

VARIATION, HERITABILITY AND ASSOCIATION OF YIELD, FIBER AND MORPHOLOGICAL TRAITS IN A NEAR LONG STAPLE UPLAND COTTON POPULATION

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Abstract

Development of near long staple (NLS) cotton germplasm represents a remarkable improvement in fiber properties of upland genotypes without compromising yield potential. This study aimed to evaluate a NLS population for variability in yield, fiber and morphological traits, investigate heritability and genetic advance of these traits, and analyze the interrelationships among them. The NLS lines exhibited large variation for lint yield per hectare and bolls per plant, while little variation for fiber properties. The highest genotypic (GCV) and phenotypic (PCV) coefficient of variation were recorded by lint yield per hectare (25.10%, 23.00%) followed by bolls per plant (18.88%, 16.38%). High heritability along with high response to selection was documented in plant height, bolls per plant and lint yield per hectare indicating that the additive gene function model in the inheritance of these traits and direct selection can be profitably applied on them. Favourable associations were found among fiber length, strength and fineness in this population. It is concluded that there is a great potential in the NSL population for further enhancing yield while maintaining high fiber quality.

Key words: Upland cotton, Near long staple, Variability, Heritability, Genetic advance, Correlation.

Introduction

Cotton is the most important fiber crop in the world. The cultivation varieties of cotton are originated from four species, viz. two diploids *G. herbaceum* L. and *G. arboretum* L., and the two tetraploid species of *G. hirsutum* L. (upland cotton) and *G. barbadense* L. (sea island cotton). Upland cotton is the leading species for cultivation and accounts for about 90% of worldwide cotton fiber production followed by sea island cotton constituting about 8% of the total world production (Han *et al.*, 2004). The former has higher yields and wider adaptability to varied growing environments, but produces ordinary quality fiber; while the latter exhibits lower yields and limited acclimation ability, but achieves excellent fiber (Liu *et al.*, 2011). Cotton breeders have been taking efforts to transfer alleles from sea island genotypes into upland genotypes in order to improve fiber properties of upland genotypes (Smith *et al.*, 1999).

Near long staple (NLS) upland cotton in China has been identified as having High Volume Instrument upper half mean length (UHML) ≥ 31 mm, fiber bundle strength (Str) ≥ 34 cN tex⁻¹ (for northern and northwestern growing regions) or 35 cN tex⁻¹ (for southern growing region), and micronaire (Mic) between 3.6 and 4.3 (for northern and northwestern growing regions) or between 3.8 and 4.4 (for southern growing region) (Anon., 2002). This type of fibers can be incorporated into the manufacture of large size yarn (above or equal to 60S) by combining with sea island cotton fibers in a certain proportion, which is used for the production of high-quality fabrics. Thus, the consumption of expensive sea island fibers can be reduced and in turn production cost decreases for the yarn and textile industry. Currently, the widely grown upland cotton cultivars in China possess medium fiber properties. According to a survey to the fiber quality of 523 commercial upland cotton cultivars extensively cultivated during 1998 to 2011 by

Supervision Inspection and Testing Center of Cotton Quality, Ministry of Agriculture, China, It was showed that 77.1% of them exhibited UHML ranging from 28.0 to 30.9 mm, and 44.51% with Str readings of 26.0 to 28.9 cN tex⁻¹, and 49.34% with Mic readings of 4.3-4.9 (Tang *et al.*, 2012). Thus, high fiber quality cotton production in China fails to meet the domestic demand by the textile industry and has become dependent on imports.

North Jiangxi province belongs to southern growing region with average temperature in summer above 25°C, and long frost-free production period (240-307 days), and availability of moisture, and abundant sunshine (1900-2000 hours per year). The climate conditions are suitable for cotton plant growth, development, and ripening. So, North Jiangxi province is considered as an optimum producer for high fiber quality cotton. However, such cotton varieties are scarce in that region. A breeding program with an aim to develop NSL upland cotton lines was initiated in 2001 in JXAU. Twenty cotton inbred lines carrying the NLS traits have been obtained by multiple crossing followed by pedigree selection. To make the most effective use of these NLS germplasms, it is important to evaluate the genetic potential for improving cotton yield and fiber traits in them. The objective of this study was (i) to assess the phenotypic and genetic variation of yield, yield parameters, fiber quality and morphological traits; (ii) to investigate heritability and genetic advance of all traits in that population; and (iii) to analyze interrelationships among them.

Materials and Methods

Experimental material

Breeding material consisted of 20 NLS upland cotton lines, and which developed by multiple crosses involving four or eight upland parents with better fiber quality but differing in other agronomic traits followed by pedigree selection (Table 1).

Table 1. Pedigrees of near-long staple germplasm lines.

Designation	Pedigree
A101, A105, A106, A107, A112, A113	Bellsiro/Sulian8908//FJA/Sulianmian12
A201, A203, A204, A205, A207, A210	AcalaSJ-2/Yimian no.2//Acala1517E-2/CSJS
A301, A303	AcalaSJ-1-9/Sicala34//SiDe/Kemian no.1
A402, A405, A406, A407, A408, A409, A413	Hopicala/AcalaSJ-4//20-5/CSKE100
A601	Bellsiro/Sulian8908//FJA/Sulianmian12// AcalaSJ-2/Yimian no.2//Acala1517E-2/CSJS
A001, A007, A009, A011, A016, A705, A708, A709	AcalaSJ-1-9/Sicala34//SiDe/Kemian no.1/// Hopicala/AcalaSJ-4//20-5/CSKE100

Experimental design: Field experiment was carried out during 2014 at Jiangxi Agricultural University (JXAU), Nanchang, China. Twenty genotypes were grown in a nursery on 9th April and transplanted to the field on 16th May, 2014. The experiment was arranged in a randomized complete block design with three replicates. The plot size was 9.5 m² having two rows, with rows and plant spacings of 1 m, 0.4 m, respectively. Control of weeds and insects, and furrow irrigation were performed as needed during the growing seasons according to local agronomic recommendation.

Traits measurement: Ten randomly selected plants in the middle of each plot were investigated for bolls per plant and three morphological characters, viz. plant height (PH), first sympodial branch height (FSBH) and total sympodial branches (SB) in late September 2014. Close to harvest, 40 open bolls from each plot were collected and ginned using a laboratory roller gin for boll size (BS), seed index (SI), lint index (LI) and lint percentage (LP) determination. The total seed cotton weight of each plot was calculated as sum of the seed cotton weight of the sampled bolls and the remaining bolls in that plot. Lint yield was calculated by multiplying the seed cotton yield by the lint percentage from the 40 boll samples. Twenty grams of lint from each boll sample was sent to Supervision Inspection and Testing Center of Cotton Quality, Ministry of Agriculture, Anyang, Henan, for high volume instrument (HVI) fiber analyses. The following parameters were analyzed: UHML, Str, Mic and elongation at break (EI).

Statistical analyses: All the data were subjected to analysis of variance (ANOVA) in order to determine the significance of differences in all investigated characters among the genotypes by using the general liner model (GLM) procedure of SPSS 18.0 (Kong, 2006). For each trait the genetic, environmental, and phenotypic variances, broad sense heritability (H^2) expected response to selection (Re) were further estimated from the ANOVA mean squares according to Ahsan *et al.* (2015) and Khan *et al.* (2010). The phenotypic and genetic correlation coefficients were also worked out following the formula outlined by Kempthorne (1957).

Results and Discussion

Genetic, phenotypic, and environmental Variability: The mean performance and the range of variations in all traits investigated are presented in Table 2. The analysis of variance showed significant differences among the lines for all characters. The greatest variance was observed in lint yield ranging from 506.1 to 1253.3 kg ha⁻¹ followed by

bolls per plant with a wide range of 16.3–29.3. The other yield components showed smaller variation ranges compared to bolls per plant. The size of variability available in the NSL lines for economically important characters determines the breeding value of the population. Phenotype variance can be divided into genetic (heritable) and environmental (non-genetic) components. The breeders should separate genetic variance from the phenotypic variance to exercise proper selection in a breeding project since environmental effects influence the genetic variation (Mahaingam *et al.*, 2013). Saleem *et al.* (2016) stated that genetic variability is the basic prerequisite for success in a breeding program. Lint yield per hectare exhibited the largest genotypic and phenotypic variances i.e. 43593.98 and 51927.15 followed by plant height (163.39, 178.33) (Table 3). The smallest genotypic and phenotypic variances were recorded for fiber elongation i.e. 0.01 and 0.01. In difference from the variations affected by the magnitude of the measurement units of different traits, coefficients of variation are not pertinent to the measuring units so they are more useful in studying the NSL cotton population. Genotypic coefficient of variation (GCV) had the same trend as phenotypic coefficient of variation (PCV). The GCV and PCV estimates were higher in lint yield, yield components than fiber qualities. The GCV range varied from 5.95 (boll size) to 23.00% (lint yield per hectare) for the former, while from 1.37 (fiber elongation) to 5.06 % (micronaire) for the latter. The highest PCV and GCV estimates were recorded for lint yield per hectare (25.10%, 23.00%) followed by bolls per plant (18.88%, 16.38%). This suggested that selection pressure can be imposed on the two characters to isolate more promising NSL line. Similar results in cotton were given by Dheva & Potdukhe (2002), Preetha and Raveendran (2007), Dhivya *et al.* (2014) and Ahsan *et al.* (2015). Moderate PCV and GCV within the range of 10 to 15% were observed for plant height, first sympodial branch height and the number of sympodial branches. These traits can be improved by rigorous selection. Fiber properties exhibited low PCV and GCV indicating that there was little potential for fiber quality improvement in the NLS cotton population. In fact, most of NLS lines exhibited the desirable combination of longer fiber length, stronger fiber strength and lower micronaire. The characters such as boll size, lint percentage, seed index and lint index also presented low PCV and GCV suggesting that source of high variability for these characters should be sought to make improvement. Environmental coefficient of variation (ECV) was the highest for lint yield per hectare (17.42%) followed by first sympodial branch height (17.01%), bolls per plant (16.29%) and number of sympodial branches (10.82%), which suggested that these traits were considerably influenced by environmental factors.

Table 2. Estimates of variability for yield, yield components, morphological traits and fiber properties in the near long staple (NLS) cotton population.

Characters	Mean	Range	Mean squares		PCV/%	GCV/%	ECV/%
			Genotypes	Error			
PH/cm	100.80	76.3-127.0	534.98**	44.81	13.25	12.68	6.64
FSBH/cm	27.16	18.8-35.8	47.25*	21.35	14.61	10.82	17.01
SB	13.87	11.0-17.8	7.21**	2.24	11.17	9.28	10.79
BPP	21.06	16.3-29.3	47.45**	4.03	18.88	16.38	16.29
BS/g	4.96	4.5-5.6	0.37**	0.11	7.04	5.95	6.53
LP/%	40.24	34.0-43.9	20.32**	1.63	6.47	6.20	3.17
SI/g	11.30	10.1-13.3	2.80**	0.24	8.54	8.17	4.36
LI/g	7.59	6.4-8.8	1.02**	0.18	7.67	6.96	5.57
LY/kg ha ⁻¹	907.71	506.1-1253.3	155781.44**	24999.49	25.10	23.00	17.42
UHML/mm	31.98	29.7-34.7	5.74**	1.90	4.33	3.54	4.30
Mic	4.89	4.3-5.6	0.27**	0.08	6.08	5.06	5.82
El/%	6.26	6.1-6.5	0.03**	0.01	1.65	1.37	1.60
Str/cN tex ⁻¹	33.57	29.9-36.9	8.07**	1.88	4.89	4.28	4.09

PCV: phenotypic coefficient of variation, GCV: genotypic coefficient of variation, ECV: environmental coefficient of variation, PH: plant height, FSBH: first sympodial branch height, SB: sympodial branches, BPP: bolls per plant, BS: boll size, LP: lint percentage, SI: seed index, LI: lint index, LY: lint yield per hectare, UHML: upper half mean length, Mic: micronaire, El: elongation, Str: fiber bundle strength

Table 3. Estimates of genetic variance, phenotypic variance, broad sense heritability (H^2) and predicted selection response (Re) for yield, yield components, morphological traits and fiber properties in the near long staple (NLS) cotton population.

Characters	Genetic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Heritability/ % (H^2)	Predicted response with selection intensity of 10% Re	
				Re	Re (%)
PH/cm	163.39	178.33	91.62	21.47	21.30
FSBH/cm	8.63	15.75	54.81	3.82	14.06
SB	1.66	2.40	68.94	1.88	13.52
BPP	11.89	15.82	75.20	5.25	24.92
BS/g	0.09	0.12	71.31	0.44	8.81
LP/%	6.23	6.77	92.00	4.20	10.44
SI/g	0.85	0.93	91.31	1.55	13.69
LI/g	0.28	0.34	82.38	0.84	11.09
LY/kg ha ⁻¹	43593.98	51927.15	83.95	335.74	36.99
UHML/mm	1.28	1.91	66.99	1.63	5.08
Mic	0.06	0.09	69.43	0.36	7.41
El/%	0.01	0.01	68.75	0.12	1.99
Str/cN tex ⁻¹	2.06	2.69	76.67	2.21	6.57

PH: plant height, FSBH: first sympodial branch height, SB: sympodial branches, BPP: bolls per plant, BS: boll size, LP: lint percentage, SI: seed index, LI: lint index, LY: lint yield per hectare, UHML: upper half mean length, Mic: micronaire, El: elongation, Str: fiber bundle strength

Heritability and predicted selection response: GCV alone is not helpful for effective selection, but together with heritability estimates could determine the extent of selection response (Mahaingam *et al.*, 2013). Broad sense heritability estimates ranged from 71.31 (boll size) to 92.00% (lint percentage) for lint yield and yield components and from 66.99 (UHML) to 76.67% (fiber bundle strength) for fiber properties (Table 3). It was the highest for lint percentage (92.00%) followed by plant height (91.62%) and seed index (91.31%) indicating these traits were affected less than the others by the environmental conditions. This is contradiction with the result of Killi *et al.* (2005) that heritability estimates for

100-seed weight (6.67%) and plant height (20.60%) were fairly low level. The difference might be accredited to the various experimental materials used with diverse genetic background. The predicted selection response associated with the retention of the top of 10% of NSL lines for each character in the preferred direction indicated that the shift in population mean over an unselected population would be the greatest for lint yield per hectare and bolls per plant, moderate for seed index, lint index and lint percentage, and small for boll size in case of yield and yield components. It was also small for all fiber properties. The integration of high heritability with high response to selection will provide a high reliability in selection of those specific traits

(Dhivya *et al.*, 2013; Ahsan *et al.*, 2015). High heritability coupled with high response to selection was noticed for plant height, bolls per plant and lint yield per hectare, which revealed the additive gene action model in the inheritance of these characters and the scope for improvement of them through simple selection procedures (Vineela *et al.*, 2013). The studies conducted by Ravikesavan & Iyanar (2008) and Hussain *et al.* (2010) indicated that plant height and number of bolls per plant were under the control of additive gene action. High heritability along with moderate response to selection was observed in lint index, seed index and lint percentage, which revealed the involvement of both additive and non-additive gene action in the inheritance of these characters and offered the best possibility of improvement of these traits through progeny selection or any modified selection procedures (Vineela *et al.*, 2013). The result is in accord with the reports of Muhammad *et al.* (2004) and Ahsan *et al.* (2015).

Trait associations: Correlations among these traits both at phenotypic and genotypic levels were listed in Table 4. In this study, genotypic correlation coefficient (r_g) exhibited the same trend as phenotypic correlation coefficient (r_p), and in most cases r_g exhibited a greater magnitude than r_p indicating that genetic causes were greater than environmental causes in expression of these traits. Lint yield was positively correlated with all yield components investigated except seed index. This is accord

with the finding of Zeng *et al.* (2007). Bolls per plant contributed more variation to lint yield than the other yield components. The correlations between lint yield and three morphological traits (PH, FSBH and SB) were significant and positive. Killi *et al.* (2005) reported positive correlations between seed cotton yield and plant height and number of sympodial branches. Naveed *et al.* (2004) observed that plant height was positively and significantly associated with yield of seed cotton at phenotypic and genotypic levels. These results are accord with our findings. Lint yield was negatively correlated with UHML and Str at phenotypic and genotypic levels, as were lint percentage with UHML and Str. This agrees with previous reports that lint yield correlations with fiber strength and length were negative (Meredith, 1984; Ulloa, 2006; Zeng & Meredith 2009; Hinze *et al.*, 2011). This type of negative association has created enormous challenge and barrier to achieve high yield and high fiber quality in cotton cultivars (Meredith & Bridge, 1971; Percy *et al.*, 2006; Zeng & Meredith, 2009). Boll size exhibited positive relationship with seed index and lint index at both levels and with Mic only at genotypic level. The correlations between boll size and seed weight and lint weight per seed were significant and positive, which is agreement with the findings of Zeng *et al.* (2007) and Tang and Xiao (2013). UHML showed highly significant positive correlation with Str, but highly significant negative correlation with Mic, suggesting a possibility to simultaneous selection for long, strong and fine fibers.

Table 4. Phenotypic and genotypic correlation coefficients among yield, yield components, morphological traits and fiber properties in the NLS population.

Traits	FSBH	SB	BPP	BS	LP	SI	LI	LY	UHML	Mic	El	Str
PH	0.381 0.511*	0.885** 1.000**	0.665** 0.761**	0.621** 0.727**	-0.006 -0.006	-0.037 -0.039	-0.055 -0.060	0.659** 0.713**	-0.299 -0.363	0.183 0.215	0.433 0.523*	-0.122 -0.139
FSBH		0.077 0.119	0.060 0.088	0.343 0.517*	0.376 0.503*	-0.164 -0.389	0.358 0.507*	0.315 0.441*	-0.385 -0.604**	0.105 0.161	0.464* 0.706**	-0.224 -0.604**
SB			0.759** 1.000**	0.408 0.550**	-0.175 -0.209	-0.039 -0.047	-0.301 -0.379	0.544* 0.679**	-0.087 -0.122	0.086 0.115	0.233 0.328	0.081 0.106
BPP				0.176 0.226	0.268 0.306	-0.392 -0.450*	-0.059 -0.071	0.798** 0.954**	-0.246 -0.329	0.287 0.374	0.307 0.407	-0.215 -0.270
BS					0.018 0.021	0.382 0.450*	0.452* 0.561**	0.496* 0.607**	-0.351 -0.485*	0.368 0.499*	0.245 0.337	-0.143 -0.185
LP						-0.712** -0.738**	0.638** 0.607**	0.594** 0.642**	-0.633** -0.765**	0.386 0.458*	0.608** 0.720**	-0.673** -0.762**
SI							0.083 0.078	-0.379 -0.360	0.376 0.357	-0.194 -0.228	-0.442 -0.522*	0.351 0.695**
LI								0.428 0.490*	-0.503* -0.644**	0.362 0.159	0.364 0.460*	-0.578** -0.693**
LY									-0.539* -0.684**	0.450* 0.557**	0.541* 0.679**	-0.538* -0.637**
UHML										-0.600** -0.833**	-0.784** -1.000**	0.811** 1.000**
Mic											0.156 0.216	-0.401 -0.521*
El												-0.710** -0.937**

PH: plant height, FSBH: first sympodial branch height, SB: sympodial branches, BPP: bolls per plant, BS: boll size, LP: lint percentage, SI: seed index, LI: lint index, LY: lint yield per hectare, UHML: upper half mean length, Mic: micronaire, El: elongation, Str: fiber bundle strength. Values followed by *, ** are significantly different at $p < 0.05$, $p < 0.01$, respectively. Upper values are phenotypic correlation coefficients, and lower values are genotypic correlation coefficients.

Conclusions

There were large variations among the NLS lines for lint yield per hectare and bolls per plant, while little variation for fiber properties. High heritability along with high response to selection was found in plant height, bolls per plant and lint yield per hectare indicating that the role of additive gene action in the inheritance of these characters and direct selection can be profitably applied on them. The NLS population exhibited the desirable combination of fiber length, strength and fineness. It comes to a conclusion that the NSL population is a useful genetic germplasm for improving lint yield and fiber quality.

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