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**Project ID: FY10-NW-012**

**FY09 ARS Agreement #: 59-0206-9-059**

**Research Category: VDHR-NWW**

**Duration of Award: 1 Year**

**Project Title: Mapping QTL in Biparental Populations.**

### **PROJECT 6 ABSTRACT**

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The objective of this project is to complete Fusarium head blight (FHB) mapping projects for three soft red winter wheat varieties possessing potentially novel sources of 'native' FHB resistance. Varieties include: 'Truman' from the University of Missouri, 'IL97-1828' from the University of Illinois, and 'NY91017-8080' from Cornell. Among the limitations of phenotypic data for FHB resistance traits is the widely-reported magnitude of the environmental component of the variance associated with field evaluations of FHB incidence, severity, Fusarium damaged kernels (FDK), and deoxynivalenol (DON) content of FHB infected grain therefore multiple years and/or environments of phenotyping are required to generate reliable FHB data. Statistical rigor also demands replicated data from each environment but replication is often precluded by the scarcity of seed of individual lines in the first year of phenotyping. This project will add one additional year of funding of multi-state and/or multi-year, replicated, phenotyping to complete mapping projects of these three resistant lines. For Truman, a set of 239 RILs from the cross Truman/MO 94-317 will be phenotyped in three environments including nurseries at the University of Missouri, the University of Kentucky and Purdue University. For IL97-1828, 217 RILs from the cross IL97-1828/Clark will be phenotyped at University of Illinois while for NY91017-8080, 219 RILs from the cross NY91017-8080/Caledonia will be phenotyped for an additional year at Cornell. In all cases, incidence and severity, FDK, and DON will be phenotyped in field nurseries following the protocols of the principle investigators and cooperating scientists. Molecular marker analyses will be conducted either at the originating institution or in collaboration with the genotyping center at Raleigh NC under the direction of Dr. Gina Guedira-Brown. DArT analysis will be done by Diversity Arrays Technology Pty Ltd, (Triticarte) Yarralumla, Australia. The identification of genes associated with these resistances will provide information on the uniqueness of these sources of resistance and where they are novel, will permit the pyramiding of resistance genes without the linkage drag currently associated with markers linked to resistance from more exotic sources. Markers associated with resistance genes will be made immediately available to the genotyping centers for use in ongoing marker-assisted-selection programs and will be published in the peer-reviewed literature, and reported at the Fusarium Head Blight Forum and other relevant meetings so that interested scientists may make use of them in their own breeding programs.