



Research Note

Variability, heritability and genetic advance for yield and quality components in interspecific F₁ hybrids of cotton

Isong Abasianyanga and P. Amala Balu

Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore – 641003, India

E-mail: isongplus@yahoo.com

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Abstract

Assessment of genetic variability using appropriate parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), and genetic advance (GA) are really necessary to start an efficient breeding program. Cultivated tetraploid cotton (*G. hirsutum* x *G. barbadense*) hybrids were subjected to variability evaluation, heritability and genetic advance in a randomized complete block design during the summer 2016. The analysis of variance was highly significant for the eighteen characters studied. Elongation % recorded the highest coefficient of variation followed by number of seeds/boll, boll weight, lint index and number of monopodia. Phenotypic coefficient of variation (PCV) recorded higher values than their corresponding genotypic coefficient of variation (GCV) for all the characters, this indicated obviously the presence of environmental interaction in phenotypic expression of the traits. Number of monopodia had the highest PCV and uniformity ratio recorded the least. The highest GCV was recorded by number of monopodia followed by seed cotton yield/plant while least GCV was recorded by days to first bursting followed by 2.5% span length and elongation %. Heritability was expressed very high by seed cotton yield followed by number of bolls/plant. Other characters had high heritability except elongation %, 2.5% span length and days to first bursting which recorded low heritability. The most favourable selection response was demonstrated by number of monopodia and micronaire value. Number of monopodia, micronaire value, lint index and boll weight had demonstrated an additive gene effects by having high heritability and high genetic advance over mean, directional selection would have positive effect for their genetic improvement.

Key words

Cotton, interspecific hybrid, variability, heritability, genetic advance

Global textile industry depends largely on natural fibre. Majority of plant trichomes are multicellular, but *Gossypium* spp. produce unicellular seed trichomes known as fibre, making cotton the leading cash crop with significant economic and social impact on Indian economy (Boopathi *et al.*, 2011). Cotton provides numerous useful products and supports millions of jobs as it moves from field to fabric. The major target of cotton breeding in the world has been to improve fibre yield and quality. Remarkable advances in cotton yield and quality improvement has been recorded in both conventional and molecular approaches in the last few decades. Yield potential is reportedly plateaued due to complex and antagonistic genetic relationship amongst the cultivated species. For instance, continuous incorporation of genes and selection from the same breeding stock of cultivated species has resulted in narrow genetic base for most of the elite types which is a major bottleneck for cotton breeding, cultivation and production. Selection changes the genetic structure of population due to preservation of superior alleles and discarding the undesirable alleles (Budak *et al.*, 2004). Positive cotton improvement by selection therefore will largely depend on discovery and creation of genetic variability. Superior genotypes resulting from the recombination of superior alleles at different loci

are then precisely selected at different breeding stage. Often the selection is based solely on phenotypic expression which is often misleading because of the influence of environment. Therefore, data information on genotypic, phenotypic and environmental variability is of great importance in making effective selection. They are measured by their coefficient of variation. However, genotypic coefficient of variation does not give an exact idea on the total heritable variation. According to Magadum *et al.* (2012), the relative amount of heritable variation could be assessed by heritability. To account for the proportion of phenotypic variance attributable to genetic variance, heritability will have to be estimated. This is vital as it also provides the basis for effective selection. Magadum *et al.*, (2012) also pointed out that genetic variability along with heritability of a character will indicate the possibility and extent to which improvement is feasible through selection on phenotypic basis. Heritability value alone may not provide clear predictability of the breeding value (Mishra *et al.*, 2015). Hence, combination of heritability with genetic advance over mean is more effective and reliable in predicting the resultant effect of selection (Ramanjinappa *et al.*, 2011 and Patil *et al.*, 1996). Genetic Advance according to Hamdi *et al.*, (2003) will ostensibly show the magnitude of

the expected genetic gain from one cycle of selection. In view of the aforementioned, the present investigation is an attempt to assess the genetic variability, heritability and genetic advance of some yield and quality characteristics in F_1 interspecific -hybrid of cultivated cotton.

The experiment was conducted in the research field of the Department of Cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore during summer 2016. Coimbatore has a mean maximum temperature during summer and winter to vary between 35 °C to 18 °C. The town has an annual rainfall of 700 mm with the northeast and southwest monsoons contributing to 47% and 28% respectively to the total rainfall.

Genetic materials for the experiment were 42 F_1 hybrid derived from a cross of 13 parents in a Line x Tester fashion. Seven *G. hirsutum* genotypes (COD-5-1-2, African1-2, VS-9-S11-1, TCH1705-101, KC2, TSH0250 and Surabhi) as female and Six *G. barbadense* genotypes (TCB 26, TCB 37, TCB 209, CCB36, DB 3, SUVIN) as males, having varying agronomic and morphological characters were crossed during the Kharif 2015. The 42 progenies used for the experiment were sown in summer 2016 after due treatments on the seeds.

The 42 hybrids were sown in a Randomized Block Design (RBD) with three replications. Four rows each were planted at a spacing of 90 cm between rows and 60 cm between plants. Standard procedure for field maintenance was adhered to, basic agronomic practices like irrigation, fertilizer application, weed and pest control measures were taken. Data were recorded from five selected plants in each entry for fifteen characters *viz.*, seed cotton yield (g), plant height (cm), number of bolls per plant, number of sympodia branches per plant, number of monopodia branches per plant, boll weight (g), number of seeds per boll, ginning percentage, lint index, seed index, 2.5% span length (mm), bundle strength, fibre fineness, elongation percentage and Uniformity ratio and the remaining three characters namely days to flowering, days to 50% flowering and days to boll bursting were taken from the plants in each entry. Seed cotton was pooled from the sampled plants, ginned and the lint obtained was evaluated for fibre quality characters estimation using High Volume Instrument 900 classic.

The means for all the observed parameters were worked out and further subjected to Analysis of variance (ANOVA) according to Johnson *et al.*, (1955) and Falconer (1967). PCV, GCV, h^2 and GA from the replicated data were obtained from the analysis using the AGRISTAT statistical analyses software.

The analysis indicated that all the hybrids used for the study were significantly different for all the eighteen characters. Days to flowering ranges from 44 to 53.3 days with a mean of 48.91 days and a coefficient of variation of 4.52. The phenotypic and genotypic variances for this character was 7.72 and 2.84 respectively, the phenotypic and genotypic coefficients of variability for days to flowering was 5.68 and 3.45 respectively. Plant height recorded a mean value of 113.08 cm, ranges between 57.5 cm and 145.5 cm and coefficient of variation of 10.46. The phenotypic variance, genotypic variance, phenotypic coefficient of variation and genotypic coefficient of variation were found to be 328.53, 188.52, 16.03 and 12.14 respectively. Number of bolls/plant and number of seeds/boll recorded a mean value of 40.82 and 20.17 respectively. The phenotypic and genotypic coefficient of variation for number of bolls per plant was found to be 13.48, 12.85 and for number of seeds per boll 16.13, 10.26 respectively. Boll weight had a mean value of 3.08g while the seed cotton yield/plant was 139.96g. Seed cotton yield also recorded a phenotypic and genotypic coefficient of variance of 18.32 and 18.27 respectively. The moderate phenotypic and genotypic coefficient of variation was recorded 18.6 and 15.35 respectively by micronaire value whereas low PCV and GCV was recorded by elongation %, bundle strength, uniformity ratio and 2.5% span length. Similar results were reported by Preetha and Raveendran (2007). Venkatesan (2008) observed equally low PCV and GCV for days to flowering.

Seed cotton yield, number of monopodia/plant, plant height, number of bolls per plant, number of sympodia branches, boll weight, number of seeds per boll, ginning outturn, lint index, seed index and micronaire value had moderate PCV and GCV indicating an inherent but not sufficient variability. However, earlier work by Ganesan and Raveendran (2007) showed a higher PCV and GCV values for seed cotton yield. The PCV values were found to be higher than GCV in all the characters studied, therefore the environmental effect also influenced for these characters. This result is in agreement with the findings of Sakthi *et al.* (2007) and Tomar *et al.* (1992).

Moderate to high heritability in broad sense was observed in all the characters except days to first bursting, 2.5% span length and elongation %. The highest was observed in seed cotton yield/plant (99.41) followed by number of bolls/plant (90.78). Chee and Campbell (2009) and Liu, *et al.*, (2010) reported on heritability similar to the range as obtained in this interspecific hybrid. The implication for these on the characters is that the additive genetic variance has been fixed during breeding. Heritability is a property of a character in

the population, environment and the conditions of the genotypes (Yadav *et al.*, 2011). It is influenced by variability existing between the population and the extent to which a character is affected. Hence it lacks the information about genetic gain that is expected in the selection. In combination with genetic advance, the idea about the gene action involved in the expression of various polygenic traits was provided. High genetic advance as % of mean was observed for number of monopodia per plant, boll weight, lint index and micronaire value while moderate genetic advance as % of mean for seed index. High heritability and high genetic advance as a percentage of mean were recorded for number of monopodia, boll weight, lint index and micronaire value. This indicated that the heritability is due to additive gene effect and selection may be effective. High heritability with low genetic advance was recorded for seed cotton yield and number of bolls/plant. The implication for these characters is that they were under the control of non-additive (dominant) gene action. Heterosis breeding would be of much advantage to improve them. Days to first boll bursting, 2.5% span length and elongation % recorded low heritability and low genetic advance which indicates that the characters were highly influenced by environmental effects and selection would be ineffective.

It is of note that in an early generation like the interspecific F_1 , heritability and genetic advance are of minimal use in guiding the selection process, since most of the alleles for these quantitative characters are yet heterozygous. More so, the phenotype expression is subject to influence of additive and dominant gene effects, and epistasis is assumed to be absent.

In conclusion, hybridization and effective selection of the characters like number of bolls per plant, number of monopodia, seed cotton yield, micronaire value, boll weight, lint index and seed index would be of great benefit in a breeding program because of the number of variability parameters that recorded high values.

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Table 1. Mean, variability, heritability and genetic advance for yield and quality parameters in hybrid cotton

S. No.	Characters	Mean	Range	CV	Phenotypic Variance	Genotypic Variance	PCV	GCV	Heritability (bs) (%)	Genetic advance (GA)	G A as % of mean
1	Days to flowering	48.91	44 – 53.3	4.52	7.72	2.84	5.68	3.45	36.80	0.46	0.94
2	Days to 50% flowering	56.38	47 – 67.5	4.00	10.71	5.62	5.81	4.21	52.47	0.78	1.39
3	Days to First Bursting	90.70	85.5 - 98	3.79	12.66	0.88	3.92	1.03	6.92	0.04	0.04
4	Plant height (cm)	113.08	57.5 –145.5	10.46	328.53	188.52	16.03	12.14	57.38	0.89	0.79
5	Number of bolls per plant	40.82	32.1 - 56.3	4.09	30.29	27.50	13.48	12.85	90.78	1.78	4.36
6	Number of sympodia/plant	18.14	11.4 - 22	7.51	4.41	2.55	11.57	8.80	57.90	0.91	5.00
7	Number of monopodia /plant	2.22	1 – 3.1	11.15	0.23	0.17	21.67	18.58	73.51	1.29	58.41
8	Boll weight	3.08	2.3 – 4.1	11.49	0.25	0.13	16.35	11.63	50.56	0.74	24.03
9	Number of seeds per boll	20.17	13.3 - 26	12.44	10.58	4.28	16.13	10.26	40.48	0.53	2.63
10	Seed cotton yield per plant	139.96	115.6 -227.7	1.41	657.36	653.53	18.32	18.27	99.41	2.04	1.46
11	Ginning outturn	29.13	23.1 – 39.7	10.39	18.39	9.23	14.72	10.43	50.19	0.73	2.52
12	Lint index	3.58	2.3 – 4.7	11.20	0.37	0.21	16.96	12.73	56.36	0.87	24.38
13	Seed index	8.92	5.6 – 12.4	10.36	2.75	1.89	18.59	15.45	68.98	1.18	13.24
14	2.5%Span length	36.19	29.8 - 39	7.37	7.52	0.41	7.58	1.77	5.47	0.03	0.07
15	Uniformity ratio	46.34	42.6 – 51.3	4.28	5.21	2.89	4.93	3.67	55.47	0.73	1.23
16	Bundle strength	26.39	20.1 – 30.9	7.64	6.76	2.69	9.85	6.22	39.88	0.52	1.97
17	Elongation %	5.93	4.8 – 7.3	14.21	0.73	0.02	14.37	2.14	2.21	0.01	0.11
18	Micronaire value	3.39	2.6 – 6.4	10.50	0.41	0.27	18.60	15.35	68.12	1.16	34.14