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Early generation selection strategies for breeding better combinations of cotton yield and fibre quality

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ABSTRACT

This research investigated the use of elite parents and breeding selection strategies for reducing the negative association between cotton yield and fibre quality. Three populations, each with 100 lines developed from high yielding and high fibre quality parents were advanced in a pedigree method to the replicated stage with no selection in any generation. A yarn quality index (YQI) was used as a measure to integrate different fibre properties of length, strength and fineness. Each population had similar means and good genetic variation existed for lint percent (LP) and fibre quality traits in the single plant (SPS) stage; as well as for yield, fibre quality and YQI traits in the Progeny Row (PR) stage and in the following two years of replicated experiments. There were significant associations between SPS ($P < 0.05$) or PR ($P < 0.01$) and subsequent replicated data for yield and fibre quality traits. LP at the SPS and yield at PR stage could successfully select highest yielders as measured in subsequent replicated experiments; broad sense heritability was high for all measures. Retrospective analysis determined the proportion required in early generation selections of SPS and PR to successfully identify the highest ranked lines for mean yield and quality in subsequent replicated experiments. Populations had similar proportions (10%) with high yield (>2000 kg lint ha^{-1}) and high quality (YQI > 62), but the populations differed in the numbers of lines with low yield (<1800 kg lint ha^{-1}). For combining high yield and YQI, to capture all 29 lines which subsequently had high yield and YQI in replicated experiments, it would have been necessary to select 55–89% of the highest yielding lines in PR, which would lead to large numbers if lines were to be assessed in replicated experiments. A selection strategy to improve yield and fibre quality combinations which would successfully keep the majority of best lines, would be to select the best 27% of yielders and best 11% of YQI from PR, then select for the best combinations of yield and YQI in replicated experiments. We identified one line which broke the negative relationship between yield and fibre quality within these populations. We conclude that early generation selection for LP, yield and quality would enable unsuitable lines to be discarded so chosen lines could be better assessed in later generations.

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1. Introduction

Cotton is the leading natural fibre crop internationally, but due to competition with synthetics, changes to spinning techniques and shifts to finer yarns, there is a continual need to improve fibre

quality. Longer, stronger and finer premium fibre quality allow for finer yarns and upscale garments which have more spinning value and may have a better price. The drawback is that a negative association between yield and quality prevents the highest yielding cultivars from possessing premium fibre quality (Clement et al., 2012). Breeding efforts have been successful in improving yield of premium fibre quality cultivars, but not as much as yield improvements in cultivars with base fibre quality (Campbell et al., 2014). Yield penalties incurred by fibre quality improvements deter producers from embracing cultivars with superior fibre quality.

Cotton breeding programs ultimately supply new improved cultivars. Australian gains in yield through time have been due mainly to genetics, management and the interaction of the two (Liu et al., 2013). Most cotton breeding programs have accomplished genetic improvement by using a modified pedigree breeding method (Bowman, 2000; Keim, 2007). In a pedigree breeding scheme

Abbreviations: AR1, Autoregressive Process; ACRI, Australian Cotton Research Institute; CSIRO, Commonwealth Scientific and Industrial Research Organisation; EBLUE, Empirical best linear unbiased estimates; EBLUP, Empirical best linear unbiased predictions; HVI, High Volume Instrument; LP, Lint Percent; PR, Progeny row; REML, Restricted Maximum Likelihood; SPS, Single Plant Selection; YQI, Yarn Quality Index.

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(Fehr, 1991), it is necessary to go through a single plant stage (SPS), with seed from each plant subsequently sown as an individual Progeny Row (PR), which then provides seed for future replicated experiments. The finer detail on when to make breeding selections for particular traits varies widely (Calhoun and Bowman, 1999). May and Green (1994) assessed breeding methods and selection criteria for improving fibre quality and concluded that the selection of F_2 bulk populations for fibre traits was more beneficial than selecting individual F_2 plants when initiating a pedigree breeding scheme for quality improvement.

A breeder has a considerable dilemma with deciding on number of crosses to do each year, the size of subsequent populations developed, the traits to be screened, the proportion selected to be applied and the generation to apply that selection. PRs may be used for observations with heavy selection pressure based on plant type and other traits such as disease resistance (Keim, 2007). Visual selection has long been practiced in cotton breeding as a way to cull out undesirable phenotypes in early generations (Jensen, 1988) and it was effective in early breeding efforts due to the distinct phenotypes from exotic material (Richmond, 1951). However there may be merit in measuring desirable traits in SPS and PR. Lint percent (LP) is one yield component (Coyle and Smith, 1997) that has been found to be positively correlated with lint yield (Bridge et al., 1971) and could be used as an early generation selection criteria. In PR, yield can be measured directly and fibre quality can be used as selection criteria especially if Nearest Neighbour and Mixed Model statistical analyses are used to improve the accuracy of trait measures (Jensen, 1988; Cullis et al., 2006; Liu et al., 2014). Selection is necessary in SPS and PR, otherwise the logistics in numbers of entries into replicated experiments become problematical. Early generation selection allows undesirable lines to be discarded and not consume resources unnecessarily which allows more effort on lines selected with desirable traits and on making additional crosses.

In order to develop more targeted breeding strategies to combine high yield and premium fibre quality, elite parents for yield and quality were used to develop three separate populations that would be advanced in a pedigree breeding method from SPS, PR and two years replicated stages with no selection. Once all generations were processed, selection criteria were applied to the data in each generation to determine the usefulness of the selection methods in identifying what were subsequent superior lines for yield, quality or combinations of yield and quality. A simplified yarn quality index (YQI) was used to create a criteria for fibre quality by integrating fibre length, strength and fineness (Hunter, 2004).

2. Methods

A pedigree-breeding study with no selection at any generation was performed in the field at the Australian Cotton Research Institute (ACRI), Narrabri, NSW, starting with field crosses in 2008–09. The soil type was grey clay with heavy texture, classified as Ug 5.2 (Isbell, 1996); the US classification is Typic Haplustert (USDA, 2010). This environment has been proven favourable for cotton, with a season length from sowing to harvest about 180 days; the seasonal conditions have been presented previously (Clement et al., 2013). All field experiments were sown in early to mid October with a cone seeder in rows 100 cm apart aiming at 10 plants per metre of row. Crops were managed with full irrigation, fertilizer, spraying for pests as required and weed management by pre-planting herbicides such as trifluralin and fluometuron followed by inter-row cultivation prior to flowering.

High yielding parents were crossed with high fibre quality parents to develop three separate populations, CSX206, CSX211 and CSX218 (Table 1); the parents were representative of breeding

material from within the local CSIRO cotton breeding program. The crosses consisted of approximately 40 successful crosses per population; the F_1 seeds were sown for selfing in the glasshouse in winter of 2009. Individual F_2 plants were grown in a spaced (40 cm on 100 cm rows) SPS nursery in 2009–10. The population size was limited to 100 in each cross to make a practical size of subsequent replicated experiments. One hundred single plants from each population along with 20 individual plants of control cultivars Siokra V-18 (Reid, 2003a) or Sicot 71 (Reid, 2003b) were hand harvested. The data from the control cultivar plants were used to determine a nominal standard error for SPS plants.

In 2010–11, $F_{2:3}$ PRs were grown in single 100 cm row plots, 12 m long in an augmented design where each line was entered once and two local controls, Sicot 71 and Siokra 24 (Stiller and Reid, 2005) were planted alternatively, once in every six plots (i.e. 16% controls). Local experience has been that single row plots are adequate when plant growth habit was similar, which was the case for these populations. The $F_{2:4}$ lines were grown in 2011–12 as a replicated experiment in two separate fields at ACRI with two replications per site. In 2012–13, $F_{2:5}$ lines were grown as a four replication experiment in one field. In the replicated experiments, Sicot 71 and Siokra 24 were included as controls. Replicated experiments were planted in a Latinized alpha design consisting of one row plots \times 12 m. All PR and replicated experiments were harvested with a single row spindle picker at maturity.

A 200 g hand harvested sample from each SPS plant or 250 g subsample from machine harvested plots was used for determining LP on a 20-saw gin. Fibre quality was tested on a HVI 1000 (USTER Technologies Inc., Charlotte, NC) with fineness and maturity ratio measured on a Shirley Fineness Maturity Tester (FMT-3; Shirley Developments Ltd., Stockport, England). A yarn quality index (YQI) was calculated which combines fibre length, strength and fineness ($YQI = \text{length} \times \text{strength}/\text{fineness}$) (Hunter, 2004). The units of this index are $\text{m kN m kg}^{-1} (\mu\text{g m}^{-1})^{-1}$. This is an alternate, simplified version of other published YQI (Iyengar and Gupta, 1974; Subramanian et al., 1974), yet it is an integrated measure to use in selection of fibre quality relevant to yarn tenacity. The Q-score developed by Bourland et al. (2010) is based on length, micronaire, length uniformity and strength and is aimed at predicting US loan value.

Spatial models based on the first order separable autoregressive process (AR1) (Gilmour et al., 1997) were applied in the analysis of individual and combined trial datasets in this study. For individual experiments, the treatment effect (populations and controls) was fitted as fixed effect and lines within the population as random effect. Liu et al. (2014) demonstrate the common presence of different forms of spatial variations in cotton breeding trials. When such variations existed, they were taken into account in the analysis. The combined analysis followed a one stage approach under the mixed model framework (Smith et al., 2005) with the detail as follows: for experiments (or site in 2011–12), population and their interaction were fitted as fixed and test lines within individual populations and interactions with site were fitted as random. For the three year pooled data, year, treatment and the year \times treatment interaction were fitted as fixed and lines within populations and their interaction with year were fitted as random. Year was fitted as a fixed effect as the experiments in this study as it was conducted in a small number of years. Either for individual or for combined datasets, when appropriate models were fitted, empirical best linear unbiased estimates (E-BLUEs) were obtained for population, parents and controls. Similarly, empirical best linear unbiased predictions (E-BLUPs) were obtained for individual test lines in populations. All analyses used ASREML-R software (Butler et al., 2009).

Broad sense heritability (H^2) was calculated as the ratio between genotypic and phenotypic variance (i.e. V_g/V_p). Phenotypic variance (V_p) is the sum of REML estimated variance for genotype or

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