

Genomic Evaluation of the Defense Response of Maize (*Zea mays* L.) against Herbivory
by the Western Corn Rootworm (*Diabrotica virgifera virgifera* LeConte)

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The western corn rootworm (WCR) is the most important insect pest in the U.S. Corn Belt. In the past, breeding programs were not successful improving native host plant resistance of corn against root feeding by WCR larvae in maize. This lack of progress was due to the lack of resistant plant materials and detailed information about the defense responses of maize against WCR larvae root feeding and wounding. Recently maize germplasm with improved levels of native WCR resistance were developed by using exotic maize sources. The main goal of the present project is to investigate the genetic basis of WCR resistance in these newly developed maize cultivars using a quantitative trait loci (QTL) mapping approach. Given the genetic complexity and the low to moderate levels of resistance of the parental inbreds used for the development of the initial mapping population, we decided to develop new and more informative mapping populations. A total of four populations were developed using the double haploid technology in 2006/2007 and two mapping populations were test-crossed in 2007. Populations AG1×NGSDRW1 (250 DHL-TC) and AG1× AR17056-16 (200 DHL-TC) were planted in Illinois, Missouri, South Dakota and evaluated for WCR resistance, root size, and root regrowth in the summer season of 2008. The statistical analysis and quantitative genetic interpretation of the phenotypic data is underway.