

PI: Steven Xu**PI's E-mail:** Steven.Xu@ARS.USDA.GOV**Project ID:** FY18-DU-004**ARS Agreement #:** *N/A***Research Category:** DUR-CP**Duration of Award:** 1 Year**Project Title:** Development and Characterization of Elite Durum Wheat Germplasm with Scab Resistance.**PROJECT 1 ABSTRACT**

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Durum wheat (*Triticum durum*) is known to be highly vulnerable to Fusarium head blight (FHB) or scab. The objectives of this project are to continue developing elite durum germplasm with improved FHB resistance derived from other tetraploid wheat subspecies and hexaploid wheat (*T. aestivum*) and to determine the expression of the FHB-resistant quantitative trait loci (QTL) derived from hexaploid wheat. We previously developed a large number of durum lines with improved FHB resistance derived from *T. dicoccum*, *T. carthlicum*, and hexaploid wheat. Five of the durum lines developed from the crosses involved in hexaploid wheat lines exhibited a high level of FHB resistance, low DON, and good agronomic traits. Three lines (D151343, D151344, and D151345) have been crossed with six durum lines (D101073, D08900, D09555, and three isogenic lines (Carpio LCd, Divide LCd, and Joppa LCd) carrying *Cdu1* for low cadmium accumulation). Approximately 7,600 F₂ plants have been genotyped with the STARP (semi-thermal asymmetric reverse) markers for *Fhb1* and *Cdu1* and approximately 400 F₂ plants that are homozygous for *Fhb1* and *Cdu1* have been selected. In this project, the advanced lines (F₅ and beyond) derived from the F₂ plants will be evaluated for FHB resistance in the multiple environments and the top lines (30 - 40 lines) will be evaluate for major agronomic traits, yield, and quality in field trials. To further improve the FHB resistance, we will continue pyramiding the FHB resistance QTL from different sources, including *Fhb1* and the QTL derived from hexaploid wheat (PI 277012) and tetraploid subspecies (*T. dicoccum*, *T. carthlicum*, and *T. timopheevii*). In addition, we observed that the durum lines carrying the homozygous allele for *Fhb1* segregated in their resistance to FHB. Therefore, we proposed to identify the suppressor or enhancer gene(s) using a population of recombinant inbred lines that are homozygous for *Fhb1* derived from the cross between D151343 and Joppa LCd using molecular mapping. By implementation of this project, we expect that a number of elite durum lines with combination of low grain cadmium, high yield, and excellent quality with a high level of FHB resistance will be developed and directly entered the pipelines of durum variety releases. The genomic region(s) that either enhance or suppress the expression of *Fhb1* and other QTL will be identified. Thus, the outputs of this project meet the overall goal of the USWBSI.