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Global Change and the Cryptic Invasion by Transgenes of Native and Weedy Species

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According to the U.S. Department of Agriculture (USDA): “The sustainability of agriculture, forest and rangelands depends on understanding the factors that influence climate change, the mechanisms that may enhance or mitigate this change, and its effects on food and fiber production and natural resources.” (USDA: <http://www.csrees.usda.gov/>). A global issue in agriculture is the increasing incidence of herbicide resistant weeds. Weeds may become resistant to herbicides by mutation or by gene flow from sexually compatible crop species genetically modified for herbicide resistance. The adventitious presence of transgenes in the environment represents a potential threat to U.S. agriculture, and is an understudied aspect of global change. The investigators have adopted commercially available canola genetically modified for herbicide resistance as a model system. Canola is sexually compatible with a number of weeds in the United States; this project will focus on field mustard (*Brassica rapa* L.) and black mustard (*Sinapis arvensis*). The investigators will travel to sites in the midwestern United States to collect weeds and their seed progeny to: (1) evaluate the incidence of gene flow from crop to weed, and (2) to assess population variability in the likelihood of hybridization. The population measures, including flowering phenology and sexual compatibility, will be mapped and merged with predictive models of climate change in the United States. The result will be an understanding of regional variation in the likelihood of transgene flow, a predictive model of how these risks will change in the advent of climate change, and a heightened awareness of the impact of global change on agriculture and food supply in the United States.

The primary goal of this research project is to develop a predictive model of how populations of plant agricultural pests may expand or contract in the face of climate change. The study system is genetically modified canola (*Brassica napus* L. [Brassicaceae]) and native and weedy plant species that are sexually compatible with canola. To this end, the investigators will conduct plant surveys of the upper midwestern United States where canola is currently an important crop system, greenhouse experiments to evaluate population variability in compatibility, and GIS modeling efforts that incorporate these data with accepted models of predicted climate change. This collaborative work will involve scientists from the University of Arkansas, California State University (CSU), Fresno, and the U.S. Environmental Protection Agency’s National Health and Environmental Effects Laboratory, Western Ecology Division. It is anticipated that one postdoctoral fellow and two graduate students will be recruited to the project. The results of the work will be published in a series of peer-reviewed publications (at least three), one review article, four papers presented at national or international meetings, and a symposium arranged by the collaborators to be held in the last year of the project.

This research approach adopts methods from plant population biology and rapidly evolving geospatial technologies. The investigators visit sites in the upper midwest (Montana, North Dakota, Minnesota, and Wisconsin); midwest (Iowa, Illinois); and southeast (Arkansas, Oklahoma) to collect seeds of weed pests that are sexually compatible with canola (primarily *B. rapa* and *S. arvensis*). These seeds will be used to address a number of questions that include estimating the rate of gene flow from GM herbicide resistant canola, and determining population variability in sexual compatibility with canola. Greenhouse studies will be completed at the University of Arkansas, Fayetteville. Spatially explicit information regarding rates of gene flow, sexual compatibility, and environmental data will be incorporated into a GIS layer, which in turn will be incorporated into an emerging predictive model of climate change. The majority of the geospatial modeling will be completed at CSU, Fresno. This work constitutes a novel approach to assessing the risks of transgene escape in the face of climate change. This project is unique in melding traditional plant population biology with emerging spatial technologies.