



## Gene Flow among Transgenic Plants and Their Wild Relatives: Implications for Risk Assessment

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Research on gene flow from transgenic plants marches on! For example, the North Central Weed Science Society hosted the second biannual symposium on gene flow on December 12 – 13, 2007, in St. Louis, Missouri. Abstracts of the 38 oral presentations and posters are available at <http://www.ncwss.org/>. The meeting brought together academic, industry, government, and other interested scientists to discuss recent research on 1) within-species gene flow, 2) crop-wild hybridization and gene introgression, 3) consequences of gene flow, 4) approaches to managing gene flow, and 5) modeling gene flow. The organizing committee included Michael Horak (Monsanto Company; Committee Chair), David Gealy (USDA), Hector Quemada (Crop Technology Inc.), Neal Stewart (University of Tennessee), Mark Westgate (Iowa State University), and Allison Snow (Ohio State University). More than fifty people from at least six countries participated.

The arrival of transgenic crops in the 1990's triggered an explosion of research on the extent and consequences of gene flow from crop species to their wild, weedy, or feral relatives. More recently, many gene flow studies have focused on problems that can arise from the unwanted, adventitious presence of transgenes in non-GE seed and food supplies. This later phase of gene flow research was well represented in presentations about crop-to-crop transgene dispersal in corn, alfalfa, canola, and wheat. Underscoring the need for managing pollen- and seed-mediated dispersal of transgenes, David Gealy summarized a new report from CAST (Council on Agricultural Science and Technology) on "Implications of Gene Flow in the Scale-Up and Commercial Use of Biotechnology-Derived Crops" (<http://www.cast-science.org/>).

Meanwhile, gene flow to wild, weedy, or feral relatives is still a very active area for research. Investigators discussed new findings about the extent of hybridization in wild/weedy relatives of corn, rice, wheat, sugar beet, canola, squash, sunflower, sorghum, radish, and cowpea. Most of these crops have weedy relatives that could become more challenging to manage if they acquire new types of herbicide resistance, whether transgenic or not. This issue was raised in several presentations, and three invited speakers described gene flow from GE canola in Canada, where herbicide resistance traits have spread to wild *Brassica rapa*, volunteer canola, and feral populations that establish from spilled seeds. Michael Owen's group also presented studies of the potential for spontaneously evolved herbicide resistance to spread *via* hybridization among closely related weed species in the Asteraceae and Amaranthaceae families.

A poster by Remy Pasquet et al. examined possible risks of Bt genes that could enter wild cowpea populations in West Africa, where Bt cowpea is being developed. Otherwise, few presentations included crop-wild systems in which it was possible to examine the consequences of gene flow, as opposed to its mere occurrence (which is often referred to as "exposure" to a given "hazard"). Two speakers discussed current regulations and the challenges of evaluating the "hazard" component of risk assessment, while others indicated that *any* transgene could be considered a commercial hazard if it spreads adventitiously to non-GE seeds or food.

Given the regulatory, commercial, and environmental incentives for confining transgenes, research on bioconfinement methods such as sterility, chloroplast transformation, and site-specific recombination to remove transgenes is also receiving attention. Christiane Koziol presented ongoing research by the EU project known as Transcontainer (<http://www.transcontainer.org>), and Neal Stewart's group described plans for related studies in tobacco and canola.

Several important research areas were not represented at the meeting. These included studies of 1) gene flow from new types of GE plants that are being developed for biofuels, forage, landscaping, and forestry applications; 2) fitness effects of transgenic drought resistance, cold tolerance, or better nutrient use efficiency in wild/weedy relatives; 3) whether increased fitness due to transgenes could result in weedier or more invasive plant populations; and 4) whether transgene introgression could threaten the genetic diversity of wild relatives, above and beyond the effects of ongoing gene flow from conventional crops. To address these and other types of questions, investigators noted that weed scientists need to have greater access to transgenic materials and more opportunities for funding from federal agencies.

In summary, this symposium offered a great opportunity for researchers to share recent results and for other interested parties to gauge the status of gene flow research in the USA and elsewhere.

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