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Seed dormancy may hold key to improved weed management

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Weeds are the primary pests that cause yield losses in producing the nation's food and fiber crops. Weeds flourish in agricultural, urban, and natural settings because they have certain characteristics, such as seed dormancy, that provide for their persistence.

Seed dormancy, which denotes a relatively inactive or resting condition, slows down or stops weed seed germination. The dormant seeds in the soil allow weeds to escape – or avoid exposure to – control practices that target emerging and emerged weed seedlings.

With support from USDA's National Research Initiative (NRI), researchers from the USDA-Agricultural Research Ser-

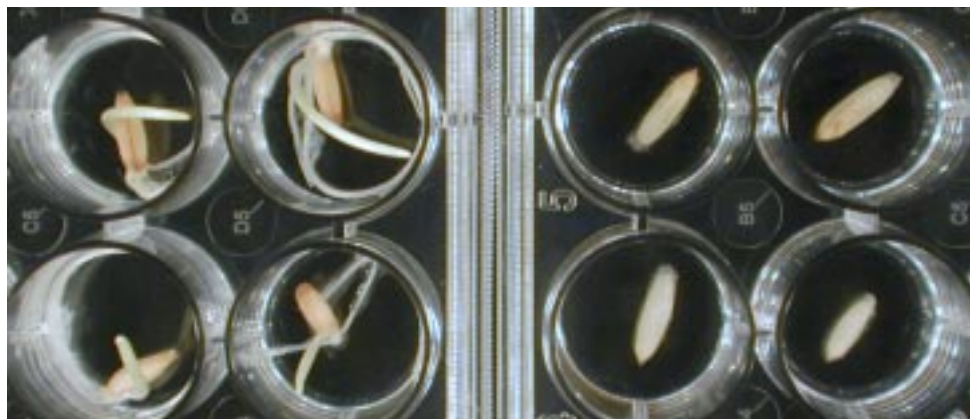
vice (ARS) and North Dakota State University (NDSU) are using molecular and genetic approaches to develop fundamental knowledge of seed dormancy in wild oat.

WILD OAT

Wild oat is an economically important annual weed that competes effectively with small grain crops for light, space, nutrients, and water, thereby reducing crop yields in many parts of the world. In North Dakota alone, field losses and additional production costs for wild oat are estimated at \$150-200 million annually.

Several herbicides are available for controlling wild oat, but their repeated use leads to herbicide-resistant strains

GERMINATION OF NON-DORMANT (LEFT) AND DORMANT (RIGHT) WILD OAT CARYOPSES.



The potential benefit from this research is new knowledge that will be critically important as biologically based weed management strategies are considered and developed.

growing in farmers' fields. Crop producers need new biologically based methods to control problem weeds like wild oat.

Wild oat has been used by scientists worldwide for nearly a century in a model system to investigate the environmental, physiological, biochemical, and molecular bases for dormancy and to seek natural and artificial means to break seed dormancy.

Scientists have known for some time that the dormancy trait is controlled by a combination of genetic and environmental factors. As a step toward understanding the signaling pathways and regulatory mechanisms for seed dormancy, the research team is evaluating the genetics of dormancy.

They are also identifying molecular markers for dormancy quantitative trait loci (QTLs), and evaluating a genotype by environmental interaction as it relates to dormancy in wild oat.

APPLYING GENETICS TO WEEDS

With funding help from the National Science Foundation, the researchers first cross-pollinated a dormant and a non-dormant strain of wild oat to develop several genetic populations, segregating for dormancy. Using these populations and classical genetics, they determined that at least three QTLs control seed dormancy. They used molecular techniques to identify markers for two QTLs.

In this phase of the project, they further developed an advanced generation recombinant line (RIL) population and used the population to construct a rudimentary genetic linkage map for wild oat. This map is essential in locating the position of existing and newly discovered QTLs in the genome.

In addition, RIL seeds were germinated at temperatures from 10 to 30 °C to evaluate a genotype by germination temperature interaction and to determine which dormancy QTLs are influenced by the germination temperature.

IMPACT

This NRI-funded research program has facilitated development of a RIL population and linkage map, which are critical tools for investigating genetic and environmental factors that regulate dormancy in wild oat.

Future goals are to clone and characterize genes that regulate seed dormancy using dormant strains of weedy grasses and a comparative genetics approach.

The potential benefit from this research is new knowledge that will be critically important as biologically based weed management strategies are considered and developed. In addition, fundamental information on dormancy in seeds may be applied to solve problems related to pre-harvest sprouting in seeds of cereal grain crops like barley, rice, and wheat.



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