Heritability and selection response of yield components and fibre properties in an inter-specific derived RIL population of cotton

Shiming Liu · Danny J. Llewellyn · Warwick N. Stiller · John Jacobs · Jean-Marc Lacape · Greg A. Constable

S. M. Liu · W.N. Stiller · G.A. Constable (✉)
CSIRO Plant Industry, Narrabri, NSW 2390, Australia
e-mail: greg.constable@csiro.au

D.J. Llewellyn
CSIRO Plant Industry, P.O. Box 1600, Canberra, ACT 2601, Australia

J. Jacobs

Bayer BioScience N.V., Technolgiepark 38, Gent, Belgium

J-M. Lacape
UMR-DAP, CIRAD, Avenue Agropolis, 34398, Montpellier Cedex 5, France
Abstract  Exploiting genetic variation through inter-specific breeding has improved cotton yield, fibre properties and adaptability. The objectives of this study were to examine heritability and selection response of yield components and fibre properties in a recombinant inbred line (RIL) population from an inter-specific cross between *Gossypium hirsutum* (Gh) variety, Guazuncho 2 and *G. barbadense* (Gb) line VH8-462. A population of 93 and 82 RILs was tested in two seasons, with two parents and local controls, Sicot 75 (Gh) and Sipima 280 (Gb) in field experiments. Seed cotton samples hand harvested before and after defoliation were used to measure lint percent, boll weight, 100 seed weight and the lint to measure fibre length, uniformity, short fibre index (SFI), elongation, strength, micronaire, maturity ratio (MR), percent of maturity (PM) and fineness. There was large phenotypic variation for individual traits and transgressive segregation occurred in lint percent, lint weight/seed, fibre N%/seed, uniformity, SFI, elongation, MR and PM. Narrow sense heritabilities were moderate for yield components (34.3% ~ 41.2%) and for key fibre properties, length, strength, micronaire and fineness (38.3 to 42.1%), which led to a predicted response of 6.7% to 24.0% for yield components and 3.9% to 10.9% for key fibre properties under a selection intensity of 10%. Favourable associations were seen between key fibre properties, but an adverse association between lint percent and each of the fibre properties. Only five RILs were identified with desirable combinations. The results demonstrate the value of exploiting inter-specific variation to develop cotton germplasm and how breeding strategies can be improved.
Key Words  Inter-specific breeding · heritability · selection response · phenotypic correlation · recombinant inbred lines · *Gossypium hirsutum* L. · *G. barbadense* L.
Introduction

Of the two main tetraploid species of cotton that are cultivated for fibre, *Gossypium hirsutum* L. (Gh) achieves higher yields and is more widely adapted to different growing environments, but produces average quality fibre; while *G. barbadense* L. (Gb) has lower yields and limited adaptation, but produces excellent fibre (i.e. extremely long, strong and fine) that attracts a price premium from textile manufacturers. This nexus has continued to attract attention from cotton breeders aimed at moving desirable traits between the species. Such efforts have led to improved Gh fibre quality and Gb yield (Meredith 1991; Bowman *et al.* 1996; Bowman and Gutierrez 2003; Percy 2009). In segregating generations of Gh x Gb crosses, however, genetic breakdown can be substantial, due to plant loss from physiological disorders and male sterility (Brown and Ware 1958; Meyer 1974; Lubbers and Chee 2009). Molecular genetic evidence demonstrates that multi-locus epistatic interactions in Gh x Gb crosses are responsible for maintaining individual genome integrity and limiting inter-genomic recombination and/or introgression. However, some specific genomic regions were prone to inter-genomic exchange (Jiang *et al.* 2000) and these may be responsible for the limited improvements so far achieved with inter-specific Gh x Gb breeding. More recently Gh x Gb crosses have been used to find and apply molecular markers (for example, Lacape *et al.* 2005; Chee and Campbell 2009; Lacape *et al.* 2009) for facilitating trait introgression as the level of intra-specific DNA polymorphism within either cotton species is generally quite low and impractical for marker-assisted breeding.

Quantitative genetic evidence in cotton so far has demonstrated that lint yield is governed by additive and non-additive gene effects. Lint yield is known as an outcome of
a number of yield components including boll number, boll weight, seed weight, lint
percent as well as seed N%/boll and lint/seed (Worley et al. 1976). These components
show high heritability, and selection based on them is more effective for manipulating
lint yield when trait relations are properly considered (Meredith 1984; Calhoun and
Bowman 1999; Coyle and Smith 1997).

Fibre quality described by length, length uniformity, strength, short fibre index,
elongation, maturity and fineness impact on the abilities of the fibre to be spun into yarn
of different qualities and are mainly subject to additive gene effects and are moderately
heritable (Meredith 1984; May 1999). With the evolution of spinning technologies, there
has been an increased demand for longer, stronger, more uniform, mature and finer cotton
fibres (Chee and Campbell 2009; Foulk et al. 2009). Fibre quality properties reflect
different physical aspects of individual cotton fibres and in particular the mass of the
fibre, which is to some extent a yield component. This is particularly true for length,
uniformity, maturity and fineness (Bange et al. 2009). However, relationships between
yield and fibre properties are complex. Yield and/or lint percent are negatively correlated
with fibre strength possibly due to the existence of unfavourable linkages and/or gene
pleiotropy (Meredith 1984; Smith and Coyle 1997). Mitigation of such adverse
associations requires exploiting genetic/allelic variation for fibre properties in both intra-
and inter-specific crosses (Culp and Harrell 1973; Meyer 1974; Culp et al. 1979; Smith
and Coyle 1997; Liang et al. 2002; Chee and Campbell 2009).

Recombinant inbred lines (RILs) of a Gh x Gb cross developed by CIRAD,
Montpellier, France were evaluated under Australian conditions over two seasons as part
of an international effort for QTL mapping of fibre quality properties (Lacape et al. 2009;
Lacape et al. 2010). In this paper, we report heritability and selection response of yield components and fibre properties in this population. Breeding strategies are discussed in terms of using inter-specific crosses as an additional approach for developing diverse germplasm in cotton breeding programs.

Materials and Methods

Origin of the RIL population and field experimental designs

The RIL population generated by CIRAD was derived from an inter-specific cross between Gh variety Guazuncho 2 (Gz2) and Gb accession VH8-462 (VH8), through single seed descent from the F2 generation as described by Lacape et al. (2009). A small quantity of seed of 140 individual RILs at F6 to F9 generation were obtained in 2006 and then grown in the CSIRO quarantine glasshouse for seed multiplication and to meet Australian quarantine conditions. RILs used in the field experiment in this study were thus at least at the F7 – F10 generation in 2007/08 and at the F8 – F11 generation in 2008/09.

The number of RILs used in field experiments in the two cropping seasons varied (Table 1). In the 2007/08 season, the amount of seed was limited for most test RILs after initial seed multiplication and was only sufficient in many cases to plant single plots, although some were replicated. Because some of the RILs exhibited extremely vigorous growth and very late maturity under Australian conditions they failed to have any mature bolls by the end of the 2007/08 season, so in the 2008/09 season, only 82 of the original 140 RILs were retained for further testing, although again seed supplies of some RILs were limited because of their poor productivity. Over half of them were planted in two or
more replicate plots and the rest were planted as a single plot each. In both seasons, the
two parents and two locally bred controls, Sicot 75 (Gh) and Sipima 280 (Gb) were
planted in the experiment.

The experiments were set out according to a partial replicate design generated using
DIGGER software (Coombes 2002). In 2007/08, the experiment was laid out in a
rectangular grid with 9 rows and 15 columns in which test RILs took single or 2 or 3
plots (Table 1), the parents had a single plot each and the two Australian controls had 11
plots each. In 2008/09, the experiment was arranged in a rectangular grid with 10 rows
and 20 columns where individual RILs had unequal replicate plots ranging from single to
4 (Table 1) and Gz2, VH8, Sicot 75 and Sipima 280 had 14, 6, 15 and 23 plots,
respectively. In these experiments, single rows of 12 m in length were used as the plot
size with 1 m row spacing. Seeding rate was 18-22 g per plot and the final plant stand
was 7-14 plants/m. The experiment was located in the CSIRO Leitch Lease (E 30° 10’,
S149° 35’) at Myall Vale, NSW, Australia, which has a self mulching vertisol. Standard
commercial practices were used for fertilizer, irrigation and control of pests and weeds.

Seed cotton sampling, yield component & fibre property measurements

In order to obtain seed cotton samples representing bolls developed and matured at
different time, two hand harvests were carried out in the experiment each season. The
first harvest was prior to the initial defoliation and the second after final defoliation. The
two harvests were separated by about four weeks. Seed cotton samples were taken from
15 to 70 open bolls representing those that had matured prior to and post defoliation in
the plots. The samples were then weighed and ginned using a 20 saw gin to obtain lint
and seed weight. Lint samples were then used for fibre testing and seeds used to measure
100 seed weight.

Due to large differences of maturation within the population, 24 and 9 RILs had no open
bolls at the end of each season, with some only having sufficient mature bolls post
defoliation to get a minimal weight of lint sample for fibre testing (Table 1). As a result,
only 68 RILs had phenotyping data in common across both seasons for lint percent,
within-boll yield components and fibre property measures.

Average boll weight was derived from seed cotton sample weight and the number of
harvested bolls for individual plots and lint percent was the ratio of lint weight after
ginning and seed cotton weight. Two 100 seed sub-samples were obtained from
individual seed samples post ginning and the average represented 100 seed weight. Based
on Worley et al. (1976) ontogenetic cotton yield model, lint weight, seed weight and boll
number of each harvested sample were used to derive lint and seed weight/boll; and then
seed N°/boll and lint weight/seed were estimated using 100 seed weight as a conversion
factor.

Fibre properties were determined with an Uster High Volume Instrument (HVI 900)
and Shirley Fineness Maturity Tester (FMT3). HVI gave the measures of length,
uniformity, short fibre index (SFI), elongation, strength and micronaire and FMT gave
maturity ratio (MR), percent maturity (PM) and fineness.

Fibre N°/seed was determined for each sample using the formula: 1000,000 * lint
weight per seed (g)/(length (mm) * uniformity (%) * micronaire). Fibre perimeter was
determined by applying Montalvo’s (2005) formula: $\sqrt{4\pi^{*}\text{fineness}}/(0.577*1.52*\text{maturity}
\text{ ratio})$. 
At the end of each season, a plot harvester was used to pick the rest of the seed cotton in each plot, which contained considerable amounts of trash and plant residuals particularly for those RILs with few open bolls (Table 1). The bulk harvest data was not used for statistical analysis, but used as a yield potential measure of RILs with elite fibre properties.

Data analysis

There was one independent dataset for each harvest time within each season, thus, the full dataset for the analysis could be viewed as four experiments with the degree of their connectivity determined by whether seed cotton samples of particular genotypes were present at the different harvests. Structurally, it mimics the dataset of a multi-environment trial used in crop improvement programs for evaluating advanced breeding lines or varieties, but with limited environments. With this regard, the mixed model approach was appropriate for a combined data analysis (see Smith et al. 2005).

The analysis regarded test season and harvest time as fixed terms and test genotypes (RILs, parents and controls) and genotype × environment interaction (i.e test season and harvest time within each test season) as random terms. In terms of the design features of the experiment, spatial variation at the experiment level was modelled through including appropriate fixed and/or random effects of row or column or both to account for global and extraneous variation and by using a covariance structure of a separable autoregressive process of order one (AR1 × AR1) for the residual. Once the best model was fitted, variance components for each random term and empirical best linear unbiased predictions (E-BLUPs) for 72 genotypes (68 RILs, two parents and two controls) were obtained.
In order to determine the variance of the RIL population, a new factor was created with five different levels which represent the RILs, two parents and two controls. Then the model was refitted including this new factor as a fixed term to obtain variance components of genotypes only related to the RIL population ($V_{RIL}$) rather than all test genotypes (Smith et al. 2006).

In theory, $V_{RIL}$ represents two fold additive variance of the F$_2$ population in this case where they are derived from two inbred parents through selfing with the assumption of the absence of epistasis (Bernardo 2002). Heritability in the narrow sense ($h^2$) was then calculated using the formula of $100 \times 0.5 \times \frac{V_{RIL}}{V_P}$, where $V_P$ represents phenotypic variance and is the sum of variance components of genotype ($V_g$), genotype × environment interaction ($V_{gxe}$) (i.e. genotype × season and genotype × harvest time within test season) and the error variance ($V_{error}$). The selection response was predicted for the scenario in which the top 10% RILs is retained using the equation of $R = k \times \sqrt{V_P} \times h^2$, where $k$ is the standardised selection differential and can be estimated when the trait phenotype follows a normal distribution in a breeding population (Falconer, 1989).

Pearson’s correlation analysis was conducted between traits using E-BLUPs of 68 RILs. All analysis was carried out using Asreml-R (Butler et al. 2009) and R software.

**Results**

Phenotypic variation of lint percent and within boll yield components

The difference between the two parents was large across the six yield traits examined (Fig. 1). Gb parent VH8 had lower lint percent, smaller bolls, lower seed N°/boll, lint weight/seed and fibre N°/seed and larger seed size compared to Gz2. When compared
with locally bred counterparts, both parents had lower lint percent, lint weight/seed, and
VH8 also had lower seed N\text{\textsuperscript{o}}/boll and fibre N\text{\textsuperscript{o}}/seed. In the field, VH8 was very tall with late maturity (data not shown), highlighting its poor adaptation to the local conditions.

Histograms of individual traits indicated a broad variation but normal distribution for all the traits examined, except for seed N\text{\textsuperscript{o}}/boll and fibre N\text{\textsuperscript{o}}/seed that were skewed towards lower and higher values, respectively (Figure 1). The mean of the population deviated from the mid-parent values to different extents for different traits, and towards the parent Gz2 for lint percent (33.4%), 100 seed weight (11.7 g), lint weight/seed (59.2 mg) and fibre N\text{\textsuperscript{o}}/seed (15,919), or towards VH8 for boll weight (3.3 g) and seed N\text{\textsuperscript{o}}/boll (18.6). Transgressive segregants better than the best parents were present for lint percent (17 out of 68), lint weight/seed (31 out of 68) and fibre N\text{\textsuperscript{o}}/seed (40 out of 68). There were 4, 5 and 21 RILs superior to the better local control for boll weight, lint weight/seed and fibre N\text{\textsuperscript{o}}/seed, respectively.

Phenotypic variation of fibre properties

VH8 had the expected longer, stronger and finer fibre than Gz2, but its fibre was extremely immature and poor in elongation (Fig. 2). The absence of many mature bolls in VH8 prior to defoliation could explain the observed poor fibre maturity. When compared with the locally adapted controls, Gz2 had shorter but finer fibre than Sicot 75, and VH8 had much longer, finer but weaker and immature fibre than Sipima 280.

Segregation in the RILs resulted in large phenotypic differences for all fibre properties (Fig. 2). Length, uniformity, SFI, strength, elongation, micronaire, PM and
fineness were distributed normally (the distribution of MR is not given as being almost
identical to that of PM), but fibre perimeter appeared bimodal. Uniformity and PM, were
skewed towards high values and for SFI towards low values. Except for uniformity and
SFI that were near the mid-parent value, the population means tended to be closer to the
parent, Gz2 for length (1.22 inch), strength (33.2 g/tex), elongation (3.9), micronaire
(3.8), MR (0.88), PM (77.4%), fineness (145.2 µg/m) and perimeter (48.6 µm).
Transgressive segregation resulted in a large proportion of individuals with shorter,
weaker and coarser fibre than the worst parent. However, there were 21, 27, 22, 19 and
19 RILs with improved uniformity, SFI, elongation, MR and PM, respectively, over the
better parent. A proportion of the RILs possessed fibre properties within the range of the
two locally adapted controls, and this is most obvious for length (26%, 18 RILs), strength
(74%, 50 RILs), micronaire (38%, 26 RILs), fineness (40%, 27 RILs) and perimeter
(46%, 31 RILs).
(Fig. 2 here)
Heritability estimates and predicted selection response amongst the RILs

The components of variance shown in Table 2 indicate that genotypic (RIL) differences
were the most important source of variation for yield components, fibre length, strength,
micronaire, MR, PM and fineness. There were significant G × Season interactions for all
traits except for SFI and strength and significant G × S × Harvest time interactions for all
traits except for fibre N^0/seed, elongation and perimeter. The size of the variances due to
G × E interactions were proportionally smaller than that of the RILs, and for those traits
subject to the influence of various G × E interactions, the variance of G × Season was
much larger than that of G × S × Harvest time, i.e. 1.9 to 6.3 fold for yield components
and 1.2 to 3.7 fold for fibre properties. For uniformity, SFI, elongation and perimeter, the error variance exceeded the sum of genotype and $G \times E$.

(Table 2 here)

Narrow sense heritability estimates ranged from 34.3% (100 seed weight) to 41.2% (lint weight/boll) for yield components and from 32.0% (uniformity) to 42.1% (strength) for fibre properties (Table 3). The reduced estimates appeared to be due to either large $G \times E$ interactions, for example with 100 seed weight, or to large experimental error variance, for example, uniformity, elongation and perimeter (Table 2). The predicted selection response associated with the retention of the top 10% of RILs for each trait in the preferred direction indicates that the shift in population mean over an unselected population would be greatest for boll weight and seed $N\%$/boll, moderate for lint weight/seed and fibre $N\%$/seed, and small for lint percent and 100 seed weight; among fibre properties, it was large for SFI, elongation, micronaire and fineness, moderate for length, strength, MR and PM and least for uniformity and fibre perimeter. For fineness related traits, it is the optimal range rather than the lowest values that determine lint quality and sale price in the market which prefers high MR and low fineness. None of the RILs display commercially desirable combinations of these fibre properties, but from a breeding and selection viewpoint the selection response values highlight the potential for reasonable genetic gain for those traits by using this inter-specific population.

(Table 3 here)

Trait associations

Phenotypic correlations were observed in 9 out of the 15 trait pairs for yield components (Table 4). Except for an inverse association between lint percent and 100 seed weight,
they were all positive with the Pearson’s correlation coefficient ranging from 0.28 to 0.95. Boll weight components, boll weight and seed N\(^\circ\)/boll, were strongly correlated (r = 0.95), as were lint percent and lint related components (lint weight/seed and fibre N\(^\circ\)/seed) (r= 0.50 to 0.82).

Correlations were also observed in 30 out of the 36 trait pairs among the nine fibre properties (Table 5). The relationship was moderate to strong between PM (or MR), micronaire, fineness and perimeter. Among HVI measures, SFI is calculated from uniformity through an inverse relationship, so it is expected that a strong negative association would be seen between these traits (r=-0.92). Interestingly, in this RIL population, length, uniformity and strength were all positively related to one another to a moderate extent (r=0.36 to 0.56), suggesting a possibility to improve these properties through simultaneous selection. Length as well as strength showed an inverse association with the measures of fibre fineness (micronaire, fineness and/or perimeter: r=-0.34 to -0.33), so clearly favouring the selection for long, strong and fine fibres. However, undesirable, but weak, associations existed between fineness or micronaire and uniformity, SFI, and elongation (-0.33≤ r ≤0.33), and also between elongation and length, SFI and strength (r=-0.22 to -0.33).

(Tables 4 & 5 here)

Considering the associations between yield components and fibre quality properties, significant correlations were found in 26 out of the 63 trait pairs in this RIL population (-0.40≤ r ≤0.49) (Table 4): Lint percent was negatively associated with length and strength; and this translated into positive correlations between 100 seed weight and length and strength. Boll weight and seed N\(^\circ\)/boll were positively correlated with uniformity, but
negatively correlated with SFI, although all being weak. Seed N\(^0\)/boll was negatively, but
weakly, correlated with strength (r=-0.22). The other important associations included
positive correlations of maturity and fineness properties with lint percent, boll weight,
seed N\(^0\)/boll and lint weight/seed. This is in accord with the fact that uniformity, maturity
and fineness properties are all measures of individual fibre mass. Fibre N\(^0\)/seed showed
negative associations with uniformity, micronaire, fineness and perimeter (r=-0.40 to -
0.28), but positive associations with SFI (r=0.33), suggesting selection for high fibre N\(^0\)
on individual seeds would tend to result in finer, but less uniform fibres.

**Discussion**

Trait segregation and recombination

There were large phenotypic differences within this RIL population for both yield
components and fibre properties. This supports recent similar studies on different RIL
populations of Gh × Gb crosses (e.g. Percy *et al.* 2006; Zeng and Meredith 2009) and on
Gh intra-varietal breeding families (Meredith 1984; May 1999). In addition to the large
variation between individuals, the bimodal distribution for perimeter suggest a tendency
for segregation in the inter-specific cross towards the parental genotypes which is
consistent with earlier observations (Meredith 1991). Even for the traits where the
individuals followed a normal distribution, the mean of the population appeared to tend
towards the agronomically inferior parent, as observed for boll weight and seed N\(^0\)/boll
which were biased towards VH8, while for 100 seed weight, and also key fibre properties
including length, strength and fineness related traits it was biased towards Gz2. Such bias
was noted by He et al. (2008) for length, strength and micronaire and by Percy et al.
(2006) for boll size.

Despite transgressive segregants for a number of yield components and fibre
properties in this study, only five RILs (~3%) would have potential for further breeding
as they combine better yield (data not shown) and fibre properties, which is in agreement
with the other studies (He et al. 2008; Zeng and Meredith 2009). As the family mean and
level of variation determine the potential of a breeding population, when using Gh × Gb
inter-specific crosses to generate novel germplasm it is essential to choose high
performing genotypes as the parents for crossing and to use large population sizes in the
segregating generations. In this instance the population size was clearly too small to
uncover any highly desirable recombinants (only about 68 of the original 140 had
productive phenotypes). It is also clear that this RIL family was not desirable for
Australian conditions.

The negative association between lint percent and fibre length and strength and the
positive association between lint percent and fineness related traits are indicative of the
ongoing breeding challenge to achieve high yield and high fibre quality in cotton varieties
(Meredith and Bridge, 1971; Percy et al., 2006 and Zeng et al., 2009). Similar challenges
are faced in combining some desirable fibre properties, particularly because of the inverse
correlation between elongation with length and strength, as seen here and in other studies
(for example, Miller and Rawlings 1967; He et al. 2008) and between strength and PM.
The evidence also explains to some degree the low frequency of desirable RILs from this
relatively small inter-specific population.
The other interesting relationships found in this study are of fibre N°/seed with lint percent, 100 seed weight, fibre length and strength (Table 4) and between fibre length, strength, uniformity and fineness related traits (Table 5). The former suggests that selecting for increased fibres on individual seeds can increase lint percent, but be neutral on those other characters, which is opposite to the undesirable effect associated with selecting just for high lint percent (Table 4). In other words, selection for high density of fibres on the seed coat would contribute to simultaneous improvement of yield and key fibre properties, which is supported by some previous studies (Zhang et al. 2005; Zeng and Meredith 2009) and deserves more attention by breeders. The latter suggests that it is possible to improve these properties simultaneously through inter-specific breeding.

Breeding implication of heritability and selection response estimates

Heritability estimates for the traits in this study are within the range of those reported previously (Meredith 1984; May 1999; Chee and Campbell 2009). Taking into account how this population was derived, the estimates imply that the genetic variance has been fixable (additive) during inbreeding. The magnitude of selection response suggests that there is a chance of shifting means in favourable directions for each trait except length uniformity and perimeter. Marani (1968b) concluded similarly for fibre length and strength after examining F1’s, F2’s and BCF1’s of a number of Gh x Gb crosses.

It is important to be aware that neither heritability nor predicted selection response in this study are of any use in guiding how selection should proceed in early segregating generations (F2 to F4) of inter-specific crosses, since a large proportion of the alleles for these quantitative traits would still be heterozygous and the phenotype subject to the influence of both fixable (additive) and non-fixable (dominant) gene effects, even
assuming the absence of epistasis. In Gh x Gb crosses, genetic variances due to
dominance and/or epistasis are common and more important than additive effects in early
generations for lint yield, yield components, fibre length, strength and micronaire
(Marani, 1968a,b). However, once advanced generations (F₅ onwards) are reached, most
alleles for individual traits become homozygous, and the attribution of non-fixable gene
effects to genetic variance become small (Allard, 1960). Selection by that stage should be
effective as that predicted in this study. Thus delaying selection until advanced
generations can be particularly important in inter-specific breeding to ensure selection
gain for quantitative traits. This is different to selection strategies used for intra-species
cotton breeding where initial selection for yield components and fibre properties starts in
the early segregating generations (Calhoun and Bowman, 1999).

Conclusions

The population used here would be useful to select desirable inbreds with long, strong
and fine fibre properties. It is also clear that the large genetic variation between Gh and
Gb species can be recombined to improve yield components and fibre properties using
conventional breeding. To ensure the best outcome of such an effort, selection and
breeding strategies should emphasise:

1. Choice of elite and well-adapted Gh and Gb germplasm as parents for crossing

and the use of a large population size during inbreeding, particularly in early
generations.
2. Elimination of plants and/or progeny with morphological and growth deficiencies in early segregating generations and rapid progression through these generations using an off-season nursery or glasshouse.

3. Selection for yield components and fibre properties in advanced generations based on replicated experiments over a few locations and seasons.

Furthermore, as RILs with desirable combinations of fibre properties and yield potential are going to be rare, a standard single cross, followed by a single selection cycle is unlikely to deliver lines with commercial potential and there is a need to consider the incorporation of other breeding strategies. This could include modified backcross, random inter-mating and even mutagenic approaches (Culp et al. 1979; Meredith and Bridge 1971; Meredith 1991) to promote inter-genomic trait recombination and/or introgression. Applying optimal selection strategies and taking account of inter-trait relationships would maximise the chance of discovering desirable genotypes from inter-specific crosses with the limited use of resources.
Acknowledgements

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Table 1  The number of test RILs and their plots and seed cotton samples harvested in two cropping seasons

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<th>2008/09</th>
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<tr>
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</tr>
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</tr>
<tr>
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<td>82</td>
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<td>9</td>
</tr>
<tr>
<td>Post-defoliation only</td>
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<td>Prior &amp; post-defoliation</td>
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<td>52</td>
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**Table 2** Significant sources of variation revealed in a combined data analysis of 68 RILs, their parents and two controls for six yield components and ten fibre properties

<table>
<thead>
<tr>
<th>Trait</th>
<th>Source (%)</th>
<th>Source (%)</th>
<th>Source (%)</th>
<th>Source (%)</th>
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<td>Genotype x Season x Harvest time</td>
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<td>19.1</td>
<td>3.2</td>
<td>26.4</td>
</tr>
<tr>
<td>Seed weight</td>
<td>43.3</td>
<td>24.4</td>
<td>3.9</td>
<td>28.4</td>
</tr>
<tr>
<td>Seed N⁰/boll</td>
<td>53.3</td>
<td>20.4</td>
<td>4.1</td>
<td>22.3</td>
</tr>
<tr>
<td>Lint weight/seed</td>
<td>57.6</td>
<td>9.5</td>
<td>5.0</td>
<td>27.9</td>
</tr>
<tr>
<td>Fibre N⁰/seed</td>
<td>53.3</td>
<td>6.5</td>
<td>1.3&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>38.9</td>
</tr>
<tr>
<td><strong>Fibre properties</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Length</td>
<td>53.0</td>
<td>16.3</td>
<td>4.4</td>
<td>26.3</td>
</tr>
<tr>
<td>Uniformity</td>
<td>34.9</td>
<td>9.2</td>
<td>3.2</td>
<td>52.6</td>
</tr>
<tr>
<td>Short fibre index</td>
<td>44.4</td>
<td>1.5&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>3.9</td>
<td>50.3</td>
</tr>
<tr>
<td>Strength</td>
<td>59.1</td>
<td>2.3&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>5.3</td>
<td>33.2</td>
</tr>
<tr>
<td>Elongation</td>
<td>33.4</td>
<td>12.8</td>
<td>0.2&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>53.5</td>
</tr>
<tr>
<td>Micronaire</td>
<td>56.5</td>
<td>8.8</td>
<td>7.6</td>
<td>27.2</td>
</tr>
<tr>
<td>Maturity ratio</td>
<td>52.6</td>
<td>10.1</td>
<td>7.7</td>
<td>29.6</td>
</tr>
<tr>
<td>Percent maturity</td>
<td>53.3</td>
<td>14.0</td>
<td>7.6</td>
<td>25.1</td>
</tr>
<tr>
<td>Fineness</td>
<td>59.9</td>
<td>5.9</td>
<td>2.7</td>
<td>31.5</td>
</tr>
<tr>
<td>Perimeter</td>
<td>37.9</td>
<td>6.1</td>
<td>0.0&lt;sup&gt;ns&lt;/sup&gt;</td>
<td>55.9</td>
</tr>
</tbody>
</table>

<sup>ns</sup> means not significant
Table 3  Estimates of narrow sense heritability ($h^2$) and predicted selection response for lint percent, within-boll yield components and 10 fibre properties in the RIL population based on a combined data analysis.

<table>
<thead>
<tr>
<th>Trait</th>
<th>$h^2$ (%)</th>
<th>Predicted response with selection intensity of 10% $^a$</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>In units of the trait</td>
<td>In % of the RIL mean</td>
</tr>
<tr>
<td><strong>Yield components</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lint percent (%)</td>
<td>40.6</td>
<td>2.7</td>
</tr>
<tr>
<td>Boll weight (g)</td>
<td>37.8</td>
<td>0.8</td>
</tr>
<tr>
<td>100 seed weight (g)</td>
<td>34.3</td>
<td>0.8</td>
</tr>
<tr>
<td>Seed N°/boll</td>
<td>37.3</td>
<td>4.2</td>
</tr>
<tr>
<td>Lint weight/seed (g)</td>
<td>41.2</td>
<td>6.9</td>
</tr>
<tr>
<td>Fiber N°/seed</td>
<td>40.2</td>
<td>1589.9</td>
</tr>
<tr>
<td><strong>Fibre properties</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Length (inch)</td>
<td>38.3</td>
<td>0.05</td>
</tr>
<tr>
<td>Uniformity (%)</td>
<td>32.0</td>
<td>0.8</td>
</tr>
<tr>
<td>Short fibre index</td>
<td>36.9</td>
<td>-0.6</td>
</tr>
<tr>
<td>Strength (g/tex)</td>
<td>42.1</td>
<td>2.2</td>
</tr>
<tr>
<td>Elongation</td>
<td>33.1</td>
<td>0.3</td>
</tr>
<tr>
<td>Micronaire</td>
<td>40.7</td>
<td>-0.4</td>
</tr>
<tr>
<td>Maturity ratio</td>
<td>39.0</td>
<td>0.05</td>
</tr>
<tr>
<td>Percent maturity</td>
<td>38.7</td>
<td>3.8</td>
</tr>
<tr>
<td>Fineness ($\mu g/m$)</td>
<td>42.0</td>
<td>-15.9</td>
</tr>
<tr>
<td>Perimeter ($\mu m$)</td>
<td>33.6</td>
<td>-1.3</td>
</tr>
</tbody>
</table>

$^a$ minus symbol before the value means the preference of selection to small value. For fibre fineness related properties, in breeding practice, selection prefers to keep those RILs within optimal ranges rather than with the smallest value, thus their predicted response is overestimated.
Table 4  Pearson’s correlation coefficients of yield components and between yield component and fibre properties of 68 RILs from an inter-specific cross based on a combined data analysis

<table>
<thead>
<tr>
<th>Trait</th>
<th>Lint percent</th>
<th>Boll weight</th>
<th>100 seed weight</th>
<th>Seed N°/boll</th>
<th>Lint weight/seed</th>
<th>Fibre N°/seed</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Yield components</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Boll weight</td>
<td>0.37**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>100 seed weight</td>
<td>-0.41***</td>
<td>0.13</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Seed N°/boll</td>
<td>0.36**</td>
<td>0.95***</td>
<td>-0.13</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lint weight/seed</td>
<td>0.82***</td>
<td>0.45***</td>
<td>0.15</td>
<td>0.28*</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fibre N°/seed</td>
<td>0.50***</td>
<td>0.09</td>
<td>0.11</td>
<td>-0.06</td>
<td>0.59***</td>
<td></td>
</tr>
<tr>
<td><strong>Fibre properties</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Length</td>
<td>-0.23*</td>
<td>0.00</td>
<td>0.36**</td>
<td>-0.07</td>
<td>-0.01</td>
<td>-0.10</td>
</tr>
<tr>
<td>Uniformity</td>
<td>0.10</td>
<td>0.31**</td>
<td>0.10</td>
<td>0.27*</td>
<td>0.19</td>
<td>-0.28*</td>
</tr>
<tr>
<td>Short fibre index</td>
<td>-0.02</td>
<td>-0.27*</td>
<td>-0.10</td>
<td>-0.23*</td>
<td>-0.11</td>
<td>0.33**</td>
</tr>
<tr>
<td>Strength</td>
<td>-0.29*</td>
<td>-0.11</td>
<td>0.44***</td>
<td>-0.22*</td>
<td>-0.03</td>
<td>-0.01</td>
</tr>
<tr>
<td>Elongation</td>
<td>0.10</td>
<td>-0.02</td>
<td>-0.06</td>
<td>-0.04</td>
<td>0.08</td>
<td>-0.08</td>
</tr>
<tr>
<td>Micronaire</td>
<td>0.43***</td>
<td>0.41***</td>
<td>-0.15</td>
<td>0.44***</td>
<td>0.37***</td>
<td>-0.36**</td>
</tr>
<tr>
<td>Percent of maturityᵃ</td>
<td>0.49***</td>
<td>0.46***</td>
<td>-0.13</td>
<td>0.48***</td>
<td>0.44***</td>
<td>-0.20</td>
</tr>
<tr>
<td>Fineness</td>
<td>0.39***</td>
<td>0.37***</td>
<td>-0.10</td>
<td>0.38***</td>
<td>0.39***</td>
<td>-0.40***</td>
</tr>
<tr>
<td>Perimeter</td>
<td>0.12</td>
<td>0.08</td>
<td>-0.05</td>
<td>0.09</td>
<td>0.15</td>
<td>-0.36**</td>
</tr>
</tbody>
</table>

ᵃ Maturity ratio has a perfect correlation with percent of maturity (r=0.997), thus correlation coefficients between maturity ratio and other traits are not given here.

*, ** and *** indicate significance at the probability level of .05, .01, .001, respectively.

Table 5  Pearson’s correlation coefficients of nine fibre properties of 68 RILs from an inter-specific cross based on a combined data analysis

<table>
<thead>
<tr>
<th>Trait</th>
<th>Length</th>
<th>Uni</th>
<th>SFI</th>
<th>Strength</th>
<th>El</th>
<th>Mic</th>
<th>PM</th>
<th>Fineness</th>
</tr>
</thead>
<tbody>
<tr>
<td>Uniformity (Uni)</td>
<td>0.36**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Short fibre index (SFI)</td>
<td>-0.43***</td>
<td>-0.92***</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Strength</td>
<td>0.56***</td>
<td>0.45***</td>
<td>-0.44***</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Elongation (El)</td>
<td>-0.33**</td>
<td>0.11</td>
<td>-0.23*</td>
<td>-0.22*</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Micronaire (Mic)</td>
<td>-0.33**</td>
<td>0.27*</td>
<td>-0.23*</td>
<td>-0.33**</td>
<td>0.29*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Percent of maturityᵃ</td>
<td>-0.17</td>
<td>0.37***</td>
<td>-0.29*</td>
<td>-0.26*</td>
<td>0.22*</td>
<td>0.86***</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fineness</td>
<td>-0.34**</td>
<td>0.26*</td>
<td>-0.24*</td>
<td>-0.29*</td>
<td>0.33**</td>
<td>0.93***</td>
<td>0.73***</td>
<td></td>
</tr>
<tr>
<td>Perimeter</td>
<td>-0.34**</td>
<td>0.02</td>
<td>-0.05</td>
<td>-0.16</td>
<td>0.24*</td>
<td>0.50***</td>
<td>0.12</td>
<td>0.74***</td>
</tr>
</tbody>
</table>

ᵃ Maturity ratio has a perfect correlation with percent of maturity (r=0.997), thus correlation coefficients between maturity ratio and other traits are not given here.

*, ** and *** indicate significance at the probability level of .05, .01, .001, respectively.
Fig. 1 Mean distribution of 68 RILs of the inter-specific cross, their parents and two locally bred controls for lint percent and five within-boll yield components (Closed triangles(▼), VH8; Open triangles(▽), Guazuncho 2; Closed circles (●), Sipima 280; Open circles(○), Sicot 75; Closed diamonds (◆), mean of all RILs)
Fig. 2 Mean distribution of 68 RILs of the inter-specific cross, their parents and two locally bred controls for nine fibre properties (Closed triangles (▼), VH8; Open triangles (▽), Guazuncho 2; Closed circles (●), Sipima 280; Open circles (○), Sicot 75; Closed diamonds (◆), mean of all RILs).