Genetic basis of variation for within-boll yield components in cotton

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Abstract: Cotton productivity on a per-hectare basis is low in Pakistan. As boll is the basis for seed cotton yield, within-boll yield components can potentially serve as the most basic determinants of cotton productivity on a per unit land area basis. Before attempting the improvement of any trait, it is necessary to know the genetic mechanism lying behind its inheritance. The current study aimed to estimate the genetic basis of within-boll yield components in cotton. The research trials were conducted at the research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. Epistasis was found to be involved in all traits such as average boll weight, seed number boll–1, seed mass boll–1, lint mass boll–1, lint mass seed–1, seed index, seed volume 100-seeds–1, seed density, and surface area seed–1. Additive variance was greater in magnitude than dominance variance for traits such as lint mass boll–1 and lint mass seed–1 in cross I and for seed number boll–1, seed mass boll–1, and lint mass seed–1 in cross II. The magnitude of both variances was nearly equal for seed density in cross I and seed number boll–1 in cross II. While dominance variance was found to be greater in magnitude than additive variance for all the remaining traits in both crosses, the degree of dominance √(H/D) in cross I was partial for lint mass boll–1 and lint mass seed–1. We found complete dominance for seed density and overdominance for the remaining traits. While in cross II the degree of dominance was partial for seed mass boll –1 and lint mass seed–1, complete dominance was found for seed number boll –1 and overdominance for the remaining traits.

Key words: Genetics, cotton, triple test cross, within-boll yield components, epistasis

1. Introduction

Cotton (Gossypium hirsutum L.) is an important agricultural commodity in the world economy. It is primarily grown for fiber, but it also provides food in the form of edible oil for human consumption and feed for farm animals, such as protein-rich seedcake (Alford et al., 1996; Ali and Awan, 2009). Pakistan is the fourth major cotton-producing country worldwide. However, the yield level on a per-hectare basis is still low, i.e. 769 kg ha–1 (Ministry of Finance, 2012–2013) as compared to Australia, China, Mexico, and other leading cotton producing countries (USDA, 2013). To enhance productivity, conventional breeding methods have been used in recent years (Rathore et al., 2008; Schwartz and Smith, 2008). There are many pathways that contribute to the final yield of the cotton plant, one of which may be the exploitation and selection of several basic traits related to seed and boll (synonymously known as within-boll yield components) e.g., seed number per boll, seed size, seed index, weight of seeds per boll, lint mass per seed, seed volume, surface area of seed, and number of fibers produced per unit seed surface area, and their impact on seed cotton yield and fiber quality.

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Limited selection has been done for these traits other than lint percentage, mainly because of the difficulty in their measurement.

Within-boll yield components are the most basic determinants of seed cotton and/or lint yield in cotton (Gossypium hirsutum L.). Worley et al. (1974) revealed that the number of bolls on unit land area played a primary role in the total contribution to lint yield. Lint mass produced by individual seeds and the number of seeds per boll played a secondary and tertiary role, respectively. Culp and Harrell (1975) reported that increased lint yield resulted by increasing the number of seeds per boll, which increased the seed surface area for greater lint production. Significant general combining ability (GCA) was detected in fiber length, uniformity, strength, yield, and lint percentage, which suggested early generation selection to improve these traits (Green and Culp, 1990). Some evidence of nonadditive genetic effects was also found in several fiber traits. No single parent exhibited high GCA effects for yield and all fiber traits. Coyle and Smith (1997) revealed positive GCA effects for the upper half of mean length, micronaire value, maturity, and strength of fiber, while negative GCA
variances were observed for the most basic boll-related yield components in the same genetic material.

A negative relationship was obvious between fiber length and strength with seed surface area, number of spinnable fibers per unit seed surface area, number of seeds per boll, lint percentage, and other boll-related traits (Smith and Coyle, 1997). Plant density exhibited a direct relation with total seed surface area per unit of land area, yet an inverse relation with lint mass per boll, individual seed mass, and seed number per boll (Bednarz et al. 2006). The genotypes with smaller seed size produced more seed surface area but low lint mass and fiber numbers, and vice versa (Bednarz et al., 2007). It was concluded that seed size was the determinant of lint weight and number of fibers on unit seed surface area. The number of seeds per boll was additively controlled due to higher GCA than specific combining ability estimates, which were also additively controlled (Basal et al., 2009). Lint mass per seed, seed mass per seed, and boll per weight were controlled primarily by an additive type of gene action. Lint mass per boll, number of seeds per boll, and seed mass per seed exhibited dominant genetic effects (Tang and Xiao, 2013).

Keeping in view the importance of a seed's physical traits in determining the seed cotton yield and fiber quality, the present study aimed to investigate the genetic basis of these basic yield determinants so that effective breeding procedures and selection methods could be adopted to improve these traits and to achieve the ultimate objective of increased seed cotton yield and lint quality.

2. Materials and methods

The study was conducted at the research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. Two crosses, namely NIAB-999 × BH-89 and NIAB-228 × BH-160, were made involving 4 parents selected on the basis of their contrasting characters relating to plant morphology, seed cotton yield, and fiber quality traits. The parents originated from different breeding stations and parentage; they also evolved through different methods of evolution. The 4 parents were NIAB-999, a heat-tolerant, medium-statured variety with small to medium boll size (3.4 g) and medium seed size (seed index = 8.0 g), evolved by mutation breeding and with good fiber quality; BH-89, an advanced strain with small boll size and a lower number of seeds per boll (seed index = 6.8 g), having less lint percentage and low fiber quality; NIAB-228, an advanced strain evolved by mutation breeding with small boll size but a higher number of bolls per plant, small seed size (seed index = 7.0 g), and critical fiber quality traits; and BH-160, a high yielding, heat-tolerant, and medium-maturing variety with medium to large boll size (4.3 g), medium bold seed size (seed index = 8.5 g), and excellent fiber quality traits. The F1 population was grown with the relevant parents, and 10 other genetically diverse genotypes and crosses were made according to the modified triple test cross (TTC) suggested by Ketata (1976). The 10 genotypes used to generate TTC progeny were CIM-70, a semidwarf early-maturing variety with determinate growth habit, medium boll size, and bold seeds (seed index = 8.5 g), possessing good fiber quality but low lint percentage; Russian, an exotic genotype with dark red pigmentation on the stem, leaves, and flowers, with short stature, small boll size, lower number of bolls per plant, small seed size, and low fiber quality; CIM-496, an early-maturing heat-tolerant variety with medium boll size (4.2 g), bold seeds, and excellent fiber quality; CIM-1100, a late-maturing variety with a bushy plant shape, medium boll size containing bold seeds, and good fiber quality, but somewhat less lint percentage; Reshami-90, a cotton hybrid possessing good yield potential, medium to large boll size with a higher number of bold seeds, and good fiber quality parameters; FH-634, a tall-statured variety with spreading growth habit, medium- to late-maturing, large boll size (4.6 g) containing a higher number of bold seeds (seed index = 8.7 g), and good quality traits, but lower lint percentage; S-12, a short-statured early-maturing variety with large boll size but a lower number of small seeds, and good fiber traits with high lint percentage; NIAB-78, a short-statured, semispreading, and early-maturing variety evolved by mutation breeding, which produces lower medium bolls (3.7 g) containing bold seeds (seed index = 8.2 g) and possesses good fiber traits but low lint percentage (36%); CIM-240, a short-statured, late-maturing variety with big sympodia and rare monopodia, whose leaves incline downwards, with a large boll size (4.6 g) containing a higher number of large-sized seeds (seed index = 10.2 g), with acceptable fiber quality but low ginning out-turn/ lint percentage; and VH-144, possessing a high potential for seed cotton yield and producing a higher number of small- to medium-sized bolls, representing marginally fit fiber quality parameters but with typical fiber fineness.

The TTC progeny of crosses I and II, comprising 3 lines (P1, P2, and F1), 10 testers, and 30 crosses (20 single and 10 three-way crosses), were grown in field conditions. The standard practices followed during the entire crop duration were fertilizer NPK @ 120, 60, and 60 kg ha–1, respectively. One-third of nitrogen (urea) and total phosphorus (SSP) and potassium (K 2SO4) were applied at the time of sowing, while the remaining nitrogen was split into 2 doses, one at square formation stage and the other at peak flowering and boll formation stage. A total of 7 irrigations (flooding) were applied by observing the crop demand. Weeds were controlled by a preemergence herbicide (S-metolachlor) @ 1.50 L ha–1, and a postemergence herbicide (glyphosate) @ 2.7 L ha–1 was applied with the help of a protective shield at 50 days after
Insecticides (diafenthiuron and imidacloprid @ 600 mL ha$^{-1}$) were applied to control sucking insects such as aphids, jassids, whiteflies, and thrips, while emamectin benzoate and lambda-cyhalothrin were sprayed at a dose of 500 mL ha$^{-1}$ and 1 L ha$^{-1}$, respectively, to control pink bollworm, spotted bollworm, and army worm when their population was above economic threshold level. All agronomic practices were kept uniform and normal for all the treatments. Weather data of the site are presented in the Figure. At maturity, 5 bolls were picked from each of the 5 tagged plants in each experimental plot. In this way, 43 samples (each sample containing 25 bolls) of seed cotton were collected from each of the 2 crosses. These samples were weighed and ginned by laboratory saw gin. Data on various seed-related traits were recorded/calculated according to the ontogenetic yield model of Worley et al. (1976), also reported by Coyle and Smith (1997). These were as follows: boll weight (BW) = (seed cotton weight per sample/number of bolls); seeds/boll (S/B) = (number of seeds in the sample/number of bolls); seed mass/boll (SM/B) = (seed weight of the sample/number of bolls); lint mass per boll (LM/B) = (lint weight of the sample/number of bolls); lint mass/seed (LM/S) = (lint mass per boll/number of seeds per boll); seed index (SI) = weight of 100 seeds; seed volume/100 seeds = measured by alcohol displacement method; seed density (SD) = seed weight/seed volume; surface area/seed (SA/S) = seed volume converted to SA/S by Hodson’s (1920) table.

To analyze the recorded data, the TTC suggested by Kearsey and Jinks (1968), which is an extension of design III of Comstock and Robinson (1952), was employed, as it not only provides a precise test for epistasis but also gives estimates of additive (D) and dominance (H) components. The various phenotypes of the TTC technique are presented in the model below:

$$L_{ijk} = \mu + G_{ij} + R_k + E_{ijk},$$

where $L_{ijk}$ denotes the phenotypic value of the cross between tester $i$ and line $j$ in the $k$th replication, $\mu$ denotes the overall mean of all single and three-way crosses, $G_{ij}$ denotes the genotypic value of the cross between tester $i$ and line $j$, $R_k$ presents the effect of the $k$th replication, and $E_{ijk}$ is the error associated with that particular cross in replication $k$.

2.1. Detection of epistasis
The test of significance of difference $[(L_{i1} + L_{i2} - 2L_{i3})$, where $i =$ number of lines] provides information about the presence or absence of epistasis. Therefore, $L_{i1} + L_{i2} - 2L_{i3}$ for each line and each replication was first computed and then tested.

2.2. Estimation of additive variance component (D)
The sum of $L_{i1} + L_{i2}$ for each line was calculated replication-wise and subjected to analysis.

2.3. Estimation of dominance variance component (H)
The sum of $L_{i1} - L_{i2}$ for each line was calculated replication-wise and subjected to analysis of variance as following.

2.4. Degree of dominance
Degree of dominance was calculated as $(H/D)^{1/2}$, where $H$ and $D$ are the dominance and additive variance components, respectively.

2.5. Correlation coefficient ($r_{sd}$)
The correlation coefficients ($r_{sd}$) between the sum $(L_{i1} + L_{i2})$ and the genotypic differences $(L_{i1} - L_{i2})$ was calculated as:

$$r_{sd} = \frac{\sum XY - \sum X \sum Y / N}{\sqrt{\left(\sum X^2 - \left(\sum X\right)^2 / N\right) \left(\sum Y^2 - \left(\sum Y\right)^2 / N\right)}}.$$

3. Results
Analysis of variance for various agronomic and within-boll yield components under TTC revealed that the genotypes represented significant variability among themselves, which permitted a further analysis of the data for both crosses (Tables 1 and 2). Parents (lines and testers) originating from different breeding stations, distinct strategies of development, and diverse pedigrees exhibited significant differences for nearly all traits under study, which is the basic requirement for their use in TTC analysis. Partitioning of variation among genotypes into components revealed that both parents and hybrids exhibited significant variability with respect to the traits under study. Further partitioning of the parental variation into lines (3), testers (10), and their interactions revealed significant results; thus, the 30 produced hybrids showed significant variation regarding seed cotton yield attributes and boll related traits. Line v tester interaction was found to be significant for all the traits except for the number of bolls per plant, seed cotton yield per plant, and lint mass.
per boll. Genetic analysis of the data for various boll- and seed-related traits revealed that the mean square values due to deviation of \((L_{1i} + L_{2i} - 2L_{3i})\) from zero indicated the presence of highly significant epistasis for all the traits under study (Tables 3 and 4). Further partitioning of the total epistasis into components revealed that \([i]\) type (additive \(\times\) additive) epistasis was significant for seed index, highly significant for seed density, and nonsignificant for the remaining traits, whereas \([j + l]\) type (additive \(\times\) dominance and dominance \(\times\) dominance) epistasis was found to be highly significant for all the traits.

Analysis of variance for sums \((L_{1i} + L_{2i})\) and differences \((L_{1i} - L_{2i})\) provides information about the prevalence of additive and nonadditive genetic components. In the present case both the sums and differences of mean squares were highly significant for all the traits in both crosses, which suggested that the role of both additive and nonadditive components of genetic variation was important in the inheritance of these traits (Tables 5 and 6). The value of \(D\) and \(H\) indicates the relative importance of the additive and dominance components of the genetic variation. Additive (\(D\)) variance was higher in magnitude than dominance (\(H\)) variance for traits such as lint mass per boll and lint mass per seed in cross I, and seed number per boll, seed mass per boll, and lint mass per seed in cross II. This indicated the relative importance of additive gene action in the inheritance of these traits. The differences in the relative values of \(D\) and \(H\) were nonsignificant for seed density in cross I and seed number per boll in cross II, indicating complete dominance of the genes controlling these traits. However, the dominance (\(H\)) variance for all the remaining traits was stronger, indicating the preponderance of dominant behavior of the genes controlling the expression of these traits.

Relative importance of additive and dominant behavior of the genes was further confirmed by the estimates of degree of dominance (\(\sqrt{H/D}\)), which were less than 1, showing the partial dominance nature of genes controlling...
Table 3. Test of epistasis for various seed-related traits in cross I.

<table>
<thead>
<tr>
<th>Items</th>
<th>d.f.</th>
<th>Average boll weight/plant</th>
<th>Seed number/ boll</th>
<th>Seed mass/ boll</th>
<th>Lint mass/ boll</th>
<th>Lint mass/ seed</th>
<th>Seed index</th>
<th>Seed volume/ 100 seeds</th>
<th>Seed density</th>
<th>Surface area/ seed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total epistasis</td>
<td>10</td>
<td>1.000**</td>
<td>88.962**</td>
<td>0.373**</td>
<td>0.479**</td>
<td>0.0008**</td>
<td>3.664**</td>
<td>6.908**</td>
<td>0.016**</td>
<td>0.072**</td>
</tr>
<tr>
<td>i type epistasis</td>
<td>1</td>
<td>2.431**</td>
<td>10.585**</td>
<td>0.070**</td>
<td>1.668**</td>
<td>0.0020**</td>
<td>0.397**</td>
<td>4.880**</td>
<td>0.028**</td>
<td>0.051**</td>
</tr>
<tr>
<td>j + l type epistasis</td>
<td>9</td>
<td>0.840**</td>
<td>97.670**</td>
<td>0.407**</td>
<td>0.346**</td>
<td>0.0007**</td>
<td>4.028**</td>
<td>7.133**</td>
<td>0.015**</td>
<td>0.074**</td>
</tr>
<tr>
<td>Total epistasis × replicates</td>
<td>20</td>
<td>0.125</td>
<td>6.011</td>
<td>0.026</td>
<td>0.065</td>
<td>0.0001</td>
<td>0.051</td>
<td>0.180</td>
<td>0.002</td>
<td>0.002</td>
</tr>
<tr>
<td>i type epistasis × replicates</td>
<td>2</td>
<td>0.608</td>
<td>2.646</td>
<td>0.018</td>
<td>0.417</td>
<td>0.0005</td>
<td>0.099</td>
<td>1.220</td>
<td>0.007</td>
<td>0.013</td>
</tr>
<tr>
<td>j + l epistasis × replicates</td>
<td>18</td>
<td>0.072</td>
<td>6.385</td>
<td>0.027</td>
<td>0.026</td>
<td>0.0000</td>
<td>0.045</td>
<td>0.064</td>
<td>0.002</td>
<td>0.001</td>
</tr>
</tbody>
</table>

Table 4. Test of epistasis for various seed-related traits in cross II.

<table>
<thead>
<tr>
<th>Items</th>
<th>d.f.</th>
<th>Average boll weight/plant</th>
<th>Seed number/ boll</th>
<th>Seed mass/ boll</th>
<th>Lint mass/ boll</th>
<th>Lint mass/ seed</th>
<th>Seed index</th>
<th>Seed volume/ 100 seeds</th>
<th>Seed density</th>
<th>Surface area/ seed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total epistasis</td>
<td>10</td>
<td>4.270**</td>
<td>411.848**</td>
<td>1.308**</td>
<td>1.715**</td>
<td>0.0014**</td>
<td>6.558**</td>
<td>4.230**</td>
<td>0.123**</td>
<td>0.044**</td>
</tr>
<tr>
<td>i type epistasis</td>
<td>1</td>
<td>17.511**</td>
<td>1488.679**</td>
<td>2.548**</td>
<td>6.678**</td>
<td>0.0006**</td>
<td>0.413**</td>
<td>6.533**</td>
<td>0.148**</td>
<td>0.069**</td>
</tr>
<tr>
<td>j + l type epistasis</td>
<td>9</td>
<td>2.798**</td>
<td>292.201**</td>
<td>1.170**</td>
<td>1.163**</td>
<td>0.0015**</td>
<td>7.241**</td>
<td>3.974**</td>
<td>0.120**</td>
<td>0.041**</td>
</tr>
<tr>
<td>Total epistasis × replicates</td>
<td>20</td>
<td>0.480</td>
<td>44.061</td>
<td>0.093</td>
<td>0.197</td>
<td>0.0001</td>
<td>0.137</td>
<td>0.199</td>
<td>0.006</td>
<td>0.002</td>
</tr>
<tr>
<td>i type epistasis × replicates</td>
<td>2</td>
<td>4.378</td>
<td>372.170</td>
<td>0.637</td>
<td>1.670</td>
<td>0.0002</td>
<td>0.103</td>
<td>1.633</td>
<td>0.037</td>
<td>0.017</td>
</tr>
<tr>
<td>j + l epistasis × replicates</td>
<td>18</td>
<td>0.047</td>
<td>7.604</td>
<td>0.032</td>
<td>0.034</td>
<td>0.0001</td>
<td>0.141</td>
<td>0.040</td>
<td>0.003</td>
<td>0.004</td>
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Table 5. Mean squares due to sums (L₁i + L₂i) and differences (L₁i – L₂i), estimates of additive (D) and dominance (H) components, degree of dominance (V(H/D)), and correlation coefficient (rₓᵧ) for various seed-related traits in cross I.

<table>
<thead>
<tr>
<th>Items</th>
<th>d.f.</th>
<th>Average boll weight/plant</th>
<th>Seed number/ boll</th>
<th>Seed mass/ boll</th>
<th>Lint mass/ boll</th>
<th>Lint mass/ seed</th>
<th>Seed index</th>
<th>Seed volume/ 100 seeds</th>
<th>Seed density</th>
<th>Surface area/ seed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sums</td>
<td>9</td>
<td>0.428**</td>
<td>33.481**</td>
<td>0.118**</td>
<td>0.276**</td>
<td>0.0003**</td>
<td>0.791**</td>
<td>2.131**</td>
<td>0.012**</td>
<td>0.022**</td>
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<tr>
<td>Differences</td>
<td>9</td>
<td>0.676**</td>
<td>90.073**</td>
<td>0.209**</td>
<td>0.211**</td>
<td>0.0002**</td>
<td>1.198**</td>
<td>2.476**</td>
<td>0.011**</td>
<td>0.026**</td>
</tr>
<tr>
<td>D</td>
<td>9</td>
<td>0.545</td>
<td>43.123</td>
<td>0.147</td>
<td>0.356</td>
<td>0.0003</td>
<td>1.041</td>
<td>2.829</td>
<td>0.016</td>
<td>0.0294</td>
</tr>
<tr>
<td>H</td>
<td>9</td>
<td>0.878</td>
<td>115.490</td>
<td>0.251</td>
<td>0.270**</td>
<td>0.0002</td>
<td>1.566</td>
<td>3.289</td>
<td>0.015</td>
<td>0.0342</td>
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<tr>
<td>V(H/D)</td>
<td></td>
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<td>(rₓᵧ)</td>
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</tbody>
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Table 6. Mean squares due to sums (L₁i + L₂i) and differences (L₁i – L₂i), estimates of additive (D) and dominance (H) components, degree of dominance (V(H/D)), and correlation coefficient (rₓᵧ) for various seed-related traits in cross II.

<table>
<thead>
<tr>
<th>Items</th>
<th>d.f.</th>
<th>Average boll weight/plant</th>
<th>Seed number/ boll</th>
<th>Seed mass/ boll</th>
<th>Lint mass/ boll</th>
<th>Lint mass/ seed</th>
<th>Seed index</th>
<th>Seed volume/ 100 seeds</th>
<th>Seed density</th>
<th>Surface area/ seed</th>
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<tr>
<td>Sums</td>
<td>9</td>
<td>1.079**</td>
<td>141.855**</td>
<td>0.741**</td>
<td>0.291**</td>
<td>0.0008**</td>
<td>2.445**</td>
<td>1.232**</td>
<td>0.036**</td>
<td>0.013**</td>
</tr>
<tr>
<td>Differences</td>
<td>9</td>
<td>1.304**</td>
<td>129.520**</td>
<td>0.462**</td>
<td>0.426**</td>
<td>0.0006**</td>
<td>3.021**</td>
<td>2.727**</td>
<td>0.076**</td>
<td>0.028**</td>
</tr>
<tr>
<td>D</td>
<td>9</td>
<td>1.422</td>
<td>187.252</td>
<td>0.980</td>
<td>0.380</td>
<td>0.0011</td>
<td>3.251**</td>
<td>1.626</td>
<td>0.048</td>
<td>0.017</td>
</tr>
<tr>
<td>H</td>
<td>9</td>
<td>1.730</td>
<td>172.232</td>
<td>0.614</td>
<td>0.563</td>
<td>0.0008</td>
<td>4.015</td>
<td>3.620</td>
<td>0.101</td>
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<tr>
<td>V(H/D)</td>
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<tr>
<td>(rₓᵧ)</td>
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the expression of the earlier mentioned characteristics; nearly equal to 1 for seed density in cross I and seed number per boll in cross II; and greater than 1 for later-mentioned traits depicting overdominance of genes for these traits. The value of correlation coefficient \( r_{sb} \) was significant and positive for lint mass per seed, seed volume per 100 seeds, seed density, and seed surface area in cross I, and seed number per boll in cross II, indicating dominance towards decreasing parent/accumulation of more negative alleles. For lint mass per boll and seed density in cross II, the direction of dominance was towards increasing parent due to a significant negative value for \( r_{sb} \). However, the correlation coefficient was nonsignificant for the remaining traits, indicating an asymmetrical distribution of positive and negative alleles.

4. Discussion

Genetic analyses of the data revealed that epistasis affected all the traits under study. Thus, the presence of epistasis complicated the inheritance of seed physical traits. The presence of additive × additive interaction was absent in the inheritance of almost all the characters; however, additive × dominance and dominance × dominance \([j + l]\) type epistasis appeared to complicate the inheritance of these characters. The TTC analyses further showed that although both additive (D) and dominance (H) components of variation appeared to predominantly affect all the characters, the ratio of \((\sqrt{H/D})\) indicated that lint mass per seed in both crosses, and lint mass per boll in cross I and seed mass per boll in cross II, were influenced predominantly by the additivity of the genes as \((\sqrt{H/D} < 1)\). However, seed density in cross I and seed number per boll in cross II showed the importance of both additive and dominance properties of genes, since the degree of dominance in this case was almost equal to unity. The higher degree of dominance \((\sqrt{H/D} > 1)\) for all the remaining traits in both crosses showed overdominance.

Therefore, the information reported here appears consistent with the previous findings. The differences in the relative importance of additive and dominance components between the 2 crosses may be attributed to the diverse genetic background of parents (Tang et al., 1993; Patel et al., 1997; Pavasia et al., 1999; Kiani et al., 2007). Nonallelic interactions may also be vulnerable to changes in the strength of additive and dominant components (Bhatti et al., 2006). Natural mutations in the parental genetic make-up may also be responsible for these contradictions (Stebbins, 1950; Harten, 1998; Schouten, 2006).

The presence of epistasis at additive × dominance loci suggests that inheritance of seed physical traits in cotton (Gossypium hirsutum L.) is a complex phenomenon. Presence of epistasis, or more specifically \([j + l]\) type epistasis, in all the traits in both crosses may likely handicap plant breeders for making a straightforward selection. In such situations selection should be deferred until later generations, as suggested by Tripathi and Singh (1983), or heterosis breeding may be rewarding for these traits (Melchinger et al., 2007). A recurrent selection procedure may also be adopted, as it accumulates both additive and nonadditive effects of genes (Coyle and Smith, 1997).

The present study supported the hypothesis that within-yield components are basic determinants of seed cotton yield and quality and that they are genetically controlled. Intergenic interactions seemed to play the most important role in their inheritance. The most important impact of dominance variance and involvement of highly significant amounts of additive × dominance and dominance × dominance epistasis suggested a strong reason for hybrid development for the improvement of within-boll yield components. This will help attain higher seed cotton yield and maintain and improve fiber quality.

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