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A Study on Genetic Advance and Heritability for Quantitative Traits in Cotton (*Gossypium hirsutum* L.)

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Abstract: The experiment was laid out to estimate heritability, genetic correlation and genetic advance for seed cotton yield, yield components and fiber quality in F_1 populations by line x tester mating design. Seed index (0.789), ginning outturn (0.758), boll weight (0.644), days to first boll opening (0.635) and boll number (0.617) exhibited a high degree of broad-sense heritability. The significant and positive genotypic correlations with seed cotton yield recorded in boll number, boll weight, fiber strength, sympodial branch number, days to first flower and seed index. The correlated response was magnitude for boll number, boll weight and sympodial branch number. The boll number and sympodial branch number represented high heritability coupled with genetic advance. The indirect selection of the boll weight and the sympodial branch was more efficient for high yielding cotton breeding.

Keywords: correlated response, fiber quality, genetic correlation, seed cotton yield, selection

Pamukta (*Gossypium hirsutum* L.) Kantitatif Özelliklerin Kalıtımı ve Genetik İlerleme Üzerine Bir Çalışma

Öz: *Bu çalışma, line x tester eşleşme deseni uyarınca oluşturulmuş melez populasyonlarında verim, verim komponentleri ve lif kalite özellikleri yönünden kalıtımın, genetik ilerleme ve korelasyonun saptanması amacıyla yürütülmüştür. Tohum indeksi (0.789), çırçır randımanı (0.758), koza ağırlığı (0.644), ilk koza açma gün süresi (0.635) ve koza sayısı (0.617) için bulunan geniş anlamda kalıtım derecesinin yüksek olduğu görülmüştür. Koza sayısı, koza ağırlığı, lif dayanıklılığı, meyve dalı sayısı, ilk çiçek açma gün süresi ve tohum indeksi ile kütlü pamuk verimi arasındaki genetik korelasyonların pozitif ve önemli olduğu saptanmıştır. Koza sayısı, koza ağırlığı ve meyve dalı sayısına ilişkin seleksiyon tepkisinin anlamlı olduğu görülmüştür. Koza sayısı ve meyve dalı sayısının hem kalıtım derecesinin hem de genetik ilerleme katsayısının yüksek olduğu bulunmuştur. Bu iki özellik için yapılacak dolaylı seleksiyonun yüksek verimli pamuk ıslahında başarı ile kullanılabileceği kanısına varılmıştır.*

Anahtar Kelimeler: *seleksiyon tepkisi, lif kalite özellikleri, genetik korelasyon, kütlü pamuk verimi, seleksiyon*

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is one of the most profitable textile industry crop in the world. Whole world cotton planting area, lint yield and production for marketing during 2018/2019 were 33.41 million hectares, 765 kg ha^{-1} and 55.2 million tons, respectively. Planting area of Turkey expected to reach 540 thousand hectares in 2019/2020. The cotton based industry for textile and crude oil plays a major role in Turkish economy. Therefore, there is a need to improve high-yielding and quality cotton varieties to increase the seed cotton yield.

Seed cotton yield is a complex character and the results of yield attributing characters. Cotton breeding programs are based on variability existing in the base populations and selection in both pedigree and bulk methods (Kumar et al., 2019). The direct selection for seed cotton yield failed due to its polygenic nature, low heritability, non-additive gene action (Fellahi et al., 2018). The selected characters for indirect selection must have a substantially higher heritability and high genetic correlation with target characters and higher selection intensity must be applied (Percy and Kohel, 1999).

Genetic correlation studies revealed that seed cotton yield per plant exhibited positive and highly significant genetic correlation with days to fifty percent flowering, number of sympodial branches per plant, boll number, boll weight, fiber fineness, fiber strength (Iqbal et al., 2003; Chaudhary et al., 2017; Kumar et al., 2019; Naik et al., 2019; Shahzad et al., 2019; Nawaz et al., 2019). As results of these studies, it was speculated that the negative correlation between number of bolls per plant and boll weight must be broken for high seed cotton yield in a breeding program (Iqbal et al., 2003).

Genetic advance (GA) refers to the betterment of traits in genotypic value for novel population as compared with the base population and, heritability estimates along with genotypic coefficient of variation (GCV) offers a dependable guesstimate of amount of genetic advance to be anticipated through phenotypic selection (Ahsan et al., 2015; Khan et al., 2015). High genetic advance was

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recorded in seed cotton yield per plant, boll number, number of sympodial branches and seed index (Vineela et al., 2013; Dhivya et al., 2014; Kumar et al., 2019).

Keeping in view the significance of above facts, the results of a line x tester populations evaluated to i) determine genetic correlation with seed cotton yield, ii) genetic advance for observed characters in cotton.

MATERIAL AND METHODS

The present study was conducted at the Nazilli Cotton Research Institute during 2014 cotton growing season to estimate heritability, genetic correlation and genetic advance. Four genotypes, Gloria, Claudia, Carmen and Julia as lines; Stonoville-468, Carisma and Flash as tester were used, and seven cotton genotypes were crossed to produce 12 F_1 combinations according to line x tester mating design in 2013. The 12 crosses and 7 parents were arranged in Randomized Complete Block Design with three replications. The plant height (cm), number of monopodial branches, number of sympodial branches, days to first flowering, days to boll opening, boll number per plant, boll weight (g) and seed cotton yield per plant (g) were recorded on twenty random plants. Ginning outturn (%) and 100 seed weight (g) were measured in sample, and fiber fineness (mic), fiber length (cm) and fiber strength (g tex^{-1}) were analyzed by High Volume Instruments (HVI).

Heritability (broad-sense) was calculated by using the following formula according to Singh and Chaudhary (1985);

$H^2= \sigma^2_g$ (genotypic variance) / σ^2_p (phenotypic variance)

Genetic correlations with seed cotton yield were calculated using the following formula;

$r_g = COV_{GCA,(i,j)} / [\sigma^2_{gca(i)} \times \sigma^2_{gca(j)}]^{1/2}$

where $COV_{GCA,(i,j)}$ represents the covariance parameter of GCA (general combining ability) between seed cotton yield (i) and character (j), and $\sigma^2_{gca(i)}$ and $\sigma^2_{gca(j)}$ represent the variance components of seed cotton yield (i) and character (j), respectively (Fukatsu et al., 2013). $[1-r_g^2 / (N-2)]^{\frac{1}{2}}$ equation were used for standard error of genetic correlation and, significance was determined by "t" test (Steel and Torrie, 1980).

Correlation response (CR) was estimated according to following formula;

CR= (hx / hy) r_g (Falconer, 1989)

Where;

hx= broad-sense heritability of seed cotton yield

hy= broad-sense heritability of other character

r_g= Genotypic correlation between seed cotton yield and other character

Genetic advance was calculated according to Allard's (1964) by the following formula;

$GA= i \times H^2 \times (\sigma^2_p)^{1/2}$

Where,

i = selection intensity for trait

H^2 = heritability for trait

σ^2_p = phenotypic variance of trait

Selection intensity at 5% will be 2.063 was assumed in predicting direct selection response.

RESULTS AND DISCUSSION

It was seen that significant genotypic differences were existed for seed cotton yield and its components (Table 1). A successful selection depends upon presence of magnitude of genetic variability. Also, mean values and standard error for all characters indicated that studied population can be defined as short plant height, late maturity, large seed, high ginning outturn and good fiber quality (Table 1).

Table 1. Mean of squares of genotype and mean values

Source of Variation	Mean of Squares	Grand Mean ± SE
SCY (g)	302.63**	78.54±10.40
PH (cm)	100.41**	88.67±5.17
MBN (no.)	0.53**	2.75±0.41
SBN (no.)	4.26**	10.98±1.31
DFF (day)	0.72**	76.43±0.45
DFB (day)	6.05**	120.49±1.56
BN (no.)	43.38**	22.64±4.10
BW (g)	0.23**	5.80±0.31
GP (%)	5.57**	43.49±0.71
SI (g)	1.03**	10.42±0.29
FF (mic.)	0.27**	4.69±0.40
FS (g tex^{-1})	11.48**	32.77±1.34
FL (mm)	2.18**	30.75±0.77

*, **; significant level 0.05 and 0.01, respectively. h^2: Broad-sense heritability. GP: Ginning-out percentage, FF: Fiber Fineness, FS: Fiber Strength, FL: Fiber Length, MBN: Monopodial branches number, SBN: Sympodial branches number, DFF: Days to first flowering, DFB: Days to first open boll, SCY: Seed cotton yield per plant, PH: Plant height, BN: Boll number, BW: Boll weight, SI: seed index

Heritability broad-sense was classified as low (≤30%), moderate (30-60%) and high (60% ≤) (Srinivas et al., 2014). The high broad-sense heritability was recorded in seed index (0.789), ginning outturn (0.758), boll weight (0.644), days to first boll opening (0.635) and boll number (0.617) whereas the lowest heritability degree was registered in seed cotton yield (Table 2). The low heritability indicates that seed cotton yield was high influenced by environment. Seed cotton yield is also polygenic character and its inheritance was the most fluctuate one (Ahmed et al., 2006). In such cases, selection for these characters with high heritability could be recommended in early segregating generations, however the selected characters for indirect selection must have high genetic correlation with seed cotton yield (Percy and Kohel, 1999).

Genetic correlations among yield and yield components arise from the pleiotropic effects of genes and linkage (Cheverud, 2001). The results of this study showed significantly positive genotypic correlations of seed cotton yield with boll number, boll weight, fiber strength, sympodial branch number, days to first flower and seed index. In recent years, similar results reported by many researchers (Kumar et al., 2019; Naik et al., 2019; Shahzad et al., 2019; Nawaz et al., 2019). Although, negative associations between seed cotton yield and fiber quality characters reported by Clement et al. (2012), significantly positive genotypic correlation of seed cotton yield with fiber strength indicated that negative relationship is genetically broken (Bourland and Myers, 2015)

Correlated response (CR) showed the response in seed cotton yield due to selection on yield components by indirect selection (Falconer, 1989). The values above unit 1 indicated indirect response given more response than direct selection for seed cotton yield. It means that yield components using for indirect selection are more heritable and genetic correlation strong. Present study showed high (close to 1) correlated response for boll number, boll weight and sympodial branch number. It was concluded that greater response in seed cotton yield can be achieved through indirect selection on boll number and weight in early segregating generation of cotton breeding.

The high genetic advance with heritability degrees were one of the best indicator in predicting its resultant effects for selecting superior plants (Kumar et al., 2019). High heritability coupled with genetic advance was observed for boll number and sympodial branch number in positive direction whereas moderate genetic advance with high heritability was recorded for only seed index. These findings are parallel to Vineela et al. (2013), Dhivya et al. (2014) and Kumar et al. (2019). The indirect selection like boll number and sympodial branch number having high heritability and high genetic advance indicative of additive gene effects can be effective in the improvement of high yielding cotton genotypes.

CONCLUSION

Successful breeding program can be achieving through genetic diversity and effective selection. The association with heritability, genetic correlation and genetic advance are very important for high yielding cotton. The highest heritability with high genotypic correlation for boll number, boll weight and sympodial branch number indicated that indirect selection for these characters was more efficient to improve seed cotton yield compared to direct selection in future cotton breeding.

Table 2. Heritability, genetic correlation and advance, correlated response in observed characters

	Heritability (h^2)	**Genetic Correlation with Seed Cotton Yield (r_g)**	**Correlation Response (CR/R)**	**Genetic advances as percent of mean (GA)**
SCY (g)	0.286	-	-	10.42
PH (cm)	0.569	0.026	0.019	9.07
MBN (no.)	0.421	0.477	0.398	16.73
SBN (no.)	0.412	0.877**	0.724	11.75
DFF (day)	0.400	0.736**	0.623	0.68
DFB (day)	0.635	0.388	0.260	1.78
BN (no.)	0.617	0.986**	1.00	28.93
BW (g)	0.644	0.972**	0.950	7.93
GP (%)	0.758	-0.288	-0.177	5.33
SI (g)	0.789	0.514*	0.310	9.88
FF (mic.)	0.416	-0.261	-0.217	7.04
FS (g tex^{-1})	0.562	0.917**	0.654	8.21
FL (mm)	0.416	-0.276	-0.229	3.02

*, **; significant level 0.05 and 0.01, respectively. h^2: Broad-sense heritability. GP: Ginning-out percentage, FF: Fiber Fineness, FS: Fiber Strength, FL: Fiber Length, MBN: Monopodial branches number, SBN: Sympodial branches number, DFF: Days to first flowering, DFB: Days to first open boll, SCY: Seed cotton yield per plant, PH: Plant height, BN: Boll number, BW: Boll weight, SI: seed index

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