INTRODUCTION

Drought stress is one of the major constraints affecting crop production worldwide. Developing crops that are well adapted to water limited environments is one of the keys to overcome this agricultural constraint. One such crop, sorghum, is well adapted to hot and dry environments, and hence will play an important role in meeting the challenges of feeding the world’s growing population under a changing climate.

Ethiopia is a center of origin and diversity for sorghum and as such has a tremendous variability for a wide range of traits including drought tolerance (Singh, 1985; Reddy et al., 2009; Adugna, 2014; Wesseasoorya et al., 2016). Therefore, a better understanding of the genetic architecture of important traits in these diverse germplasm is vital for the development of more drought tolerant sorghum varieties in the long-term. During the last two decades, the identification of genomic regions underlying traits of interest in crops were primarily based on evaluation of populations derived from bi-parental crosses. However, this approach provides low mapping resolution and restricted allelic diversity (Korte and Farlow, 2013). GWAS has recently become an effective approach for dissecting the genetic basis of these complex traits in many crops, including sorghum.

Although several GWAS have been carried out in sorghum, only few examples of QTL analysis to identify genomic regions associated with agronomic traits under drought stress conditions have been reported (e.g. Sakhi et al., 2013). Here, we report findings of GWAS conducted on Ethiopian sorghum landrace collection for ten agronomic traits. We identified several new loci and candidate genes underlying important agronomic traits under drought stress conditions, which provides a basis for crop improvement through marker-assisted breeding and genomic selection.

MATERIALS AND METHODS

Germplasm Collection

A total of 300 sorghum landraces were collected from farmers’ fields of major sorghum growing regions of Ethiopia (Fig. 1).

Phenotyping Evaluations

Phenotyping was done for ten agronomic traits at two water limited environments (Kobo & Mieso) during 2017 & 2018 cropping seasons, respectively.

DNA Extraction & Marker Development

DNA was extracted from lyophilized leaf tissues following a modified CTAB protocol (Mace et al., 2003).

GBS libraries were constructed using the Apekel enzyme system & sequenced on a Nextseq platform (Illumina, San Diego, CA, USA) at the University of Georgia Genomics and Bioinformatics Core Facility.

RESULTS

Phenotypic Variation

The 300 landraces used in this study exhibited a significant variation for all the traits studied (Table 1).

Table 1 Phenotypic variation of all traits based on best linear unbiased predictions (h², heritability for each trait was calculated across environments)

<table>
<thead>
<tr>
<th>Trait</th>
<th>Mean ± SD</th>
<th>Range</th>
<th>Mean ± SD</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>DF</td>
<td>96.5 ± 14.29</td>
<td>72.80 - 174.60</td>
<td>166.42 ± 26.71</td>
<td>69.94 - 108.80</td>
</tr>
<tr>
<td>PHI</td>
<td>311.46 ± 41.12</td>
<td>115.20 - 414.79</td>
<td>276.86 ± 63.37</td>
<td>115.20 - 413.65</td>
</tr>
<tr>
<td>PE</td>
<td>613.6 ± 47.55</td>
<td>0.00 - 25.10</td>
<td>645.8 ± 8.99</td>
<td>0.00 - 25.90</td>
</tr>
<tr>
<td>TN</td>
<td>0.58 ± 0.12</td>
<td>0.00 - 2.00</td>
<td>0.60 ± 0.99</td>
<td>0.00 - 3.60</td>
</tr>
<tr>
<td>TPI</td>
<td>68.91 ± 28.07</td>
<td>7.30 - 133.40</td>
<td>62.84 ± 26.11</td>
<td>5.30 - 190.17</td>
</tr>
<tr>
<td>OGP</td>
<td>433.2 ± 23.57</td>
<td>1.10 - 299.80</td>
<td>38.94 ± 20.61</td>
<td>0.67 - 164.62</td>
</tr>
<tr>
<td>SPM</td>
<td>177.9 ± 5.52</td>
<td>5.20 - 47.15</td>
<td>23.44 ± 8.72</td>
<td>4.57 - 88.95</td>
</tr>
<tr>
<td>PPI</td>
<td>6.6 ± 0.15</td>
<td>0.04 - 4.87</td>
<td>6.6 ± 0.14</td>
<td>0.04 - 4.87</td>
</tr>
<tr>
<td>GNP</td>
<td>742.9 ± 64.45</td>
<td>31.00 - 2379.80</td>
<td>163.31 ± 92.52</td>
<td>98.03 - 413.12</td>
</tr>
<tr>
<td>BW</td>
<td>2.90 ± 0.17</td>
<td>1.00 - 4.10</td>
<td>2.23 ± 0.86</td>
<td>0.68 - 3.68</td>
</tr>
</tbody>
</table>

SNP Discovery

We identified a total of 79,754 high quality SNPs using GBS (Fig. 2).

Population Structure

A clear differentiation was observed across the Ethiopian landrace collection (Fig. 3).

Linkage disequilibrium (LD)

On average, LD decays to background levels (r² < 0.1) within 100 kb (Fig. 4).

GWAS for agronomic traits under drought stress conditions

We identified a total of 37 unique SNPs having significant association (p < 1.0e-7) with agronomic trait (Fig. 5).

CONCLUSIONS

Our results demonstrate that the phenotypic diversity of Ethiopian landraces was associated with the observed population structure, suggesting that a more detailed characterization of these populations with respect to agronomic traits of interest and/or eco-geographical variation might identify novel alleles for sorghum breeding programs.

The genomic regions associated with agronomic traits in this study, if validated in managed stress and multi-environment mapping studies could contribute to the genomic resources available for sorghum improvement efforts around the world.

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