

# **Genomic Evaluation of the Defense Response of Maize (*zea mays* L.) against Herbivory by the Western Corn Rootworm**

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## **Project Description**

### **Objectives**

The goal of this project is to develop maize (*Zea mays* L.) cultivars with improved native plant resistance against root feeding by larvae of the western corn rootworm (WCR, *Diabrotica virgifera virgifera* LeConte), the most important insect pest in the U.S. Cornbelt.

Maize germplasm with improved levels of native WCR resistance has been a major research thrust among the seed companies and university scientists. Resistance sources combined with new genetic tools enable scientists to investigate the genetic and biochemical basis of the defense response in maize against WCR. In a companion project funded by the Illinois Missouri Biotechnology Alliance (IMBA, Project 2006-6), the investigators initiated some novel approaches to evaluating gene expression patterns and metabolite profiles associated with maize and WCR larvae feeding.

This project will:

Determine the genomic location and effect of major quantitative trait loci (QTL) involved in the inheritance of WCR resistance in maize.

### **Procedure**

Candidate genes for these QTL will be identified by integrating QTL results with gene expression patterns using a root transcriptome map and confirmed using association genetics.

### **Impact**

This new knowledge and the genetic basis of WCR resistance are key requisites for increasing maize germplasm screening effectiveness for novel WCR resistance sources and to devise new methods to integrate this germplasm into elite breeding programs in the Midwestern Cornbelt.