with one or more wild relatives somewhere in the world (Table 1). The picture that is emerging is that most of the world's domesticated species probably mate with one or more wild relatives somewhere in the world (reviewed by Ellstrand et al. 1999). Hybridization rates measured by experimental studies vary with the study system, ranging from exceedingly low to quite high. It is not unusual for hybridization to be detected at distances of one hundred meters or more. An increasing number of hybrid fitness studies have been conducted under field conditions. The hybrids are rarely fully sterile; in certain instances they are actually as fit or more fit than their genetically pure wild siblings (reviewed by Ellstrand et al. 1999). Additionally, plenty of evidence has been uncovered demonstrating hybridization between crops and their wild relatives has served as a stimulus for the evolution of increased weediness and invasiveness (Ellstrand and Schierenbeck 2000). Another problem associated with crop to wild gene flow has been uncovered, the increased risk of extinction due to hybridization; many examples of this problem have been noted (reviewed by Ellstrand et al. 1999).

In summary, crop-to-wild gene flow is not uncommon, and on occasion, it has caused problems. Would we expect transgenic plants to behave any differently? The answer is "no". And indeed, experimental work on transgenics is beginning to trickle onto the scene. Transgenics spontaneously hybridize with wild relatives, their hybrids are somewhat or fully fertile, and those hybrids generally pose about the same kinds of risks as those posed by conventional crops (reviewed by Ellstrand 2003). But specific varieties may present unique risks. In many cases, transgenes will present unique phenotypes in the wild. After all, if the trait could have been obtained from a cross-compatible wild relative, it is unlikely that it would have been obtained at great expense and hassle through transformation. Also, there is a growing body of data showing unintended biochemical, physiological, anatomical, and morphological phenotypes in transgenic plants (examples in Kuiper et al.2001). It is not clear whether the rate of such pleiotropy is higher in transgenics than nontransgenics, and it is not clear how such unintended traits will be expressed in crop-wild hybrids. What is clear is that the lessons gleaned from conventional crops can only go so far in predicting the impacts of transgenes that end up in unintended genomes.

FUTURE

What does the future hold for research on gene flow from transgenic crops to wild relatives? There is no doubt that researchers in this area will continue on the research themes established over the last decade regarding hybridization rates and hybrid fitnesses. But I do not doubt that the research will increasingly utilize transgenic crops themselves instead of nontransgenic surrogates. Since it is almost a certainty that transgenes have entered natural populations, I suspect that the first report will come in the next five years. Additional key areas that are vastly underexplored are the genetic basis of traits that contribute to the evolution of weediness and invasiveness (see discussion in Ellstrand and Schierenbeck 2000) and gene flow by seed.

But the most important contribution in this area is apt to be via the evolution of a sister field on the unintended gene flow from transgenic crops to other crops (transgenic or not). This kind of gene flow has received almost no attention from those who address the risks of transgenic organisms, but crops of the same species growing in proximity are much more likely to mate with one another than with a wild relative. A few recent events have demonstrated that intercrop gene flow has already delivered transgenes into plants for which they were not intended and that gene flow may have environment, economic, agronomic, or social impacts:

- Spontaneous sequential cross-pollination between three varieties (two transgenic) of canola resistant to different herbicides resulted in the evolution of multiple herbicide resistant volunteers (Hall et al. 2000). While other herbicides are available for controlling these new weeds, the range of options has now been reduced, especially for farmers who want to remove volunteer canola from other crops resistant to the three herbicides in question.
- Apparent spontaneous intercrop gene flow of an herbicide resistant transgene into a nontransgenic variety of canola has already resulted in at least one lawsuit involving the unapproved use of intellectual property (Clark 2001).
- Interestingly, the same case drew a complaint from the defendant of genetic pollution by the transgenic variety.
- Reports of the occurrence of transgenes in remote Mexican maize landraces (Dalton 2001, Quist and Chapela 2001) after years of that country's moratorium on transgenic maize have raised discussion about whether post-commercialization transgene containment is likely or even possible (Hodgson 2002).

In addition to the foregoing events, the unintentional spread of transgenes through intercrop gene flow may have other important consequences:

- The pollination of seed crops intended for human or animal consumption by plants transformed to create industrial biochemicals may pose human or animal food safety issues (Ellstrand 2001).

- The pollination of crops intentionally grown for organic produce may have their certification jeopardized if that produce contains seeds or seed products resulting from seeds that were sired by transgenic plants (National Academy of Sciences 2002).
- Seed from plants that have been unintentionally pollinated by transgenic plants may serve as "genetic bridges" that transfer transgenes to other varieties or wild relatives (National Academy of Sciences 2002).

While there is certainly no reason to abandon research on crop-to-wild gene flow, the data and skills accumulated in this endeavor, may prove helpful in addressing the simpler, but perhaps more urgent, issues of transgene flow among crops.

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Table 1 There is more than circumstantial evidence for natural hybridization between the following domesticated plants and one or more wild relatives (Ellstrand 2003)

Cultigen	Scientific name
Alfalfa	*Medicago sativa*
Apple	*Malus x domestica*
Avocado	*Persea americana*
Banana	*Musa acuminata*
Bean, common	*Phaseolus vulgaris*
Beet, sugar	*Beta vulgaris*
Bentgrass, creeping	*Agrostis stolonifera*
Cacao	*Theobroma cacao*
Cane, sugar	*Saccharum officinarum*
Cassava	*Manihot esculenta*
Cocona	*Solanum sessiliflorum*
Coffee, arabica	*Coffea arabica*[b]
Cotton	*Gossypium barbadense*
Cotton	*Gossypium hirsutum*
Elm, Siberian	*Ulmus pumila*
Fescue, tall	*Festuca pratensis*
Gourd	*Cucurbia pepo*
Grapes	*Vitis vinifera*[b]
Juniper	*Juniperus chinensis*
Lettuce	*Lactuca sativa*
Maize	*Zea mays* ssp. *mays*
Millet, foxtail	*Setaria italica*
Millet, pearl	*Pennisetum glaucum*

Mushroom, button	*Agaricus bisporus*
Oats	*Avena sativa*
Potato	*Solanum stenotomum*
Potato	*Solanum tuberosum*
Quinoa	*Chenopodium quinoa*
Radish	*Raphanus sativus*
Rape, swede	*Brassica napus*
Rape, turnip	*Brassica campestris*
Raspberry	*Rubus idaeus*
Rhododendron, catawba	*Rhododendron catawbiense*
Rice	*Oryza glaberrima*
Rice	*Oryza sativa*
Rye	*Secale cereale*
Ryegrass	*Lolium perenne*
Salsify	*Tragopogon porrifolius*
Sorghum	*Sorghum bicolor bicolor*
Soybean	*Glycine max*
Squash	*Cucurbia pepo*
Strawberry	*Fragaria x ananassa*
Sunflower	*Helianthus annuus*
Walnut	*Juglans regia*
Watermelon	*Citrullus lanatus*
Wheat, bread	*Triticum aestivum*
Wheat, durum	*Triticum turgidum durum*