Lab Meeting 6/25/19 Bryce Askey

Sorghum QTL Mapping - Background

- Calculate phenotypic parameters from hyperspectral and RGB images
- Match phenotypic variations with presence/absence of markers in DNA (SNPs)

Result: Identification of areas of sorghum genome which control for economically valuable traits



- Problem: hyperspectral images only include top part of plant
 - Can't be used to segment plant organs
- Use hyperspectral images to measure panicle properties
 - Size
 - Openness/compactness
 - Seed pigment levels



- Seed pigment levels determine:
 - Color
 - Physical properties
 - Resistance to stresses
 - Nutritional content
- Majority of pigments accumulate in pericarp

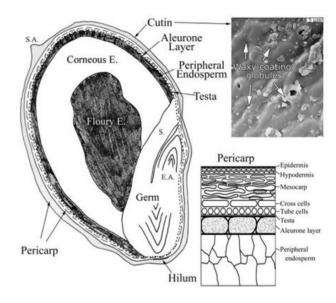
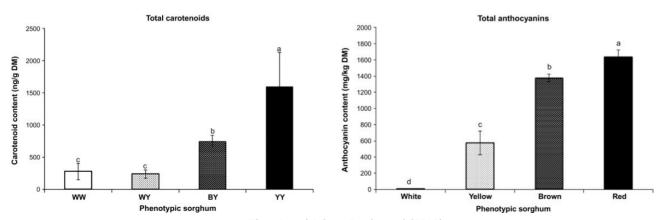


Fig. 1 from Bean et al (2016)

Sorghum seed pigments:

- Anthocyanins antioxidants
- Carotenoids vitamin A precursors
- Tannins digestibility
- Phenolic acids grain hardness



Figs. 2 and 3 from Davis et al (2019)



- Pigment measurement is possible with near-infrared spectroscopy (NIRS)
 - Not yet demonstrated with hyperspectral imaging
- Problem: sorghum pericarp thickness is variable
 - Thick opaque
 - Thin translucent (testa and endosperm are visible)
- Pericarp thickness must be determined before predicting pigment levels
 - Possible to predict pericarp thickness from images?

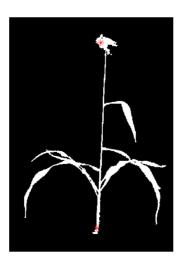
- **Problem:** # of ground-truth measurements required
 - From NIRS papers, estimate 150 250
- Use phenotypic measurements from previous papers with same recombinant inbred lines (RILs)
 - Plant genotypes will be nearly identical
 - Match pigment data from other papers to reflectance data from hyperspectral images

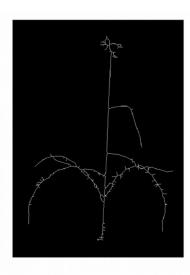
- RGB images contain entire plant
- Use to measure:
 - Number of leaves
 - Leaf angle
 - Plant height
- Unlike hyperpsectral, unable to segment leaves from stem



- Background removal thresholding in L*a*b* color space
- Identify bottom of stalk and panicle
- Skeletonize image







- Trace line on skeleton bottom of stalk to panicle
- Fit line to skeleton points represents stalk
- Segment leaves from stem based on proximity to line
- Calculate phenotypic parameters

With already segmented images:

