Project FY22-DU-008: Transcriptome Analysis of Durum with Superior Scab Resistance and Performance

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1. **What are the major goals and objectives of the research project?**
    1) Identify genes that are associated with FHB resistance.
    2) Integrate transcriptome with genome haplotypes and develop high-throughput assays.

2. **What was accomplished under these goals or objectives?** *(For each major goal/objective, address these three items below.)*

    What were the major activities?
    RNASeq data from the 2023 greenhouse season was analyzed (RNASeq #2). Additionally, another greenhouse experiment was conducted in the Fall of 2024. This experiment consisted of six durum lines including Sumai 3 and PI 277012. Samples from these nine lines were taken at 0 dpi, 5 dpi and 5 dpi of mock inoculated spikes. Non- sampled lines were also screened for disease scores. RNA samples have not been extracted until funding can be secured for sequencing.

    What were the significant results?
    RNA-Seq #2 information from the Fall 2023 GH was analyzed. Initial analysis identified many genes that are significantly regulated in response to inoculation with FHB pathogen. An interesting finding shows that resistant genotypes tend to have less genes activated in response to infection, suggesting that over-stimulation of an inadequate defense response may be the culprit to promoting disease spread. Further analysis will provide more context for these genes, particularly as they relate to cis-genomic regions and the presence of the FHB1 locus.

    List key outcomes or other achievements.
    A script was developed to identify haplotypes of a single line from the collection of potential parents using the mini-pangenome data already acquired. It automatically picks the ancestry of about 95% of the genome. The researcher then needs to investigate further to identify the specific recombination break-points.

3. **What opportunities for training and professional development has the project provided?**
    A PhD student has been investigating this data as part of his thesis. He has learned valuable lessons in setting up an FHB nursery, conducting RNA-Seq experiments and analyzing RNA data to identify differentially-expressed genes.

4. **How have the results been disseminated to communities of interest?**
    Initial results were presented at the FHB Forum.

5. **What do you plan to do during the next reporting period to accomplish the goals and objectives?**
    Once funding is released, we will submit RNA samples for sequencing and run one last greenhouse nursery to validate results from the first two experiments.