

Pollen-mediated gene flow from genetically modified herbicide resistant creeping bentgrass

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Introduction Approximately 162 ha of multiple experimental fields of creeping bentgrass (*Agrostis stolonifera* L.) genetically modified for resistance to Roundup® herbicide, were planted in central Oregon in 2002. When the fields flowered for the first time in the summer of 2003, a unique opportunity was presented to evaluate methods to monitor potential pollen-mediated gene flow from the experimental GM crop fields to compatible sentinel and resident plants that were located in surrounding, primarily non-agronomic areas.

Materials and methods A sampling grid to study the spatial pattern of gene flow was based on assumptions of pollen viability of 3 hours and prevailing winds of 10 km per hour from the northwest at the anticipated time of pollen shed. Sentinel plants of *A. stolonifera* were placed in all map directions, but primarily to the south and southeast of the control district which contained the GM fields. Sampling grid intervals for the sentinel plants were smaller close to the control district and increased with distance from the perimeter of the control district. Greenhouse methods for detecting gene flow (**Figure 1**) were based on seedling survival after treatment with Roundup® herbicide in a track sprayer and positive TraitChek™ tests for the *CP4 EPSPS* marker. Confirmatory laboratory tests for the presence of the engineered *CP4 EPSPS* marker included PCR and DNA sequencing.



Figure 1 Greenhouse assays A: Seedlings; B: Track Sprayer; C: Resistant Plants; D: TraitChek™ test

Table 1. Incidence and prevalence of gene flow from GM crop to sentinel and resident *Agrostis* spp.

Species	% Plants with positive seedling progeny	Number of seedling progeny tested	Number positive seedling progeny	% Positive seedling progeny
Sentinel <i>Agrostis stolonifera</i>	54% (75/ 138)	32,000	625	2.00%
Resident <i>Agrostis stolonifera</i>	53% (16/30)	565,000	157	0.03%
Resident <i>Agrostis gigantean</i>	33% (13/39)	397,000	159	0.04%

Results. As shown in Table 1 the overall frequency of hybridisation was higher in sentinel plants (2%) than in resident *Agrostis* spp. (0.03-0.04%). While most hybridisations were observed within 2 km in the direction of prevailing winds from the perimeter of the control district, the maximal distances to which hybridisations were observed were 21 km in sentinel plants and 14 km in resident *Agrostis* spp.

Conclusions The methods we describe study the spatial pattern of gene flow to compatible non-crop plants can contribute to the environmental risk assessment of genetically modified crops by providing estimates of exposure to marker genes from GM crops on a landscape level that may include non-target non-crop and crop plants.

Reference

Watrud, L.S., E. H. Lee, A. Fairbrother, C. Burdick, J.R. Reichman, M. Bollman, M. Storm, G. King & P. K. Van de Water (2004). Evidence for landscape level pollen-mediated gene flow from genetically modified creeping bentgrass, Proc. National Acad. Sci. (US) 101, 1433-1438.