



Full Length Article

Genetic Basis of Variation in Leaf Area, Petiole Length and Seed Cotton Yield in Some Cotton (*Gossypium hirsutum*) Genotypes

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ABSTRACT

The leaf area, petiole length and seed cotton yield were measured in six generations of a cross between cotton (*Gossypium hirsutum* L.) varieties (namely, NuCOTN-35B & NIAB-111) to study the genetic mechanisms controlling these characters, and to examine the relationship among them during 2002-2004. Five parameter models, m, [d], [i], [j], [l] for leaf area, while m, [d], [h], [i], [j] for petiole length and seed cotton yield were found adequate for genetic analysis. Genetic analysis through generation means for leaf area (cm²) indicated that this trait is controlled by the genes acting additively and complicated by (additive × additive) [i], (additive × dominance) [j] and (dominance × dominance) [l] interactions. The genetic analysis of the data for petiole length (cm) and seed cotton yield (g) revealed that both additive and dominance gene effects controlled these two traits. Potence ratio was greater than unity for leaf area and petiole length, showing over-dominance for them. For seed cotton yield, the potence ratio of 0.75 revealed partial dominance. Narrow sense heritability for leaf area (0.80), petiole length (0.62) and seed cotton yield (0.71) was moderate, suggesting the chances for improving these characters through selection from the segregating populations. Strong positive associations among the three traits suggest that indirect selection for these photosynthetic activity-enhancing traits would be helpful in improving seed cotton yield in cotton.

Key Words: Generation mean analysis; Genetic effects; Heritability; Potence ratio; Correlation

INTRODUCTION

The information on the effect of petiole length on leaf area, leaf shape and leaf orientation and consequently on the magnitude of interception of solar radiations by the cotton (*Gossypium hirsutum* L.) plant is helpful for breeding plant material with enhanced photosynthetic activities. The importance of petiole length appears even greater in selecting genotypes that have the potential to produce and retain bolls at very early nodes. The longer petiole length (even leaf size is bigger) may facilitate penetration of solar radiation to the maximum and in addition may provide protection to bolls from pests due to maximum penetration of insecticides sprayed. In contrast, smaller petioles may result in the development of dense foliage causing boll rotting at earlier nodes. This information suggests that cotton breeders should give due consideration to petiole length for selecting desirable plants in segregating populations. The information on genetic control of petiole length does not exist in the literature and previous reports on the genetics of leaf area in *Gossypium hirsutum* are very scanty.

Leaf shape in *G. hirsutum* and *G. arboreum* is under the control of additive and non-additive genes (Hammond, 1941). Furthermore, leaf area index had positive effect on

productivity of cotton plant (Dhopte & Jamadar, 1989). Baloch (2004) reported the effect of leaf modification on seed cotton yield, earliness and fiber traits in cotton and suggested that the variation in these characters may be exploited for future breeding programmes. Both additive and non-additive genetic effects control the seed cotton yield (Kalsy & Garg, 1988; Tyagi, 1988; Deshpande & Baig, 2003). More recently, however, McCarty *et al.* (2004) reported (additive × additive) epistatic effects for the inheritance of seed cotton yield and Basbag *et al.* (2008) reported heterotic effects in some cotton crosses.

The objective of this study was to find the genetic basis of variation in petiole length, leaf area and their nature of relationship with final productivity of seed cotton yield.

MATERIALS AND METHODS

Two cotton (*Gossypium hirsutum* L.) genotypes, NuCOTN-35B (P₁) exotic line from USA and NIAB-111 (P₂) were used and hybridized to develop F₁ generation. Then some of them were backcrossed with parents to develop seeds of BC_{Nu} (F₁ × NuCOTN-35B) and BC_{NI} (F₁ × NIAB-111) generations for the next year, whilst some F₁ plants were selfed to produce the seed for F₂ generation. The progenies of the six generations *i.e.*, two parents F₁, F₂,

BC_{Nu} and BC_{N1} were grown in triplicate following randomized complete block design in a field during last week of May 2003. The soil analysis results of the experimental area were sandy-clay loam type (58:23:19% sand, silt, clay, respectively) with pH 7.9, EC 1.2 dSm⁻¹, SAR 2.88, organic contents 2.3%, total N 0.06% and water-holding capacity 35.5%. The seed was sown 45 cm apart in 5.4 m long rows spaced with 75 cm apart. There was one row for each of P₁, P₂ and F₁ generation, 10 rows of F₂ generation and 5 rows each of BC_{Nu} and BC_{N1} generations. In total, there were 39 plants in 3 repeats for each of P₁, P₂ and F₁, 300 plants of F₂ and 170 plants for each of back cross generation. The growing conditions *i.e.*, agronomic and plant protection practices were identical for all the six generations.

One hundred and fifty days after planting (DAP) the data on leaf area, petiole length and seed cotton yield were recorded on per plant basis from 30 guarded plants in each of P₁, P₂ and F₁, 270 plants in F₂ and 150 plants in each of BC_{Nu} and BC_{N1} populations. Leaf area of the fully expanded leaves at 10th, 15th and 20th sympodial nodes of main stem of all the plants was measured with the help of portable leaf area meter (model CI 202, CID, Inc. USA). At the same time, petiole lengths for the same fully expanded leaves were measured and mean value of them was calculated for each family. Total seed cotton yield plant⁻¹ was recorded separately in each generations and each replication at maturity.

All obtained mean values for leaf area, petiole length and seed cotton yield per plant statistically tested with simple analysis of variance (Steel *et al.*, 1996). A weighted least square analysis of generation means was performed following Mather and Jinks (1982). Model fitting was commenced with the simplest model ('m' only) to increasing complexity (md, mdh, etc). The best-fitted model was one, which had significant parameters along with non-significant Chi-square (χ^2) value. Narrow-sense heritability (h^2_{NS}) was estimated following Warner (1952) and the potence ratio (hp), a measure of average degree of dominance, was calculated following Griffing (1950). The simple correlation among the three traits was computed using statistical package software SPSS 8.0 for windows.

RESULTS AND DISCUSSION

Analysis of variance of leaf area (LA) (cm²), petiole length (PL) (cm) and seed cotton yield (SCY) (g) revealed that there are highly significant (P≤0.01) differences among the six generations (Table I). Further partitioning of mean squares of six generations showed that interaction, P₁ vs P₂ and F₁ (P's vs F₁) was significant at P ≤ 0.01 for leaf area, petiole length and seed cotton yield. Interaction components due to backcrosses (BC_{Nu} vs BC_{N1}) was significant (P ≤ 0.05) for petiole length and seed cotton yield traits (Table I). Interaction components due to segregating populations "BC's vs F₂" and "P's, F₁ vs BC's, F₂" were also significant at P≤0.01 for seed cotton yield.

Table I. Mean squares from analysis of variances in the cross [NuCOTN-35B × NIAB-111]

Source of variation	DF	Leaf area (cm ²)	Petiole length (cm)	Seed cotton yield (g)
Replications	2	399.5	0.798	19.20
Generations	5	3521.2**	17.90**	9642.7**
P ₁ vs P ₂	1	6945.5**	39.22**	33540.3**
P's vs F ₁	1	10273.2**	48.09**	6339.4**
BC _{Nu} vs BC _{N1}	1	149.5 ^{NS}	1.79*	5821.9**
BC's vs F ₂	1	194.3 ^{NS}	0.13 ^{NS}	874.6**
P's, F ₁ vs BC's, F ₂	1	43.6 ^{NS}	0.29 ^{NS}	1637.1**
Error	10	161.1	0.23	58.7

P₁= NuCOTN-35B, P₂= NIAB-111, F₁= First generation, F₂= Second generation, P's = Parents interaction, BC_{Nu} = F₁ × NuCOTN-35B, BC_{N1} = F₁ × NIAB-111, BC's = Back crosses interactions, P's, F₁= Parents interaction with F₁ and BC's, F₂ = Back crosses interactions with F₂ generation.

* = Significant at P ≤ 0.05, ** = Significant at P ≤ 0.01 and NS = Non-significant at P > 0.05

Fig. 1. Leaf area (cm²) mean value distribution in [NuCOTN-35B × NIAB-111]

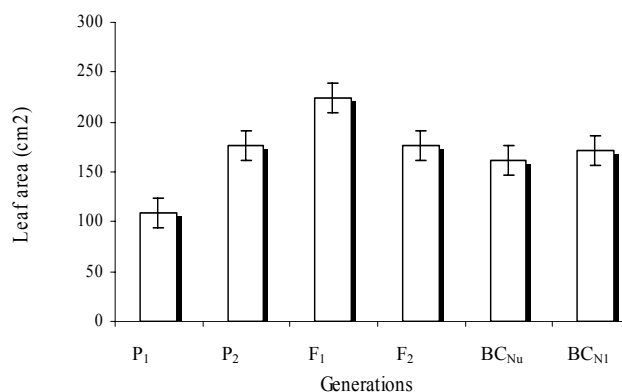
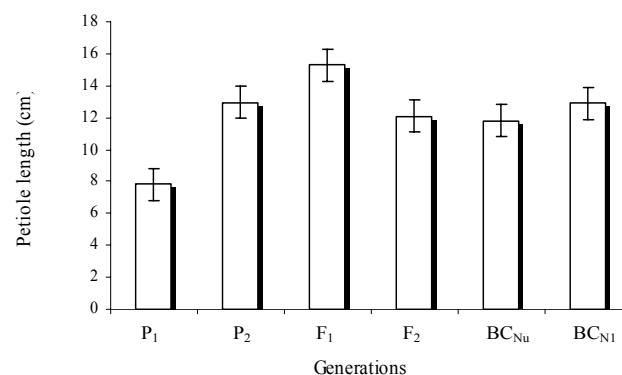


Fig. 2. Petiole length (9cm) mean value distribution in [NuCOTN-35B × NIAB-111]



The F₁ generation (Fig. 1) had the maximum mean leaf area value of 222.7 cm² and the parent NuCOTN-35B had the minimum leaf area of 108.5 cm². The mean petiole length (Fig. 2) was the longest in F₁, measuring 15.3 cm and the shortest in exotic cultivar NuCOTN-35B measuring 7.84 cm. There were striking differences for seed cotton yield among the six generations *i.e.*, P₁, P₂, F₁, F₂, BC_{Nu} and BC_{N1}

Table II. Estimation of different genetic parameters in the cross [NuCOTN-35B × NIAB-111]

Traits	Genetic effects*						χ^2 (DF)	Probability
	m	[d]	[h]	[i]	[j]	[l]		
Leaf area	160.47 ± 3.04	34.12 ± 3.60	-	-20.40 ± 4.96	-43.40 ± 4.86	52.24 ± 7.16	3.627 (1) ^{NS}	0.057
Petiole length	8.94 ± 0.36	2.54 ± 0.17	6.26 ± 0.57	1.41 ± 0.39	-3.61 ± 0.26	-	0.654 (1) ^{NS}	0.91
Seed cotton yield	79.00 ± 6.81	74.75 ± 3.13	140.68 ± 0.86	84.58 ± 7.32	-137.03 ± 4.57	-	0.013 (1) NS	0.9092

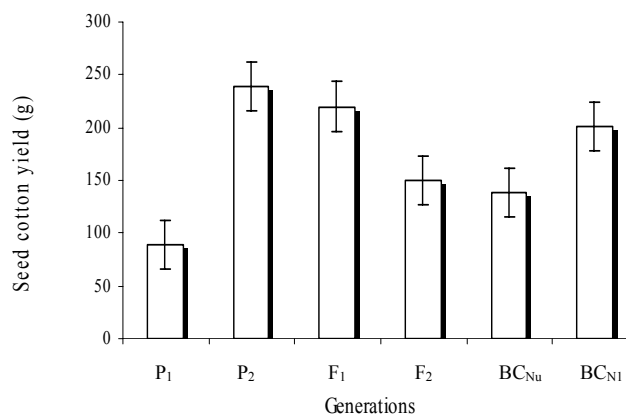
*mean (m); additive[d]; dominance[h]; (additive × additive) [i]; (additive × dominance) [j]; and (dominance × dominance) [l] epistasis

Table III. The potence ratio (hp), genotypic variances ($\hat{\sigma}_g^2$), phenotypic variances ($\hat{\sigma}_p^2$), and environmental variances ($\hat{\sigma}_e^2$), narrow-sense heritability (h^2_{NS}) of the characters

Traits	(hp)	($\hat{\sigma}_g^2$)	($\hat{\sigma}_p^2$)	($\hat{\sigma}_e^2$)	(h^2_{NS})
Leaf area	2.11	1120.03	1173.74	161.13	0.82
Petiole length	1.92	5.89	5.97	0.23	0.62
Seed cotton yield	0.75	3194.65	3214.22	58.73	0.71

Fig. 3. Seed cotton yield (g) mean value distribution in [NuCOTN-35B × NIAB-111]

P = parents, P₁ = NuCOTN-35B, P₂ = NIAB -111, F₁ = First generation, F₂ = Second generation, BC_{Nu} = F₁ × NuCOTN-35B, BC_{NI} = F₁ × NIAB -111



(Fig. 3). The mean seed cotton yield of NuCOTN-35B having a yield of 88.93 g and NIAB-111 with 238.5 g differed significantly ($P \leq 0.01$).

Generation means analysis for leaf area revealed the adequacy of five parameter model, m, [d], [i], [j] and [l], indicating that trait was controlled by the genes acting additively and complicated by (additive × additive) [i], (additive × dominance) [j] and (dominance × dominance) [l] interactions (Table II). The significant additive genetic effects for leaf area suggested that simple selection could be effective in improving the character in the segregating generations (Singh & Narayanan, 2000). The negative epistatic component suggests that fixation of additive × additive genes may reduce the leaf area in later generations, suggesting that the selection of individual plants with the desired leaf area would be advantageous in early generations. The five-parameter model, m, [d], [h], [i] and [j] was adequate for data analysis of petiole length and seed

Fig. 4. Scatter diagram for mean leaf area (cm²) and petiole length (cm) of six cotton generations

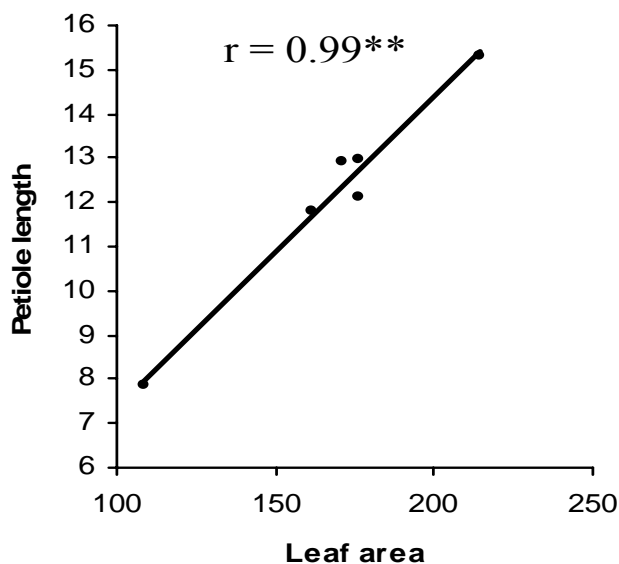
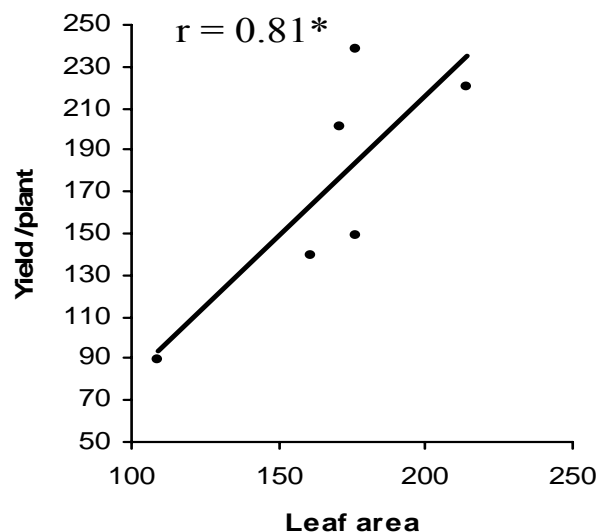
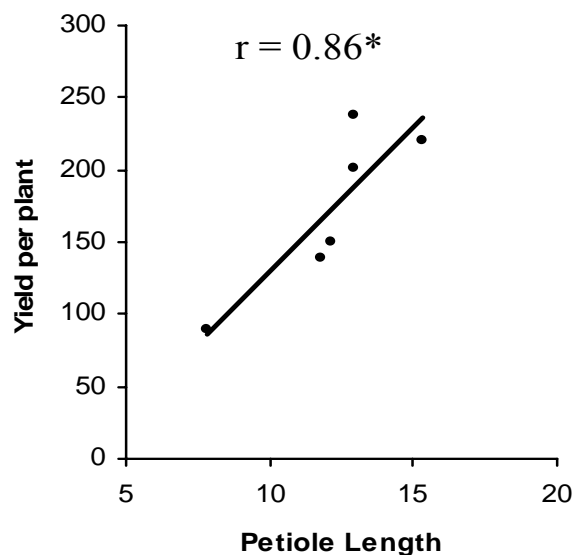


Fig. 5. Scatter diagram for mean leaf area (cm²) and seed cotton yield (g) of six cotton generations



cotton yield (Table II). The genetic analysis of the data for these three characters revealed that both additive and dominance properties of genes were important in controlling these traits. In addition, the significant additive × additive interaction [i] for these three traits suggests that fixation of favourable additive alleles would be possible in the segregating generations, as suggested by Singh and

Fig. 6. Scatter diagram for mean petiole length (cm) and seed cotton yield (g) of six cotton generations



Narayanan (2000). The involvement of both the additive and dominance gene effects and (additive \times additive) [i] epistatic effects in controlling the inheritance of seed cotton yield are in conformity with Wang and Pan (1991), Deshpande and Baig (2003), Mert *et al.* (2003), McCarty *et al.* (2004), Meredith (2005) and Mei-Zhen *et al.* (2005).

The potence ratio was greater than unity exhibiting over-dominance for leaf area and petiole length but for seed cotton yield it was 0.75, which suggested partial dominance. The narrow sense heritability (h^2_{NS}) estimates for leaf area (0.82), petiole length (0.62) and seed cotton yield (0.71) suggested the possibility of improving these traits through conventional breeding (Saranga *et al.*, 1992; Ahmed *et al.*, 2006). Nature of associations between leaf area and petiole length ($r = 0.99^{**}$, Fig. 4), leaf area with seed cotton yield ($r = 0.81^*$, Fig. 5) and petiole length with seed cotton yield ($r = 0.86^*$, Fig. 6) were positive and highly significant.

The estimates of genetic correlation facilitate the selection process especially when heritability for the target trait (s) is low (Azhar *et al.*, 2004; Naveed *et al.*, 2004). Correlation coefficients for leaf area, petiole length seed cotton yield measured in six-generations showed strong relationship among these traits. The nature of positive association of leaf area with seed cotton yield examined in the used material negate the earlier findings of Dhopte and Jamadar (1989), who reported negative correlation between leaf area and harvest index and seed cotton yield. In the present material strong positive association between seed cotton yield and leaf area of the cotton may be due to longer petiole that could have facilitated maximum harvestable bolls from the lower half of the cotton plant at maturity.

CONCLUSION

Considerable proportion of the variation in leaf area,

petiole length and seed cotton yield was heritable and the estimates of narrow sense heritability were moderate, which suggested the possibility for improving these characters through selection from the segregating populations. Strong positive associations among the three traits suggested that indirect selection for these photosynthetic activity-enhancing traits would be helpful in improving seed cotton yield in cotton.

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