Project Abstract

Project Title:	**Transcriptome Analysis of Durum with Superior Scab Resistance and Performance**	
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Durum wheat (*Triticum durum*) is global staple crop that is highly vulnerable to Fusarium head blight (FHB) or scab. Recent germplasm development efforts involving crosses with PI 277012, Sumai3, and elite durum breeding material have identified promising lines that possess scab resistance and good agronomic performance. The genetic combination of these two qualities has been very difficult to obtain.

The overall goal of the project is to understand the transcriptome of these unique durum lines.

The specific objectives of the project are to:

1) Identify genes that are associated with FHB resistance.
2) Integrate the transcriptome with genome haplotypes and develop high-throughput assays.

The expected outcomes of these objectives are:

1) Identification of gene and gene networks that are differentially expressed during infection which will improve our understanding of the resistance mechanisms in durum wheat. Additionally, we will design assays to measure expression levels of candidate genes in breeding populations to determine predictive power.
2) Knowledge of genomic regions that influence disease resistance and the production of high-throughput markers to screen for the presence of these regions. Knowledge of what portions of source genomic regions are potentially dispensable. This knowledge and the ability to screen a large number of lines will assist in the rapid breeding of FHB varieties.

The approach we will use to accomplish these goals is to perform RNA-Seq experiments on infected spikelets of resistance and susceptible lines. Network analysis will be used to identify differentially expressed genes (DEGs) and gene networks that influence disease severity. The expression information will be integrated with genomic haplotyping to assist in target selection. Causative genes will be validated with high-throughput molecular markers and expression assay screening in related breeding germplasm.

The results of this work will be useful because we will learn more about the FHB resistance mechanism of durum wheat. Additionally, the identity of DEGs will reveal the important portions of genomic linkage blocks and provide targets for breeding efforts to remove undesirable effects in resistant lines. Expression assays and molecular markers developed with this project will be made available for screening larger populations to predict performance.