

GENE ACTION AND COMBINING ABILITY FOR NEPS AND SEED COAT NEPS IN COTTON (*Gossypium hirsutum* L.)

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ABSTRACT

Information about heritability and combining ability for neps and seed coat neps is necessary for the cotton breeding strategies. Seven cotton cultivars including 4 lines and 3 testers were mated in line x tester mating design. The 19 genotypes were grown in RCBD with three replications in Aydın-Turkey conditions during 2014 growing season. Non-additive gene action was important in the expression of seed coat nep size, nep count and nep size. The parental lines Carmen and Claudia were good combiners for most neppiness characteristics. Carmen x Flash, Julia x ST-468, Claudia x Carisma and Gloria x Flash were the superior crosses for selection in further generations of neppiness breeding. It was recommended that the selection of individual plants for neppiness should be performed in later generations (F₄-F₆).

Key words: Combining ability, cotton, gene action, neps, seed coat neps

INTRODUCTION

Cotton is an important and strategic crop that has multiple contributes for the economy, widely grown in 53 countries in the world. In the 2017/18 season, global cotton production grew by 17 % to 26.8 million tons, following the 7 % production growth of the previous season. Turkey ranks ninth in the cotton sowing area, eighth in cotton production, second in cotton yield, fourth in cotton import and cotton consumption in the world (Anonymous, 2018).

Cotton breeding for fiber quality improvements has long been a primary objective of breeders. One important problem for early breeders was the lack of reliable and rapid methods to measure fiber characteristics (Baldwin et al., 1995). The AFIS (Uster Advanced Fiber Information System) instrument sizes and counts neps and seed coat neps in the lint stream. Neps and seed coat fragments remaining in fibers severely affect textile processing during spinning and dyeing (Jacobsen et al., 2001; Tekinsen, 2005; Bel and Xu, 2011). Because seed coat fragments remain in processed cotton attached to fibers, they can affect yarn quality and final fabrics by causing dyeing difficulties and holes in fabrics after “the dissolution of the seed coat tissue” (Pearson, 1955; Krifa et al., 1999). The genotypic differences and heritability on AFIS data for neps and seed coat neps have been few studies. Significant differences for neps and seed coat neps were identified among cotton cultivars in both *G.*

hirsutum L. and *G. hirsutum* L. x *G. barbadense* L. hybrid populations (Mangialardi and Lalor, 1990; Boykin, 2008; Zeng and Meredith, 2010). The information on gene action and combining ability of neps and seed coat neps are needed to identify the suitable parents and promising cross combination in breeding program. Zeng and Bechere (2012) reported that neps and seed coat neps are controlled by additive gene effect due to higher general combining ability variance than that of specific combining ability.

There is a general lack of information on gene action and combining ability of neps and seed coat neps in cotton. This study was aimed to estimate gene action for neps and seed coat neps in line x tester population and identify good combiners for these traits. The results of the present study can help predict the potential of genetic improvement for these important for fiber nep characteristics in cotton cultivars.

MATERIALS AND METHODS

The genetic population was developed from crossing four lines; Gloria, Claudia, Carmen, and Julia, and three testers; ST-468, Carisma and Flash using line x tester mating design in cotton (*Gossypium hirsutum* L.). The varieties used as line and tester were deliberately selected for high fiber quality characteristics and well adaptive capacity, respectively. Our preliminary studies (unpublished) had showed that cultivars used as lines were lower SCN count (11.25-16.70 number g⁻¹) than testers

(25.80-34.75 number g⁻¹). Totally 19 genotypes, 7 parents and their 12 F₁ crosses were grown in randomized complete block design with three replications at Cotton Research Institute, Nazilli, Aydın/Turkey. Parents and crosses were hand sown in single row of 12 m length, the rows and plant spacing was 0.7 and 0.2 m in May 2014. All the cultural managements such as fertilization and irrigation were applied as recommended for the cotton growing of Aegean Region. Twenty plants were randomly selected from F₁'s and parents. A 20-boll sample was hand harvested from middle fruiting positions of selected plants. Samples were ginned on laboratory-type roller gins with no lint cleaning. Fiber properties of nep size (µm), nep count (number g⁻¹), seed coat nep size (SCN; µm) and seed coat nep count (SCN; number g⁻¹) were measured using USTER AFIS (Figure 1) by ISKUR Textile Company.

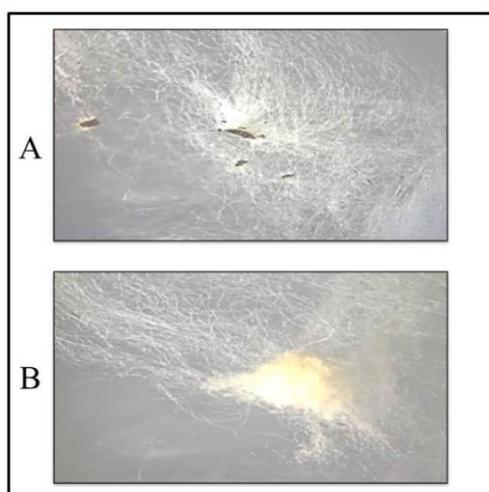


Figure 1. Seed Coat Neps (A) and Fiber Nep (B)

The combined analysis of parents and crosses was done as suggested by Arunachalam (1974) and for combining ability analysis, the following model was used:

$$Y_{ijk} = \mu + f_i + m_j + (mf)_{ij} + b_k + e_{ijk}$$

$$(i = 1, 2, \dots, l; j = 1, 2, \dots, t; k = 1, 2, \dots, r)$$

where Y_{ijk} denotes the observation recorded on the (i x j) th cross in the k th replication; μ is the general effect; f_i is the effect of the i th line; m_j is the effect of the j th tester; s_{ij} is the specific combining ability (SCA) effect of the (i x j) th cross; b_k is the k th block effect and e_{ijk} is the environmental effect (random error) associated with the (ijk) th observation which is assumed to be normally and independently distributed with a mean of zero and variance (σ^2).

σ_f^2 and σ_m^2 represent fixed type variances for lines and testers respectively. The weighted average of these two can be taken as an estimate of σ^2 GCA, i.e.

$$\sigma^2 \text{GCA} = [(l - 1) \sigma_f^2 + (t - 1) \sigma_m^2] / (l + t - 2)$$

The ratio $\sigma^2 \text{GCA} / \sigma^2 \text{SCA}$ will give an approximate idea about degree of dominance (Kaushik et al., 1984).

The variance analysis of line x tester suggested by Singh and Chaudhary (1979) were estimated using Microsoft Excel. Combining ability effects were computed for seed coat nep, seed coat nep size, number of nep and nep size.

RESULTS AND DISCUSSION

Significant variation was determined among genotypes for all the characters under study (Table 1). This reflects sufficient genetic variability and allows combining ability analysis. Also, it was shown that lines contributed higher for neppiness in this population because of significant differences among lines for SCN count, SCN size and nep size while non-significance for testers (Table 1). Genotypic differences for neppiness were determined by Mangialardi and Lalor (1990), Boykin (2008), Zeng and Meredith (2010) in cultivated species of cotton (*G. hirsutum* L. and *G. barbadense* L.).

Estimates of GCA and SCA variance ratio ($\sigma^2 \text{GCA} / \sigma^2 \text{SCA}$) which was smaller than unity revealed that non-additive gene action for the control of SCN size, nep count and nep size was higher than additive gene action (Table 1). The finding of non-additive gene effects do not corroborated by findings of Zeng and Bechere (2012) who observed greater $\sigma^2 \text{GCA}$ than $\sigma^2 \text{SCA}$ for neppiness in a hybrid populations involved exotic germplasm lines x elite germplasm in a North Carolina Design II. However, additive gene action for SCN count was found to be important in our population as reported by Zeng and Bechere (2012). The preponderance of non-additive type of gene actions clearly indicated that selection of superior plants, in terms of neppiness, should be postponed to later generation.

The mean square of parents vs hybrids for only nep size indicated that difference between the mean of parents (683.1 µm) and hybrids (651.7 µm) was significant (Table 1 and Table 2). In respect of neppiness, reduction in count and size of nep and SCN can improve yarn performance and fabric color quality (Mangialardi and Lalor, 1990). Among parents, testers, Flash, Carisma and ST-468 cultivars, were noteworthy as the parents with the worst fiber characteristics (Table 2). The lines, Claudia, Gloria, Julia and Carmen, were genotypes with lower nep count and size of fiber and SCN count. This confirms that lines and testers were deliberately selected for high fiber quality characteristics and well adaptive capacity, respectively as given in material and methods. Significant negative (desired) GCA effect of Claudia for SCN and nep count; Carmen and Flash for SCN size; Carmen for nep size was useful for the breeding of neppiness. No parent was identified with mean values and favorable GCA effects in all neppiness traits. Therefore, multiple crossing will be necessary to enhance recombination among parents.

Table 1. Mean squares for observed characters

	df	SCN (Number g ⁻¹)	SCN Size (µm)	Nep (Number g ⁻¹)	Nep Size (µm)
Block	2	3.84	24775.18	299.01	3146.68
Genotypes	18	314.05**	135228.51*	552.15*	26336.38**
Parents	6	589.71**	279073.08*	921.09**	72225.87**
Parents vs Hybrids	1	48.32	6989.60	897.52	13133.85**
Hybrids	11	187.84	68425.92**	319.52	2505.99*
Lines	3	404.99*	91462.71*	474.62	3709.51*
Testers	2	46.36	61035.53	155.58	70.19
Line x Tester	6	126.43	59370.91*	296.62	2716.15*
Error	36	108.02	22815.82	222.01	1051.22
General	56				
σ^2 (GCA)		30.95	3565.75	19.77	110.37
σ^2 (SCA)		6.13	12185.02	24.88	554.97
σ^2 (GCA) / σ^2 (SCA)		5.04	0.29	0.79	0.19

*, **, significant at 1% and 5% probability level, respectively.

Table 2. Mean values and combining ability effects of parents and crosses

Parents	SCN (Number g ⁻¹)		SCN Size (µm)		Nep (Number g ⁻¹)		Nep Size (µm)	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
Lines								
Gloria	8.0 bc	9.64*	931.3 c	-7.25	21.0 b	6.13	581.6 d	-12.94
Claudia	2.6 c	-5.91*	1159.0 b	123.75*	24.6 b	-9.63*	636.3 bc	4.94
Carmen	12 bc	-2.13	1868.3 a	-122.81*	35.3 b	-1.52	661.6 b	-18.50*
Julia	4.0 bc	-1.58	1243.0 a	6.30	40.0 b	5.02	641.3 bc	26.50*
Testers								
ST- 468	26.6 ab	0.19	1060.6 bc	-14.47	30.0 b	3.16	1030.0 a	-2.64
Carisma	10.6 bc	1.86	1069.3 bc	77.44*	73.3 a	0.75	628.6 b-d	0.53
Flash	41.3 a	-2.05	1171.6 b	-62.97*	45.3 a	-3.91	602.6 cd	2.11
LSD _(0.05)	23.03		205.13		24.5		47.2	
Mean	15.05		1215		38.5		683.1	
SE (Lines)		4.89		71.2		7.02		15.2
SE (Testers)		4.24		61.6		6.08		13.2
Hybrids	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
Gloria x ST- 468	14.00 bd	-8.97*	1355.3 ab	185.25*	47.3 ab	-8.72	650.3 b	14.19
Gloria x Carisma	31.33 a	6.69	1235.6 a-c	-26.33	54.6 ab	1.02	622.0 b	-17.30
Gloria x Flash	23.00 ab	2.27	962.6 de	-158.91*	56.6 a	7.69	644.0 b	3.11
Claudia x ST- 468	9.00 bd	1.58	1184.3 a-e	-116.7	48.6 ab	8.39	661.1 ab	7.63
Claudia x Carisma	8.00 cd	-1.08	1362.3 ab	-30.66	32.0 ab	-5.86	641.6 b	-15.52
Claudia x Flash	4.67 d	-0.50	1400.0 a	147.41*	30.6 ab	-2.52	666.6 ab	7.88
Carmen x ST- 468	11.00 bd	-0.19	1053.0 c-e	-1.52	57.0 a	8.61	652.6 b	22.08
Carmen x Carisma	14.67 bd	1.80	1219.6 a-d	73.22	49.3 ab	3.36	623.0 b	-10.75
Carmen x Flash	7.33 cd	-1.61	934.3 e	-71.69	29.3 b	-11.97	624.0 b	-11.33
Julia x ST- 468	19.33 a-c	7.58	1116.6 b-e	-66.97	46.6 ab	-8.27	631.6 b	-43.91*
Julia x Carisma	6.00 cd	-7.41	1259.3 a-c	-16.22	54.0 ab	1.47	722.3 a	43.58*
Julia x Flash	9.33 b-d	-0.16	1218.3 a-d	83.19	54.6 ab	6.80	680.6 ab	0.33
Mean	13.14		1191.8		46.75		651.7	
LSD _(0.05)	14.05		269.9		27.0		60.8	
SE (Crosses)		8.48		123.3		12.16		26.4

*, **, significant at 1% and 5% probability level, respectively.

Among crosses, three to twelve hybrids were detected significant and desired SCA for different neppiness. These hybrids were Gloria x ST-468 for SCN count; Gloria x Flash for SCN size and Julia x ST-468 for nep size. In terms of mean values and negative SCA effects Claudia hybrids (x Flash and x Carisma), Carmen x Flash and Julia x Carisma were the best combinations with lower of SCN

count. Carmen x Flash and Julia x ST-468 for SCN size; Carmen x Flash and Claudia x Carisma for nep count presented superior values while Gloria x Carisma, Carmen x Flash and Carmen x Carisma hybrids were combinations for nep size. The hybrids with favorable means, higher and positively SCA effects and involving at least one of the parents with suitable GCA effects have great

importance for favorable alleles to breed neppiness in this study (Kenga et al., 2004).

Similar to parents, it was seen that hybrid combinations with favorable mean values and SCA effects for all neppiness characteristics were obtained in these populations. However, Carmen x Flash, Julia x ST-468, Claudia x Carisma and Gloria x Flash can be identified as promising hybrids. Especially, parents as used lines of mentioned 4 hybrids exhibited favorable means and GCA, although all cultivars as testers had poor neps characteristics. SCA effects of mentioned could result from mating any combination of high (Gloria and Julia) and low (ST-468) GCA parents.

CONCLUSIONS

The genetic variability originated from parental lines for neppiness in the studied population. The lines, Carmen and Claudia cotton genotypes, were good combiners to decrease the nep and seed coat nep in breeding of neppiness. Non-additive gene action was higher than additivity in inheritance of nep and seed coat nep. The preponderance of non-additive type of gene actions clearly indicated that selection of superior plants should be postponed to later generations. Also, bulk method between F₂ and F₆ generations can be used successfully for advancing progeny generations. Carmen x Flash, Julia x ST-468, Claudia x Carisma and Gloria x Flash populations with desired mean values and SCA effects should be recommended for selection in further generations.

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