Sorghum hybrids - A contribution to future agricultural productivity and food security in West Africa

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Experimental hybrid: Yield advantages and adoption by farmers

Farmer managed on-farm yield trials*

- Seven tall and eight short experimental sorghum hybrids vs 1 local check (Tieblé) and 4 pure lines.
- 3 Malian zones (Dioila, Koutiala, Mandé).
- 3 Years (2009-2011).
- Environments grouped based on their mean yield.

Table 1: Grain yields of the highest yielding short and tall sorghum hybrids, the local check Tieblé, and the hybrid yield superiority across low, intermediate and high productivity environments in Mali. Pablo and Fadda were the best overall yielding tall and short hybrids, respectively. The “low” group of tall hybrids includes the low- and mid-low yielding groups of Fig. 1.

<table>
<thead>
<tr>
<th>Type of Hybrid</th>
<th>Number of environments</th>
<th>Fadda mean yield (g m⁻²)</th>
<th>Superiority of Fadda over Tieblé (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Low</td>
<td>9</td>
<td>153</td>
<td>161</td>
</tr>
<tr>
<td>Intermediate</td>
<td>8</td>
<td>212</td>
<td>207</td>
</tr>
<tr>
<td>High</td>
<td>10</td>
<td>284</td>
<td>250</td>
</tr>
</tbody>
</table>

Figure 1: Individual trial grain yields (g m⁻²) of hybrids and the local check ‘Tieblé’ within different productivity levels.

• Tall and short hybrid yields superior to that of local check Tieblé.
• Larger relative yield superiority of short- (compared to tall-) hybrids over the local check (Table 1).
• Tall hybrid superiority over Tieblé larger in lower input environments (Fig. 1).
• Hybrids, an option for farmers to increase yields in both low input as well as intensified production systems.
• Experimental hybrids used in these studies; more grain yield expected with high selection intensity hybrids.

Current challenges: Tools for breeders

Sorghum hybrid breeding strategies for West African sorghum hybrid development

- 91 males (R lines) and 17 females (A lines).
- 2 different trial sets: female (16 A- and 7 R-lines) and male (3 A- and 89 R-lines) combining ability trials.
- 2 years (2015-2016) in 2 locations (Samanko, Kolombada, both in Mali).
- 2 Phosphorus (P) levels, high P (HP) and low P (LP) per location.

Figure 2: Correlations between parental means and test cross performance in Samanko HP (left) and LP (right) in 2016.

Results

- Moderate correlation between parental means in low- vs high-P conditions (r²=0.43-0.61 in different locations).
- Low correlation between hybrid means in low- and high-P conditions (r²=0.06-0.15 in different locations).
- Relatively high correlations of both hybrids and parents for heading date and plant height in different P conditions.
- Weak correlation between mean per se yields and test cross performance (Fig. 2).
- Stronger correlation between per se and test cross performance in LP environments.
- Early generation test cross evaluation essential.
- Female with high yield should be favored for hybrid seed production.

Fertility restoration genes

Pollen fertility restoration genes

Fertility restoration (A, cytoplasm) gene identification/validation and KASP marker development

- Leaf sampling and seed set visual scoring of 4 F₂ populations (Fig. 3), Samanko (Bamako-Mali) 2015.
- 220 plants per F₂ population.
- GBS-SNP markers.
- Seed from completely fertile F₂ panicles sowed for the validation trial.

Figure 3: Parents of the four F₂ populations used in the mapping study.

Table 2: QTL with significant LOD score for F₂, F₂P and Pop4 populations.

<table>
<thead>
<tr>
<th>Population</th>
<th>Number of markers</th>
<th>Chr</th>
<th>Position (cM)</th>
<th>LOD</th>
<th>% Var. Explained</th>
<th>Confidence int. (Bayes) (cM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pop2</td>
<td>3859</td>
<td>5</td>
<td>10.3</td>
<td>18.9</td>
<td>8.5-15.2</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>9</td>
<td>29.8</td>
<td>6.0</td>
<td>25.0-34.0</td>
<td></td>
</tr>
<tr>
<td>Pop3</td>
<td>1574</td>
<td>2</td>
<td>24.6</td>
<td>31.0</td>
<td>24.0-25.2</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>4</td>
<td>24.0</td>
<td>17.4</td>
<td>22.0-25.0</td>
<td></td>
</tr>
</tbody>
</table>

Results

- 6 main QTL found in Pop2, 3 and 4 populations (Fig. 4, Table 2).
- Same QTL regions found on chromosome 5 in Pop2 and Pop4 (same male parent).
- KASP markers based on SNPs flanking the QTL region on chromosome 2 (Pop3) explained over 80% of the phenotypic variance in a separate F₂ population.
- No common KASP marker existing for Pop2 and Pop4 QTL.

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In Seed systems II project objectives. Available at http://ccpr.org/projects/seed-systems-i/

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