Genome-Wide Association Study of a Sorghum Collection from Niger and Senegal for its response to Anthracnose and Grain Mold

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RATIONALE
Sorghum (Sorghum bicolor, (L.) Moench) rises as a highly valuable crop in the context of climate change and food security. However, anthracnose and grain mold are among the most devastating diseases of this crop (Figures 1 and 2).

HYPOTHESIS
We hypothesized that markers for pathogen defense response could be identified through a Genome Wide Association Study (GWAS) on sorghum genotypes of a collection from Niger and Senegal.

APPROACH
A SNP dataset has been generated upon whole genome sequencing of 120 sorghum genotypes from Senegal and Niger. A subset of the collection was then planted across three locations in Senegal during the growing season and evaluated for anthracnose and grain mold responses.

GWAS was then performed for each trait and the top SNPs were mapped to the sorghum annotated genome (Sorghum bicolor v3.1.1) available in Phytozome (https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1). All analyses were performed using R version 4.2.1 and TASSEL version 5.2.89.

FINDINGS
Population Structure
The variant calling generated a dataset over 5 x 10^6 SNPs. Figure 3 shows the population structure.

GWAS for Grain Mold Response
Figures 6 and 7 show the Q-Q and Manhattan plots obtained after GWAS analysis based on grain mold scores. Most of the top hits traced back to proteins reported for their involvement in pathogen response. As an example, S02_18926114 corresponded to Sobic.002G132600.1 that codes a nuclear pore complex protein. Likewise, S03_ 68313945 fell into Sobic.003G366850 which encodes an Exportin-1. Interestingly, nucleoporins and exportins have been reported for their involvement in plant immunity mechanisms (Fang and Gu 2021).

GWAS for Anthracnose Response
Figures 4 and 5 show the Q-Q and Manhattan plots obtained from GWAS based on anthracnose severity scores. Several significant SNPs were identified. Interestingly, S07_37198002 is nearly 39.2 kb downstream of Sobic.007G105100 which product is similar to Mitogen-Activated Protein Kinase Kinase 3 (MKK3). S07_37198002 is also 68.9 kb downstream of a region coding for a Leucine-Rich Repeat (LRR) containing protein. MKK3 pathway and LRR domain containing proteins have been reported for their role in pathogen defense signaling and innate immunity respectively (Dóczi et al. 2007, Ng and Xavier, 2011).

HIGHLIGHTS
GWAS revealed interesting candidate SNPs for further identification of molecular markers for sorghum anthracnose and grain mold resistance. Specifically, deeper investigations on chromosomes 2, 3 and 7 could contribute to identify functional sources for sorghum disease resistance breeding.

REFERENCES

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