Evaluating F₃ Lines of Single Crosses for Yield Improvement in Cotton

J. Lançon
CIRAD-CA-Programme Coton, PARAB, Recherche Coton et Fibres, 01 BP 715, Cotonou, Bénin.

ABSTRACT

In Benin, average cotton yields have stagnated for several years. Although the main factors are known to be decreasing levels of inputs by the farmers, yield improvement has become a research priority for cotton research as a whole, including plant breeding. Selecting variables with low heritability like yield requires specific experimental field design, more demanding than those used for less complex characters. The design in which single crosses are evaluated through the performance of an F₃, 30 lines sample as described in this paper intends to meet this requirement. The lines are grown in cropping conditions that are similar to those of commercial fields. After examining the general parameters status under which the design is most relevant, examples show how to interpret the data: (1) from the statistical analysis, the crosses are compared and their lines ranked in each cross; then (2) with an appropriate quantitative genetics model, the genetic variability of the traits under selection can be described more precisely. Finally, the cost-effectiveness of this design is discussed and compared to more common designs.

Introduction

In 50 years, research in general and plant breeding in particular has increased cotton production appreciably in French speaking Africa. Productivity and fiber quality have improved and the varieties bred are among the best in the Upland family (CIRAD-CA, 1997). These results were obtained with pure line cotton cultivars that were bred with proven methods for average or highly heritable traits (ginning out-turn, earliness, fiber quality). However these methods have limitations for improving productivity when expression is hidden by environment and complexity of the genetic effects in action, including dominance and epistatic interactions (Lançon, 1994). Breeders have to reconsider this strategy because:

1) genetic variability and heritability of most traits tends to decrease so we can expect non additive, especially epistatic effects, to gain importance;
2) cotton production is moving to the private sector and economic and political power is shifting in favour of cotton producers;
3) weakening extension services and increases in input prices are leading to greater agronomic diversity and a trend towards extensive farming.

Cotton breeding must adapt to these changes that deal with producer priorities, in particular hardiness and yield, and to take account of the real or potential decrease in additive genetic variability.

This paper describes a design that was studied on cotton by Lançon (Lançon, 1995; Lançon 1995a), based on early evaluation of crosses (Gallais, 1988) that should fill both requirements.

Preliminary Considerations

Selection in the F₂ generation

Response to selection may be written as:

\[ R = i h²N sp = i s²A / sp \]

where \( s²p \) is the phenotypic variance, \( s²A \) the additive genetic variance and \( i \) is the selection intensity, which varies according to the fraction of selected plants.

Selection efficiency in the F₂ is then directly linked to the importance of additive genetic variance and to narrow heritability \( h²N \).

For many agronomic traits, heritability estimated on individual F₂ plants is low (Table 1). Most of the variation is not additive, rendering selection inefficient and biased by micro-environmental or non-additive genetic variation.

Selection within or between crosses?

At constant means, the option may be either to concentrate breeding efforts on crosses selected \( a \) priori or to do more crosses and select the most promising. Simulations by Fouilloux (1981) show that the choice depends on the trait’s heredity. As long as the additive genetic variance remains significant, it is preferable to cross carefully selected parents but when the additive genetic variance is low, selecting between crosses becomes more efficient. Several decades of active cotton breeding in Francophone Africa have shown that the additive part of the genetic variability utilized for improving productivity has decreased and that the best strategy involves multiplying and evaluating numerous crosses.
How to evaluate crosses?

To select few crosses among numerous, one has to consider their mean value and their additive genetic variance (Lançon et al., submitted):

1) the parents are good indicators only in the case of favourable gene repulsion and in the case of any epistatic effect;
2) the F1 generation does not segregate and its mean is biased by dominance;
3) F2 variance includes genetic and environmental variation and its mean includes some dominance;
4) the F3 generation segregates: it can be organized in lines and grown at normal plant densities that integrates competition effects. Genetic components of the mean and variance can be estimated more easily under more realistic cropping conditions.

The EE design

F3 lines are tested at crop spacing e.g. in a Fisher block layout with 3 replications. Each cross is represented by a sample of at least 30 F3 lines, in order to estimate between and within line variability. When added to the trial, the parents may be used as checks and provide an estimate of the environmental variance.

Statistical analysis

Are there differences between cross means?

In the analysis of variance and appropriate tests, if the line data are obtained from several plants, a within-line variance may be estimated directly and compared to that provided by the analysis of variance (Table 2).

Which are the best crosses?

For each cross, a genetic progress expectation may be evaluated from the F3 mean and variance (Table 3) at a given selection intensity (Lançon 1995a). Between F3 lines variance is assumed to be worth half the additive genetic variance (A) of the cross (cf § 2.2.2).

Which are the best lines in each cross?

The analysis shown in § 2.1.2 can be applied to the F3 lines. Generally, only the mean is used but if several data per line are available a variance may be estimated.

Genetic analysis

Mean genetic analysis

The EE trial can also be utilized to estimate parameters necessary for the genetic description of the trait. The model uses Kearsey and Pooni’s notation (1996) where effects are written a (additive), d (dominance), a.a (cis epistasy) and d.d (trans epistasy).

If one considers only the dominance effects, d, and dominance x dominance interaction, d.d, the F3 generation mean can be written as:

$$F_3 = m + [a] + \frac{1}{4}[d] + \frac{1}{16}[d.d]$$

Also, in the presence of additive x additive epistasy, a.a, each parent mean is written:

$$P_1 = m + [a] + [a.a]$$
$$P_2 = m - [a] + [a.a]$$

from which can be derived:

$$P_1 = m + [a.a] = \frac{P_1 + P_2}{2}$$

Genetic analysis of the variance

The F3 genetic variance may be divided into between lines variance, $s^2_B$, and within lines variance, $s^2_W$.

According to Kearsey and Pooni’s model (1996) and considering only the main 3 components of the genetic variance $ie$ A, the additive variance, D, the dominance variance and AA, the cis epistatic variance, becomes:

Total genetic variance:

$$s^2 = s^2_A + s^2_D + s^2_{AA}$$

Between lines genetic variance:

$$s^2_B = s^2_A + s^2_D$$

Within lines genetic variance:

$$s^2_W = s^2_{AA}$$

If the parents are not part of the EE trial, only two variances are computed and two parameters estimated $ie$ A and E.

From Table 2 (“mean squares expectations”) and the preceding model, we have:

$$s^2_B = s^2_A = 1/2.A$$
$$s^2_W = s^2_E + V_E = 1/4.A + V_E$$

and

$$A = 2,s^2_B$$
$$V_E = s^2_W - 1/2,s^2_B$$

When the parents are included in the trial, $V_E$ may also be estimated through:

$$(V_{P1} + V_{P2})/2$$

If the result gets close enough to that obtained in the preceding case, it can be accepted as an acceptable estimator of environmental variance.

An extra equation is available for estimating a third parameter. In general, D will be preferred to AA, even though the coefficient of AA is inferior to that of D. The system of equations becomes:

$$V_E = (V_{P1} + V_{P2})/2$$
\[ s^2_w = 1/4.A + 1/8.D + V_E \]

and

\[ A = 4/3 \left( 2 s^2_B - s^2_W + V_E \right) \]
\[ D = 16/3 \left( 2 s^2_W - s^2_B - 2 V_E \right) \]

**The Whole Breeding Design**

**Description**

A program that includes an EE trial targets low heritability traits, especially yield improvement, but selection pressure must be maintained on other traits.

The F₂ generation is sown at nursery spacing and economically important traits with good heritability and genetically not linked with yield may be screened e.g. ginning out-turn, seed index or seed coat fragments rate in the fiber. At least 30 F₂ plants are selected to produce 30 F₃ lines that are evaluated in the EE trial. On their performance in the EE trial, superior lines of the 50% best crosses are followed by conventional breeding. Note that evaluating the crosses productivity in the F₃ should reduce the number of genotypes in station yield tests in later breeding steps.

**Cost Estimates**

The respective costs of conventional pedigree-selection or EE programmes may be compared with two easy to compute parameters:

1) the total area covered by the trials;
2) the number of fiber analyses required.

With EE, the area covered by the F₃ population is obviously larger than it is with a conventional programme (Table 4). The number of observed lines must represent the whole cross and must include most of its variability, both within and between lines. An F₂ generation could be represented by 200 plants but the F₃ requires at least 30 lines with 30 plants per line.

The EE trial is kept to a reasonable size by:

1) restricting each elementary plot length (6 m); and
2) observing the lines at the crop stand (0.3 x 0.8 m).

With these restrictions, the area covered by an F₃ population is only about 450 m².

The number of fiber analyses is important because they require external, expensive expertise, their number being an indicator of laboratory work require (Table 5). Designs that include an EE trial do not require fiber analyses before the F₃ generation and then only for lines. The following generations reinforces the results.

Pedigree selection starting in the F₂ needs about the same number of analyses per cross (around 200) as programmes with F₃ EE. The number of analyses is similar for similar numbers of hybrids annually.

**Conclusion**

The ability to screen many crosses early in the breeding process under normal growing conditions, facilitates orienting a breeding program towards improvement of traits with relatively low heritability. This flexibility allows breeders to elaborate better answers to foreseeable changes in African cotton production.

**References**


Nursery spacing

<table>
<thead>
<tr>
<th>Nursery spacing</th>
<th>69</th>
<th>17</th>
<th>15</th>
<th>14</th>
<th>30</th>
<th>11</th>
</tr>
</thead>
</table>

(after Lançon et al, submitted for publication).

GOT: ginning out-turn (%); SI: seed index (g); NCF: number of bolls borne by the fruiting branches; NBV: number of vegetative branches; HT: plant height (cm); LBV: length of the longest vegetative branches (cm)

Table 2. Analysis of variance of an EE trial including c crosses, f lines per cross and r replicates.

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>df</th>
<th>MS</th>
<th>E (MS)</th>
<th>Test</th>
</tr>
</thead>
<tbody>
<tr>
<td>Between crosses</td>
<td>c-1</td>
<td>m1</td>
<td>s^2_{W1} + r s^2_{W0} + r f Q(C)</td>
<td>m1/m2</td>
</tr>
<tr>
<td>Between lines within crosses</td>
<td>c x (f-1)</td>
<td>m2</td>
<td>s^2_{W1} + r s^2_{W0}</td>
<td>m2/m3</td>
</tr>
<tr>
<td>Within lines</td>
<td>(c x f) x (r-1)</td>
<td>m3</td>
<td>s^2_{W1}</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>(c x f x r)-1</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 3. Potential genetic progress estimates in each cross.

<table>
<thead>
<tr>
<th>Cross</th>
<th>Lines mean</th>
<th>Between lines variance</th>
<th>Expected genetic progress</th>
</tr>
</thead>
<tbody>
<tr>
<td>A x B</td>
<td>X_{AB}</td>
<td>VarAB</td>
<td>X_{AB} + 0.798 x <em>{(0.20 x Var</em>{AB})}</td>
</tr>
<tr>
<td>A x C</td>
<td>X_{AC}</td>
<td>VarAC</td>
<td>X_{AC} + 0.798 x <em>{(0.20 x Var</em>{AC})}</td>
</tr>
<tr>
<td>B x D</td>
<td>X_{BD}</td>
<td>VarBD</td>
<td>X_{BD} + 0.798 x <em>{(0.20 x Var</em>{BD})}</td>
</tr>
<tr>
<td>etc</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

h^2 = 0.10; Var_{AB} represents half of the additive genetic variance of the AxB cross; and the selection pressure is 0.5 corresponding to k = 0.798

Table 4. Areas occupied by two breeding designs based on conventional pedigree selection or including an early evaluation trial.

<table>
<thead>
<tr>
<th>On station breeding activities</th>
<th>Pedigree selection (1)</th>
<th>Early Evaluation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crosses</td>
<td>1.2 per 1000 m² of selection</td>
<td>1.2</td>
</tr>
<tr>
<td>F2 generation</td>
<td>25 to 30% of the segregating material</td>
<td>10%</td>
</tr>
<tr>
<td>EE trial in F3</td>
<td>25 to 30% of the segregating material</td>
<td>55%</td>
</tr>
<tr>
<td>F4 and following generations</td>
<td>40 to 45% of the segregating material</td>
<td>35%</td>
</tr>
<tr>
<td>On station evaluation trials</td>
<td>35 to 40% of the total breeding program</td>
<td>35 to 45%</td>
</tr>
<tr>
<td>TOTAL for 10 crosses (m²)</td>
<td>13,000 m²</td>
<td>13,000 m²</td>
</tr>
</tbody>
</table>

(1) after Lançon (1994) and rectified for a 0.8 m instead of 1 m inter-row

Table 5. Number of analysis per cross.

<table>
<thead>
<tr>
<th>On station breeding activities</th>
<th>Pedigree selection</th>
<th>Early Evaluation</th>
</tr>
</thead>
<tbody>
<tr>
<td>F2 generation</td>
<td>70 plants</td>
<td></td>
</tr>
<tr>
<td>F3 EE trial</td>
<td>20 lines and 50 plants</td>
<td>2 x 30 lines</td>
</tr>
<tr>
<td>F4 generation</td>
<td>10 lines and 35 plants</td>
<td>1/2 x (30 lines and 125 plants)</td>
</tr>
<tr>
<td>F5 generation</td>
<td>5 lines and 20 plants</td>
<td>1/2 x (30 lines and 125 plants)</td>
</tr>
<tr>
<td>F6 and following generations</td>
<td>5 lines and 10 plants</td>
<td>1/2 x (5 lines and 30 plants)</td>
</tr>
<tr>
<td>Total</td>
<td>225</td>
<td>230</td>
</tr>
</tbody>
</table>