STUDIES ON GENETIC VARIABILITY IN SOME SWEET SORGHUM (Sorghum bicolor L Moench) GENOTYPES

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Studies were carried out to estimate the extent of genetic variability in some cultivated genotypes of sweet sorghum (sorghum bicolor L Moench). Thirty genotypes were evaluated in 2011 rainy season across two locations, to obtain more information on their genetic and morphological diversity. Significant mean squares were obtained for 10 traits in the individual analysis and also for the combined analysis across locations, suggesting that this sweet sorghum population was highly variable for some of the characters and as such will respond to selection. Mean performances for the combined analysis identified ICSV 93046, (SW DAURA 06-5-2 & ICSV700), SPV 422, ICSV700, (SW DAURA 06-5-2 & 38A x NR71182), SW DAURA 06-5-2, (SW DAURA 06-5-4 & E36-1), 38A*NR71182, and (SW KEBBI 07-5 & SPV 422) as the best genotypes in terms of days to 50% flowering, plant height, stem thickness, number of nodes, number of leaves, panicle weight, 1000 grain weight, grain yield and sugar content.

Key words: Variance, heritability, sweet sorghum

INTRODUCTION

Sweet sorghum (Sorghum bicolor (L) Moench) is the same species as grain sorghum, grass sorghum and broom sorghum (Doggett, 1970). Sorghum grain is the fifth most important cereal in the world after wheat, rice, maize and barley. In Africa it comes second after maize in terms of production (FAO, 2011). According to FAO (2011) estimates, the average world production of sorghum amounted to 66 million tonnes. Also according to Agricultural performance Survey of 2011 Wet Season in Nigeria, Sorghum production decline slightly from 7.02 to 6.89 million tons because the land area under cultivation decreased slightly from 5.04 million hectares to 4.89 million hectares. There is a need to improve overall income from sorghum through improving productivity or increasing value by locating and exploiting alternative uses. Sweet sorghum is similar to commonly grown grain sorghum with an increased potential to accumulate sugars in the stalk. The global energy demand and volatile prices of fossil fuels has forced nations to search for new alternative energy sources.

Sweet sorghum, with its short growing period (four months), low water requirement, high biomass and alcohol production potential and greater income potential from cultivation, is thus a preferred raw material for generating energy. In addition to its sweet stalk, it has a grain yield of about 2.0 to 6.0 t ha\(^{-1}\) (which can be used as food or feed) when harvested. Progress in plant breeding, depends on the extent of genetic variability present in the population. Therefore the first step in any breeding program is the study of the genetic variability present. This cannot easily directly measured as the phenotypic expression reflects non-genetic as well as genetic influences. The genetic basis must be inferred from the phenotypic observations which are the results of interactions of genotype and environment.

MATERIALS AND METHODS

Thirty genotypes were used for this study: seven of these
Table 1. Description of the Sweet sorghum varieties and the hybrids

<table>
<thead>
<tr>
<th>GENOTYPES/ VARIETIES</th>
<th>SOURCE</th>
<th>DESCRIPTION</th>
</tr>
</thead>
<tbody>
<tr>
<td>SPV 422</td>
<td>ICRISAT</td>
<td>High stalk yield, high grain yield and high sugar content.</td>
</tr>
<tr>
<td>ICSV 700</td>
<td>ICRISAT</td>
<td>Low stalk production</td>
</tr>
<tr>
<td>NTJ-2</td>
<td>ICRISAT</td>
<td>Lowest stalk yield, high yielding in post rainy season. Resistant to leaf diseases.</td>
</tr>
<tr>
<td>E 36-1</td>
<td>ICRISAT</td>
<td>High stalk sugar</td>
</tr>
<tr>
<td>ICSR 90304</td>
<td>ICRISAT</td>
<td>High yielding post rainy season, high sugar content and late maturing.</td>
</tr>
<tr>
<td>64 DTN</td>
<td>ICRISAT</td>
<td>High stalk sugar</td>
</tr>
<tr>
<td>ICSV 93046</td>
<td>ICRISAT</td>
<td>Moderate sugar content, tolerant to shoot fly, stem borer and leaf diseases.</td>
</tr>
<tr>
<td>ICSV 24001 X Samsorg 38</td>
<td>Hybrid</td>
<td></td>
</tr>
<tr>
<td>ICSA 344 X Samsorg 38</td>
<td>Hybrid</td>
<td></td>
</tr>
<tr>
<td>ICSA 2401 X Samsorg 41</td>
<td>Hybrid</td>
<td></td>
</tr>
<tr>
<td>ICSA 344 X Samsorg 39</td>
<td>Hybrid</td>
<td></td>
</tr>
<tr>
<td>ICSA 2401 X E 36-1</td>
<td>Hybrid</td>
<td></td>
</tr>
<tr>
<td>ICSA 2401 X NTJ-2</td>
<td>Hybrid</td>
<td></td>
</tr>
<tr>
<td>38A X Samsorg 39</td>
<td>Hybrid</td>
<td></td>
</tr>
<tr>
<td>38A X Samsorg 38</td>
<td>Hybrid</td>
<td></td>
</tr>
</tbody>
</table>

were obtained from India, eleven locally collected across Nigeria, nine genotypes resulted from crosses done and three non-sweet varieties were included from the Institute for Agricultural Research (IAR), Samaru, Zaria.

The genotypes/varieties were planted during the 2011 rainy seasons at two locations for evaluation in replicated trials. The Research Farm of the Institute for Agricultural Research (IAR), Ahmadu Bello University (ABU) Samaru Zaria (11 011’N, 07 0 38’E, 686 m above sea level) in the northern Guinea Savanna ecological zone of Nigeria; and the Irrigation Research Station, Kadawa of IAR/ABU (11 0 39’, 080 027’ E and 500 m above sea level), in the Sudan Savanna ecological zone of Nigeria.

At each location, the 30 genotypes/varieties were grown in a randomized complete block design with three replications. Each of the 30 plots consisted of 4 ridges each of which measured 5m long and were spaced 0.75m apart with 0.25m within row spacing. Proper local agronomic practices for sorghum were carried out. The two inner rows were used for data collections and observation for each plot. The data collected include:

- **Days to 50% flowering:** - the number of days from sowing to the time when 50% of the Plants flowered.
- **Number of leaves:** - was taken by counting the number of leaves from the base to the flag leaf of 6 plants taken from the two central rows and taking the average.
- **Plant height:** - was measured in cm using meter rule from the base of the plant to the top of the panicle.
- **Stem thickness:** - the diameter of the stem of six ramdomly selected plants per plot and the mean taken. It was measured in cm using vanier caliper.
- **Number of nodes:** - number of nodes on the plant from base to top taking 6 plants from the two central rows by counting the nodes.
- **Panicle length:** - the length from the base of the panicle to the tip measured in cm using a meter rule.
- **Panicle weight:** - weight of the total number of heads harvested from the two central rows in grams using measuring scale.
- **Grain yield/plot:** - after threshing and adequate drying, record the grain weight per plot to the nearest grams from the two central rows.
- **1000g grain weight:** - the weight of 1000gram grains after threshing.
- **Percentage sugar content:** - some parts of the stem were taken within each plot and analyzed at the Product Development Programme Unit Laboratory of IAR.

The data obtained were subjected to analysis of variance for each location based on plot means followed by combined analysis of data across the two locations; these were done according to methods described by Singh and Chaudhary (1985). Mean separation was carried out according to Duncans multiple range test (DMRT) described by Duncans (1955). Also components of variance ($\sigma^2_p$, $\sigma^2_e$, $\sigma^2_g$) were used for the estimation of coefficients of variation (PCV, GCV) as described by Singh and Chaudhary (1985).

**RESULTS AND DISCUSSIONS**

The significant mean values obtained from the analysis of variance for the individual location suggests that differences existed the sorghum genotypes/varieties for most traits, indicating that they are highly variable (Table...
Table 2. Sweet sorghum germplasm collected from five northern states of Nigeria.

<table>
<thead>
<tr>
<th>s/n</th>
<th>Institute assigned name</th>
<th>Place of collection</th>
<th>State</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>SW daura 06-2</td>
<td>Daura</td>
<td>Katsina</td>
</tr>
<tr>
<td>2</td>
<td>SW daura 06-5-1</td>
<td>Daura</td>
<td>Katsina</td>
</tr>
<tr>
<td>3</td>
<td>SW daura 06-5-2</td>
<td>Daura</td>
<td>Katsina</td>
</tr>
<tr>
<td>4</td>
<td>SW daura 06-5-4</td>
<td>Daura</td>
<td>Katsina</td>
</tr>
<tr>
<td>5</td>
<td>SW samaru 06-4</td>
<td>Samaru</td>
<td>Kaduna</td>
</tr>
<tr>
<td>6</td>
<td>SW makarfi 06-3</td>
<td>Makarfi</td>
<td>Kaduna</td>
</tr>
<tr>
<td>7</td>
<td>SW kebbi 07-1</td>
<td>Unguwar Lawal</td>
<td>Kebbi</td>
</tr>
<tr>
<td>8</td>
<td>SW dansadau 07-2</td>
<td>Dansadau</td>
<td>Kebbi</td>
</tr>
<tr>
<td>9</td>
<td>SW bodinga 07-3</td>
<td>Bodinga</td>
<td>Sokoto</td>
</tr>
<tr>
<td>10</td>
<td>SW bungudu 07-1</td>
<td>Bungudu</td>
<td>Zamfara</td>
</tr>
<tr>
<td>11</td>
<td>SW bungudu 07-6</td>
<td>Bungudu</td>
<td>Zamfara</td>
</tr>
</tbody>
</table>

Non sweet sorghum varieties.
Samsorg 41 (ICSV111)
Samsorg 39 (NR71182)
Samsorg 38 (NR71172)

Table 3. Mean square values for the ten traits measured at Samaru and Kadawa of 30 different sorghum genotypes in 2011.

<table>
<thead>
<tr>
<th>SOURCE OF VARIATION</th>
<th>DF</th>
<th>DTF</th>
<th>PLHT</th>
<th>ST</th>
<th>NN</th>
<th>NL</th>
<th>HDWT</th>
<th>PL</th>
<th>TGWT</th>
<th>GYLD</th>
<th>PSS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rep</td>
<td>2</td>
<td>14.27</td>
<td>76.42</td>
<td>0.07</td>
<td>0.01</td>
<td>0.04</td>
<td>0.0007</td>
<td>0.72</td>
<td>2.42</td>
<td>0</td>
<td>0.14</td>
</tr>
<tr>
<td>Location</td>
<td>1</td>
<td>96.8*</td>
<td>58056.42**</td>
<td>8.49**</td>
<td>68.45**</td>
<td>72.20**</td>
<td>113.21**</td>
<td>0.78</td>
<td>1496.75**</td>
<td>52.08**</td>
<td>68.76**</td>
</tr>
<tr>
<td>Rep(Location)</td>
<td>2</td>
<td>12.35</td>
<td>53.19</td>
<td>0.36</td>
<td>0.05</td>
<td>0.05</td>
<td>0.0003</td>
<td>0.86</td>
<td>0.06</td>
<td>0.002</td>
<td>0.09</td>
</tr>
<tr>
<td>Genotype</td>
<td>29</td>
<td>319.99**</td>
<td>12331.95**</td>
<td>3.69**</td>
<td>17.58**</td>
<td>18.82**</td>
<td>1.54**</td>
<td>232.09**</td>
<td>40.81**</td>
<td>0.74**</td>
<td>28.39**</td>
</tr>
<tr>
<td>Genotype*Location</td>
<td>29</td>
<td>95.25**</td>
<td>884.0**</td>
<td>0.49**</td>
<td>1.54**</td>
<td>1.41**</td>
<td>0.63**</td>
<td>2.58**</td>
<td>21.44**</td>
<td>0.34**</td>
<td>1.38**</td>
</tr>
<tr>
<td>Error</td>
<td>116</td>
<td>8.27</td>
<td>131.48</td>
<td>0.13</td>
<td>0.07</td>
<td>0.07</td>
<td>0.01</td>
<td>0.92</td>
<td>2.55</td>
<td>0.005</td>
<td>0.05</td>
</tr>
</tbody>
</table>

DF= degrees of freedom, DTF= Days to 50% flowering, PLHT=plant height, ST=stem thickness, NN=no of nodes, NL=no of leaves, HDWT=head weight, PL=panicle length, TGWT=1000 grain weight, GYLD=grain yield, PSS=% stem sugar, ** significant at 1%, * significant at 5%

3). The significant mean square values obtained for the location (Table 4), for some of the traits indicated that the conditions in the two locations were not similar in many ways and that is why the genotypes/varieties did not perform in the same way in the locations. The significant effects of genotype x location interaction mean squares that were observed (Table 5) in most traits also suggest that the environmental conditions in the two locations influenced the performance of the genotypes, thus suggesting the need to test genotypes over different locations across years to ascertain their stability for use as reliable genetic materials for crop improvement practices. To minimize error and consequently increase the
Table 4. Mean square values for the ten traits measured across the two locations and 30 sorghum genotypes in 2011.

<table>
<thead>
<tr>
<th>SOURCE OF VARIATION</th>
<th>DF</th>
<th>DTF</th>
<th>PLHT</th>
<th>ST</th>
<th>NN</th>
<th>NL</th>
<th>HDWT</th>
<th>PL</th>
<th>TGWT</th>
<th>GYLD</th>
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<td>0.72</td>
<td>2.42</td>
<td>0</td>
<td>0.14</td>
</tr>
<tr>
<td>Location</td>
<td>1</td>
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<td>58056.42**</td>
<td>8.49</td>
<td>68.45**</td>
<td>72.20**</td>
<td>113.21**</td>
<td>0.78</td>
<td>1496.75**</td>
<td>52.08**</td>
<td>68.76**</td>
</tr>
<tr>
<td>Rep(Location)</td>
<td>2</td>
<td>12.35</td>
<td>53.19</td>
<td>0.36</td>
<td>0.05</td>
<td>0.05</td>
<td>0.0003</td>
<td>0.86</td>
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<tr>
<td>Genotype</td>
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<td>12331.95**</td>
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<td>18.82**</td>
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<td>28.39**</td>
</tr>
<tr>
<td>Genotype*Location</td>
<td>29</td>
<td>95.25**</td>
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<td>0.49**</td>
<td>1.54**</td>
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<td>0.63**</td>
<td>2.58**</td>
<td>21.44**</td>
<td>0.34**</td>
<td>1.38**</td>
</tr>
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<td>0.92</td>
<td>2.55</td>
<td>0.005</td>
<td>0.05</td>
</tr>
</tbody>
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Table 5. Mean performance for 30 genotypes of the 10 traits across the two locations in 2011.

<table>
<thead>
<tr>
<th>GENOTYPE</th>
<th>DTF</th>
<th>PLHT</th>
<th>ST</th>
<th>NN</th>
<th>NL</th>
<th>HDWT</th>
<th>PL</th>
<th>TGWT</th>
<th>GYLD</th>
<th>PSS</th>
</tr>
</thead>
<tbody>
<tr>
<td>sw bungudu 07-1</td>
<td>69k</td>
<td>200de</td>
<td>6d</td>
<td>7g</td>
<td>9i</td>
<td>4.33abc</td>
<td>17.46jk</td>
<td>23.27hij</td>
<td>0.94kl</td>
<td>7.14abcd</td>
</tr>
<tr>
<td>sw daura 06-5 2</td>
<td>82bc</td>
<td>304a</td>
<td>6d</td>
<td>10c</td>
<td>11.5c</td>
<td>7.35a</td>
<td>32.23a</td>
<td>24.86efgh</td>
<td>0.9l</td>
<td>6.9abcd</td>
</tr>
<tr>
<td>sw samaru 06-4</td>
<td>80cd</td>
<td>187ef</td>
<td>6d</td>
<td>9d</td>
<td>11d</td>
<td>5.35abc</td>
<td>18.63ijk</td>
<td>21.59jkl</td>
<td>1.54bc</td>
<td>7.33abc</td>
</tr>
<tr>
<td>sw daura 06-5-1</td>
<td>69n</td>
<td>158hi</td>
<td>5e</td>
<td>5m</td>
<td>6m</td>
<td>4.96abc</td>
<td>19.51hij</td>
<td>26.01efgh</td>
<td>1.0jk</td>
<td>5.76k</td>
</tr>
<tr>
<td>sw daura 06-2</td>
<td>67kl</td>
<td>161hi</td>
<td>5e</td>
<td>7g</td>
<td>9i</td>
<td>6.03abc</td>
<td>24.74bcdefg</td>
<td>24.99efgh</td>
<td>1.05j</td>
<td>6.68hij</td>
</tr>
<tr>
<td>sw kebbi 07-5</td>
<td>65lm</td>
<td>209d</td>
<td>5e</td>
<td>6k</td>
<td>8k</td>
<td>4.22abc</td>
<td>17.14ijk</td>
<td>22.05ijjk</td>
<td>0.94kl</td>
<td>7.52a</td>
</tr>
<tr>
<td>sw daura 06-5-4</td>
<td>67kl</td>
<td>210d</td>
<td>5e</td>
<td>6l</td>
<td>9i</td>
<td>6.15abc</td>
<td>25.04bcdefg</td>
<td>29.81a</td>
<td>0.62o</td>
<td>7.53a</td>
</tr>
<tr>
<td>sw dansadau 07-2</td>
<td>79cdef</td>
<td>182fg</td>
<td>6d</td>
<td>8e</td>
<td>9i</td>
<td>3.79bcd</td>
<td>11.37l</td>
<td>26.01defg</td>
<td>1.0jk</td>
<td>7.14bcde</td>
</tr>
<tr>
<td>sw bodinga 07-3</td>
<td>60n</td>
<td>255b</td>
<td>6d</td>
<td>11b</td>
<td>13b</td>
<td>6.13abc</td>
<td>26.64bcdefg</td>
<td>26.01defg</td>
<td>0.95kl</td>
<td>6.84fghi</td>
</tr>
<tr>
<td>sw makarfi 06-3</td>
<td>73hij</td>
<td>162hi</td>
<td>6d</td>
<td>8e</td>
<td>10f</td>
<td>3.83cd</td>
<td>10.8l</td>
<td>28.02abc</td>
<td>1.26gh</td>
<td>7.37ab</td>
</tr>
<tr>
<td>sw bungudu 07-6</td>
<td>81bc</td>
<td>238c</td>
<td>6d</td>
<td>9d</td>
<td>11d</td>
<td>5.49abc</td>
<td>24.92bcdefg</td>
<td>26.01cdefg</td>
<td>0.51p</td>
<td>7.37ab</td>
</tr>
<tr>
<td>spv 422</td>
<td>73hi</td>
<td>236c</td>
<td>8a</td>
<td>11b</td>
<td>13b</td>
<td>6.46abcd</td>
<td>26.04bcdefg</td>
<td>28.23ab</td>
<td>1.04j</td>
<td>7.49a</td>
</tr>
<tr>
<td>nlf 2</td>
<td>67kl</td>
<td>158hi</td>
<td>7bc</td>
<td>9d</td>
<td>11d</td>
<td>5.5abc</td>
<td>19.95hij</td>
<td>26.33bcde</td>
<td>1.2hi</td>
<td>7.36ab</td>
</tr>
<tr>
<td>e 36-1</td>
<td>79cdef</td>
<td>162hi</td>
<td>6d</td>
<td>8f</td>
<td>10f</td>
<td>5.94abc</td>
<td>23.55efgh</td>
<td>29.24a</td>
<td>1.58bc</td>
<td>7.26abcd</td>
</tr>
<tr>
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<td>69jk</td>
<td>206d</td>
<td>7bc</td>
<td>9.11d</td>
<td>6.19abc</td>
<td>23efgh</td>
<td>28.09abc</td>
<td>1.6b</td>
<td>6.5j</td>
<td></td>
</tr>
<tr>
<td>64 dtn</td>
<td>62mn</td>
<td>169gh</td>
<td>7bc</td>
<td>9d</td>
<td>11d</td>
<td>5.18abc</td>
<td>19.52hij</td>
<td>28.28ab</td>
<td>1.17i</td>
<td>5.96k</td>
</tr>
<tr>
<td>icsv 93046</td>
<td>91a</td>
<td>265b</td>
<td>7bc</td>
<td>11b</td>
<td>13b</td>
<td>3.72cd</td>
<td>15.65k</td>
<td>28.04abc</td>
<td>0.71n</td>
<td>7.26abcd</td>
</tr>
<tr>
<td>icsv 700</td>
<td>84b</td>
<td>304a</td>
<td>6d</td>
<td>13a</td>
<td>15a</td>
<td>3.13d</td>
<td>10.86l</td>
<td>21.97jkl</td>
<td>0.60</td>
<td>6.92efgh</td>
</tr>
<tr>
<td>icsa24001*nr71176</td>
<td>73hij</td>
<td>173gh</td>
<td>7bc</td>
<td>9d</td>
<td>11d</td>
<td>6.76abc</td>
<td>27.42bc</td>
<td>24.61efgh</td>
<td>0.79m</td>
<td>7.26abcd</td>
</tr>
<tr>
<td>icsa 344*nr71176</td>
<td>75gh</td>
<td>206d</td>
<td>6d</td>
<td>8f</td>
<td>10f</td>
<td>6.98abc</td>
<td>26.21bcde</td>
<td>24.14efgh</td>
<td>1.31fg</td>
<td>7.02defg</td>
</tr>
<tr>
<td>icsa 24001*icsv111</td>
<td>80cd</td>
<td>164hi</td>
<td>8ab</td>
<td>9d</td>
<td>11d</td>
<td>6.67abc</td>
<td>24.06cdefg</td>
<td>23.82ghi</td>
<td>1.5cd</td>
<td>6.69hij</td>
</tr>
<tr>
<td>icsa 344*icsv111</td>
<td>77defg</td>
<td>137k</td>
<td>6d</td>
<td>8e</td>
<td>10f</td>
<td>5.39abc</td>
<td>22.47fgh</td>
<td>20.94k</td>
<td>0.95kl</td>
<td>7.28abcd</td>
</tr>
</tbody>
</table>
precision and reliability of estimates Allard and Bradshaw (1964) suggested increasing the sample size and number of locations or years during the trials. However, the disadvantage of this suggestion would be increased costs and delayed release of results, see Table 3, 4, 5 and 6.

Comparative performance of the 30 genotypes across the two locations for the 10 traits studied (Table 5) provides a clear indication of the superiority of some of the genotypes over others. All “sweet sorghum” genotypes were sweet with sugar concentrations ranging from 6-7.5% sugar. Good breeding potential therefore exists for genotypes such as ICSR 93034, E 36-1, samaru 06-4 and crosses/hybrids between ICSA24001 × ICSV111, 38A × NR71182, 38A × NR71176 as these performed very well for both yield and yield components across the two locations. Depending on the breeding objective, there was a wide range of genotypes to choose from. For instance if the breeding objective is to produce high yield and early maturing sweet sorghum varieties, then hybridization between ICSV 93046 × SAMARU 06-4 or ICSV93046 × E 36-1 or ICSV 700 × SAMARU 06-4 or DANSADAU 07-2 × SAMARU 06-4 which are early maturing and high yielding genotypes respectively could be promising.

Table 6. Shows estimates of variance components obtained from the analysis of variance. The estimates of the phenotypic, genotypic, environmental variances with their standard errors are given. All of the ten traits studied showed positive genotypic variance. Genotypic variances had relatively higher estimates compared to environmental variance estimates. For all but head weight (1.5%) and 1000 grain weight (56%) genotypic variance was > 75% of phenotypic variance.

Phenotypic and error variances estimates were all positive for all traits and they had very low standard errors. Plant height, head weight, 50% days to flowering, panicle length and thousand grain weights had large estimates of phenotypic, genotypic, and error variances. The variance components showed that most of the characters had higher phenotypic and genotypic variance estimates than the environmental variance estimates. The variance components for the two locations showed that most of the traits had high phenotypic and genotypic variance estimates (Table 6).

CONCLUSION

The success of any breeding program depends upon the genetic variation in the materials at hand. The greater the genetic variability, the higher would be the heritability. Hence the better the chances of success to be achieved through selection. Ten traits involving the leaves, stem, seed and other agronomic parameters were used.

Table 5. Continues

<table>
<thead>
<tr>
<th>Genotype</th>
<th>DTF</th>
<th>PLHT</th>
<th>ST</th>
<th>NN</th>
<th>NL</th>
<th>HDWT</th>
<th>PL</th>
<th>TGWT</th>
<th>GYLD</th>
<th>PSS</th>
<th>**</th>
<th>*</th>
<th>Means with the same letter are not significantly different</th>
</tr>
</thead>
<tbody>
<tr>
<td>icosa344*nr71182</td>
<td>71ij</td>
<td>132k</td>
<td>6d</td>
<td>7g</td>
<td>9i</td>
<td>6.06abcd</td>
<td>21.68ghi</td>
<td>21.32jk</td>
<td>1.43de</td>
<td>7.03cdefg</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>icosa24001*E36-1</td>
<td>81bc</td>
<td>205d</td>
<td>6d</td>
<td>9d</td>
<td>11d</td>
<td>5.82abcd</td>
<td>23.57defg</td>
<td>21.37jk</td>
<td>1.25gh</td>
<td>6.62ij</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>icosa24001*ntj-2</td>
<td>76efgh</td>
<td>196def</td>
<td>7bc</td>
<td>8f</td>
<td>10f</td>
<td>5.88abcd</td>
<td>26.96bcd</td>
<td>26.02defg</td>
<td>0.89l</td>
<td>6.94efgh</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>38A*nr71176</td>
<td>74ghi</td>
<td>223c</td>
<td>6d</td>
<td>8f</td>
<td>10f</td>
<td>7.3ab</td>
<td>26.06bcd</td>
<td>26.15bcde</td>
<td>1.91a</td>
<td>7.07bcd</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>38A*nr71182</td>
<td>75fggh</td>
<td>152ij</td>
<td>7bc</td>
<td>9d</td>
<td>11d</td>
<td>5.9abcd</td>
<td>23.93cdefg</td>
<td>23.77ghi</td>
<td>1.008jk</td>
<td>6.75ghij</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>icv111(samsorg 41)</td>
<td>77defgh</td>
<td>162hi</td>
<td>6d</td>
<td>7g</td>
<td>9i</td>
<td>6.35abcd</td>
<td>28.33b</td>
<td>21.23jk</td>
<td>1.85a</td>
<td>7.07bcdef</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>nr71182(samsorg 39)</td>
<td>76efgh</td>
<td>139jk</td>
<td>7bc</td>
<td>9d</td>
<td>11d</td>
<td>5.9abcd</td>
<td>24.45cdefg</td>
<td>27.72abcd</td>
<td>1.38ef</td>
<td>0</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>nr71176(samsorg 38)</td>
<td>72ij</td>
<td>197de</td>
<td>7bc</td>
<td>7g</td>
<td>10f</td>
<td>6.2abcd</td>
<td>24.12bcde</td>
<td>27.72abcd</td>
<td>1.38ef</td>
<td>0</td>
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<td></td>
<td></td>
</tr>
</tbody>
</table>

DTF= Days to 50% flowering, PLHT=plant height, ST=stem thickness, NN=no of nodes, NL=no of leaves, HDWT=head weight, PL=panicle length, TGWT=1000 grain weight, GYLD=grain yield, PSS=% stem sugar, ** significant at 1%, * significant at 5 %. Means with the same letter are not significantly different.
for this study. There was considerable variability present in the materials used. As such these results will be useful for choosing populations to be used in developing new breeding strategies to improve sweet sorghum productivity. The variations could be effectively manipulated with appropriate breeding methods to develop improved varieties, synthetics and hybrids for use by farmers and industries.

REFERENCES


Khalyani New Delhi, India, pp 318.

Table 6. Estimate of phenotypic (σ²p), genotypic (σ²g) and environmental variance for the 10 traits over the 2 locations (Samaru and Kadawa) in 2011.

<table>
<thead>
<tr>
<th>Traits</th>
<th>σ²p</th>
<th>σ²g</th>
<th>σ²e</th>
</tr>
</thead>
<tbody>
<tr>
<td>50% DTF</td>
<td>45.4172</td>
<td>37.4567</td>
<td>7.9605</td>
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<tr>
<td>plant height</td>
<td>2149.78</td>
<td>1907.99</td>
<td>241.78</td>
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<tr>
<td>stem thickness</td>
<td>0.69</td>
<td>0.5332</td>
<td>0.1568</td>
</tr>
<tr>
<td>no of nodes</td>
<td>2.748</td>
<td>2.673</td>
<td>0.075</td>
</tr>
<tr>
<td>no of leaves</td>
<td>2.9119</td>
<td>2.8433</td>
<td>0.0686</td>
</tr>
<tr>
<td>head weight</td>
<td>6.0791</td>
<td>0.0883</td>
<td>5.9908</td>
</tr>
<tr>
<td>panicle length(cm)</td>
<td>31.4402</td>
<td>24.4783</td>
<td>6.9619</td>
</tr>
<tr>
<td>1000 grain weight</td>
<td>5.7801</td>
<td>3.2283</td>
<td>2.5518</td>
</tr>
<tr>
<td>Grain yield</td>
<td>0.0713</td>
<td>0.0667</td>
<td>0.0046</td>
</tr>
<tr>
<td>sugar content</td>
<td>4.2442</td>
<td>3.95</td>
<td>0.2942</td>
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</table>