

**PI: Fusheng Wei**

**PI's E-mail: fushengw@email.arizona.edu**

**Project ID: FY10-IN-010**

**FY09 ARS Agreement #: New**

**Research Category: GDER**

**Duration of Award: 1 Year**

**Project Title: Investigation of the Barley-Fusarium Interaction using NextGen Sequencing.**

### **PROJECT 1 ABSTRACT**

(1 Page Limit)

Fusarium head blight is a devastating disease for barley and wheat by reducing yield and diminishing grain quality in the form of producing mycotoxin (DON). The overall goal of this project is to discover essential plant genes to control the disease. The project objectives are to: **1)** obtain mRNA samples from inoculated heads at five different time point (0, 16, 24, 32, and 40 hours after inoculation); **2)** sequence the stranded mRNA with the Solexa/Illumina Genome Sequencer and obtain at least 140 million sequence read, totaling 10 gigabase sequence; **3)** assemble the sequence to unique contigs by aligning to barley/wheat EST sequences or rice/sorghum/maize gene set; **4)** quantitatively analyze the expressed sequence by counting the sequence number and finalize the differentially expressed sequence set under different comparison; **5)** functionally categorize the differentially expressed sequence set through different pathways.

We will collect tissue sample and make stranded mRNA in the first four months of the project. In the next two months, we will make 14 sequencing libraries and sequence these mRNA. We will assemble the sequence and assigned them to unique genes in month 7-8. In the final four month, we will quantitatively assess the mRNA reads, finalize the differentially expressed gene set and functionally categorize the data set.

The finalized differentially gene set will be the target genes for further confirmation and transgenic verification. These genes would be in Objective 5: Identify barley genes differentially regulated in the barley-*Fusarium* interaction of **Gene Discovery and Engineering Resistance (GDER)**.