The Genetic and Biochemical Frameworks Underlying the Energy Value of Sorghum

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Introduction

- Sorghum (Sorghum bicolor (L.) Moench) is a cereal that produces grains rich in carbohydrates, predominantly starch.
- Sorghum grain is important for providing the necessary calories to both humans in Sub-Saharan Africa and Southern Asia, and livestock in the United States.
- Grain yield, composition, and digestibility in cereals all contribute to the amount of usable energy available for food, feed, and fuel uses.
- Genome-wide association studies (GWAS) are currently being utilized to elucidate genomic regions associated with grain number, size, and composition.
- Data show significant variation in grain number per panicle (63-4024), thousand-grain weight (5.36-40.56g) and starch content (53.80-74.07% dry matter) among accessions.
- Understanding the genetic and biochemical frameworks of these complex, quantitative traits will prove beneficial by creating a platform to boost cereal grain yield and value to help compensate for the steady-increasing food demand.

Figure 1. 2013 Sorghum Association Panel (Florence, SC)

Objectives

1. Characterize the natural diversity in traits directly associated with total energy value of grain sorghum per unit area.
2. Identify genomic regions that are significantly associated with these traits.
3. Investigate these regions of the genome for functional candidate genes in high linkage disequilibrium with the single nucleotide polymorphism.

Experimental Design

- Approximately 400 individuals from the Sorghum Association Panel (SAP) developed by Casa et al. (2008) was planted in 2013 (SC2013) and 2014 (SC2014) in Florence, South Carolina.
- These individuals were planted in a complete randomized design (CRD), with each individual planted in a 2 row, 6.1m (20 ft) plot with a row spacing of 0.762m (2.5 ft).
- Three main culm panicles per plot were randomly bagged at date of flowering to prevent bird and insect predation.
- Bagged panicles were harvested at physiological maturity, dried down to constant weight, and threshed by hand to allow for accurate measurement of grain number per panicle.
- The grain was cleaned using an air aspirator (AT Ferrell Company, Inc.) and wheat dehuller, and then run through a Model 900-2 seed counter (Old Mill, Inc.) to obtain grain number per primary panicle (GNP).
- Thousand-grain weight (TGW) was calculated from total weight of grains divided by total grain number per panicle.
- To determine grain composition, a DA 7250 NIR Analyzer (Perten Instruments) was used on both whole and ground grain to determine starch, amylose, amylopectin, and in vitro starch digestibility percentages. Grain was ground into 1mm particles using a CT 193 Cyclotec (Forti).

Results

Table 1. Ranges of traits showing the natural diversity that exists in sorghum.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Mean</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grain Yield</td>
<td>63.5</td>
<td>4024.5</td>
<td>1236</td>
<td>8395</td>
</tr>
<tr>
<td>Thousand-grain weight</td>
<td>5.36</td>
<td>40.56</td>
<td>25.56</td>
<td>35.10</td>
</tr>
<tr>
<td>Amylose</td>
<td>1</td>
<td>6</td>
<td>3.05</td>
<td>3.15</td>
</tr>
<tr>
<td>Amylopectin</td>
<td>1</td>
<td>6</td>
<td>3.05</td>
<td>3.15</td>
</tr>
<tr>
<td>Prolamins</td>
<td>1</td>
<td>6</td>
<td>3.05</td>
<td>3.15</td>
</tr>
</tbody>
</table>

Table 2. Correlations among traits using the Pearson method.

<table>
<thead>
<tr>
<th>Trait</th>
<th>r</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grain Yield</td>
<td>-0.46</td>
</tr>
<tr>
<td>TGW</td>
<td>0.78</td>
</tr>
<tr>
<td>Amylose</td>
<td>-0.46</td>
</tr>
<tr>
<td>Amylopectin</td>
<td>-0.46</td>
</tr>
<tr>
<td>Prolamins</td>
<td>-0.46</td>
</tr>
</tbody>
</table>

Figure 4. Additional Manhattan plots displaying overall grain starch content and starch digestibility. (A) The SNP with highest significance with grain starch is near a putative MYB-like transcription factor. The second most significant marker on chromosome 1 was in high LD with a gene orthologous to sucrose synthase 1 (SUS1) in maize. SUS1 is responsible for breakdown of sucrose and controls carbon allocation throughout the plant. (B) GWAS for in vitro starch digestibility shows a strong peak on chromosome 7. The peak is near a glycogentransferase putative transcript which is involved in carbon fixation.

Conclusions

- • Ranges from raw data for traits directly influencing energy value reveal enormous natural diversity exists and can be exploited for crop improvement.
- A weak negative correlation found between grain number per panicle and thousand-grain weight along with differences in candidate genes suggest that the biological pathways underlying these yields components can be manipulated independently. This work provides evidence that increasing grain number through proper selection and breeding can be done without compromising yield of the grain, and vice versa.
- Starch content is positively correlated with overall grain yield as well as yield components: grain number per panicle and thousand-grain weight. If the sink of carbon fixation into starch in the grain drives total yield, then it leads to the possibility of increasing starch content and total grain yield simultaneously to generate greater energy yields per unit area.
- Genome-wide association mapping tagged a SNP marker in high linkage disequilibrium with SUS1, suggesting that this gene may be responsible for the fixation of simple sugars into starch and play a role in total grain starch content in sorghum.

Future Work

- Collection and evaluation of the 2014 grain diversity panel data are in progress to provide corroborating evidence toward the trait relationships and candidate gene significance.
- The same phenotypes are also being evaluated in multiple biparental mapping populations that have lines which are segregating for grain number, size, and starch composition. The aim is to properly eliminate false positives produced from the GWAS in the diverse panel (SAP) and provide additional support toward candidate genes.
- Once confirmation of peaks across years is complete, candidate gene sequencing in selected individuals will commence to determine allelic diversity in the germplasm.

References


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