

Genome wide discovery and mapping of 3-deoxyanthocyanidin biosynthetic genes to improve anthracnose disease resistance in sorghum

**II. Abstract**

Anthracnose disease is a major threat to sorghum production worldwide. This disease is highly prevalent and severe in warm and humid environments where it causes substantial economic losses. In sorghum anthracnose is caused by *Colletotrichum sublineola*, a fungal pathogen. It causes seedling blight, leaf blight, stalk rot, head blight and grain molding, and thus limits both grain and forage production by 50% or more under severe conditions. Resistance in one location often fails in another location due to the large genetic variation in the pathogen population. Thus, continuous breeding efforts are needed to identify new sources of resistance to mitigate the constantly evolving pathotypes. One strategy is to identify the anthracnose resistant genes that impart resistant to various pathotypes. Sorghum synthesizes site-specific anti-fungal compounds known as 3-deoxyanthocyanidins (3-DAs) in response to anthracnose pathogen attack. These compounds play a major role in restricting pathogen proliferation. Thus, our goal is to identify genes involved in 3-DA biosynthesis and anthracnose disease resistance through genome wide association (GWA) mapping approach. Nested association mapping (NAM) populations (high 3-DA × low 3-DA) and selected sorghum association mapping panel (SAP) lines will be used to determine the variability, fungi-toxicity effect of 3-DAs and to identify putative genes associated with anthracnose resistance, putative genes will be further validated by using gene specific mutants. The direct impact of this project will be availability of anthracnose resistant genes and molecular markers which can be readily used in a breeding program.