

**PI: Mohsen Mohammadi**

**PI's E-mail: mohamm20@purdue.edu**

**Project ID: FY16-NW-005**

**ARS Agreement #: 59-0206-4-028**

**Research Category: VDHR-NWW**

**Duration of Award: 1 Year**

**Project Title: Genetics of, and Breeding for, Fusarium Head Blight Disease Resistance in Wheat.**

### **PROJECT 1 ABSTRACT**

(1 Page Limit)

Fusarium head blight (FHB) is a major disease of soft red winter (SRW) wheat production in the Eastern US including Indiana. The use of resistant varieties is environmentally friendly and the most economical way to manage the disease. Purdue small grains breeding program serves the SRW wheat growing regions by improving germplasm that are resistant to FHB through breeding and genetics projects. Purdue also collaborates with neighboring states in coordinated projects concerning evaluation of advanced SRW wheat lines and utilization of a male sterile population to facilitate the tedious task of crossing nurseries. We will plant three FHB nurseries.

- Nursery I includes Purdue advanced lines and the entries listed in the coordinated UESRWWN and five states preliminary and advanced trials (total 160 entries).
- Nursery II is the coordinated P+NUWWSN trials (total 92 entries).
- Nursery III includes 1044 breeding families (nearly homozygous) and 1241 recombinant inbred lines (RILs) from the six biparental mapping populations. The breeding families are progeny of crosses that pyramid native and exotic FHB resistance and also type I and type II resistance.

The three FHB nurseries will be evaluated under artificial inoculation and misting system for FHB incidence and appearance. Deliverables: the FHB nurseries will aid in decision making in variety release, selection of the most FHB resistant breeding families, and generating phenotypic data for genetics studies concerning identifications of FHB resistance loci in SRW wheat.

The 1241 RILs from six crosses were previously genotyped using microsatellite (SSR) markers. This time we will use dense Genotyping-by-Sequencing (GBS) platform for biparental QTL mapping. We will also implement genome-wide breeding technologies such as genome-wide association studies (GWAS) and will evaluate of predictive breeding. The expected outcomes will be achieving a denser genetic map of soft red winter wheat and identification of breeder's friendly molecular markers to aid in breeding for FHB resistance.

We will generate novel genetic diversity through traditional crossing nurseries and also use a male sterile population and fertilize it with our most FHB resistant germplasm for two breeding cycles. This procedure resembles half-sib selection in open-pollinated populations, eliminating the need for tedious task of cross fertilization in greenhouse. We will then use standard bulk or pedigree method to extract lines from this male sterile population.

The research proposed here will also train highly qualified PhD students, scholars, and postdoc scientists.

The financial aid requested in this proposal will be used to cover land, experimental expenses, recruiting postdocs, technician, undergraduate workers, and graduate students stipend and fees.