DETECTING GENE FLOW FROM IMIDAZOLINONE-RESISTANT WHEAT TO CONVENTIONAL WHEAT VARIETIES. Todd A. Gaines, Christopher Preston, Patrick F. Byrne, Scott J. Nissen, Dale L. Shaner, W. Brien Henry and Philip H. Westra, Graduate Student, Visiting Scientist, Associate Professor, Professor, USDA-ARS Scientist, USDA-ARS Scientist, and Professor, Colorado State University, Fort Collins, CO 80523.

Detecting rare events efficiently, such as gene flow between crop fields or between species, requires both the testing of a large number of individuals and a simple, but robust selection system. These factors make herbicide resistance an obvious marker to use. However, one of the constraints of finding rare events is the number of individuals that can be screened efficiently. For example, events occurring at low frequency require many thousands of individuals to be tested. In such cases, an efficient screen needs to be developed. In this work, gene flow between imazamox-resistant and imazamox-susceptible wheat crops was examined. In order to determine the most effective method for detecting imazamox resistance within samples; a comparison was made among three screening methods using a selected group of samples. A field evaluation used replicated field plots with a total sample size of approximately 10,000 individuals. A greenhouse method involved planting approximately 800 seeds by hand in flats, spraying at the two to three leaf stage, clipping, and evaluating re-growth. A germination method involved soaking approximately 5,000 seeds in herbicide solution for 24 hours, planting at high density in greenhouse flats, and spraying to eliminate false positives. Simply as a result of the number of individuals screened, the field evaluation method allowed detection of gene flow at the lowest levels. However, the seed soaking method required the least amount of time, space and labor.

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