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Combining ability status of naked seeded type based combiners and cross combinations in cotton (*Gossypium hirsutum* L.)

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Abstract

A study on combining ability status guides a breeder to choose elite combiners and crosses that can be released as commercial hybrids. The present study was conducted at the Botanical Garden, Department of Genetics and Plant Breeding, UAS, Dharwad during Kharif 2018-19 in a randomized complete block design with two replications. The main objective of the study was to assess the combining ability status of six parental lines and thirty cross combinations developed based on naked seeded types using the full diallel method in American cotton. Combining ability effects were estimated for important yield-related traits, viz., seed cotton yield per hectare (kg/ha), number of bolls per plant, and boll weight (g). Simple analysis of variance revealed significant differences among the parents, hybrids, and their reciprocals for all three traits studied. All three traits were found to be under the control of non-additive gene action, as revealed by the higher magnitude of SCA variance. Based on the gca effects of parents, it is revealed that DHN-3 proved to be the best general combiner due to the highest seed cotton yield and the production of the maximum number of bolls and boll weight. Based on sca effects, the specific cross DHN-1 × DHPN-2 performed better for seed cotton yield. Some unique combinations, such as DHN-1 × DHPN-2, DHN-3 × DHPN-1, DHN-2 × DHPN-1, and DHN-2 × DHPN-2, were identified as the best for the number of bolls per plant, while the crosses DHN-1 × DHPN-2, DHN-2 × DHPN-1, DHN-2 × DHPN-2, and DHPN-2 × DHN-1 were found to be the best for boll weight. It can be concluded that the expression of traits can be improved by employing heterosis breeding, as traits were inherited in a non-additive manner.

Keywords: Naked seeded types, GCA, SCA, combining ability, combiners

Introduction

Cotton (*Gossypium hirsutum* L.) is the precious gift of nature to mankind, contributed by the genus *Gossypium* to people all over the world. It is an industrial commodity of worldwide importance and occupies a place of pride in Indian agriculture and economy, earning valuable foreign exchange (ICAR-AICRP, 2018-19) [1].

Cotton seed trichomes are very long single epidermal cells that differentiate and elongate to form two types of fibers, namely lint fiber and fuzz fiber (linters) (Musaev *et al.*, 1972) [2]. The nakedness or fuzzless trait is characterized by the lack of fuzz fiber development on the seed coat (Turley, 2002) [2]. The ginning of fuzzless varieties will generate black seed and has been referred to as the naked-seed phenotype (Ware *et al.*, 1947) [4].

Naked-seeded types have important advantages over normal fuzzy types. Naked-seeded types completely eliminate the acid delinting process, thereby reducing the cost of seed production (Turley *et al.*, 2008, and Ware 1940) [5, 6]. They are advantageous during ginning because they generally require much less force to remove the lint from the seed than fuzzy-seeded cottons, resulting in less power consumption at the gin and fewer breakages of the lint fibers (Bechere *et al.*, 2012) [7]. Fuzz fibers absorb much of the oil from cotton seed, thereby reducing its content in the seed, so their absence would increase oil content in cotton seed, leading to increased oil recovery (Zhang *et al.*, 1991) [8]. Naked-seededness of a genotype can act as an easily identifiable morphological marker, helping breeders to identify/purify a genotype (Turley *et al.*, 2007) [9].

The germplasm lines and genotypes with naked-seeded types are not very productive, and fiber qualities are generally not very good (Turley *et al.*, 2007) [9]. Hence, there is a need for improving the productivity and fiber quality of naked-seeded types so that new varieties and hybrids can be consciously developed and released for cultivation. Understanding the nature of

gene action helps in choosing appropriate breeding procedures/methods to develop a cultivar in any crop (Stansfield *et al.*, 1969) [10].

Based on the nature of combining ability of parents and gene action, the breeder can determine whether developing a variety or hybrid in a crop is appropriate or not. Combining ability analysis is one of the most effective methods for determining the finest combiners for use in crosses, whether to exploit heterosis or to accumulate productive genes (Sprague *et al.*, 1942, and Subramanian *et al.*, 2005) [11, 12]. It also aids in the understanding of the genetic architecture of distinct traits, allowing the breeder to build an effective breeding plan for future material improvement.

The ability of parents and hybrids to combine traits is used to reveal the nature of gene activity involved in the inheritance of features. Combining ability is of two types, *viz.*, General Combining Ability (GCA) and Specific Combining Ability (SCA). GCA is a measure of additive gene activity that relates to the average performance of a genotype in a series of hybrid combinations (Sprague *et al.*, 1942) [11]. GCA is mainly due to additive genetic variance and additive \times additive gene interaction. It helps in the identification and selection of the best genotype to use in hybridization as a parent; it is estimated by half-sib mating and has a relationship with narrow sense heritability.

SCA is the performance of a parent in a specific cross in reference to general combining ability (Sprague *et al.*, 1942) [11]. It is due to dominance genetic variance and all three types of gene interactions. It helps in the identification and hence the selection of the best cross combinations, *i.e.*, those with the desired output. It is estimated by full-sib mating and it has a relationship with heterosis.

Biometrical designs such as diallel analysis and line \times tester analysis are used for the estimation of combining ability of the genotypes (Wandhare *et al.*, 2010a) [13]. Diallel analysis refers to the mating of selected parents in all possible combinations and the evaluation of a set of diallel crosses (Wandhare *et al.*, 2010b) [14]. The procedures of diallel cross analysis for the study of polygenic traits in self-pollinated species were developed in 1954 by Jinks and Hayman. It is used to evaluate several inbred lines in terms of combining ability variances and effects. There are four different methods of diallel analysis based on the inclusion of parents, direct crosses, and reciprocal crosses (Griffing *et al.*, 1956) [15]. A full diallel analysis includes parents, direct crosses, and reciprocal crosses in its analysis. The present study employed a full diallel analysis for assessing the combining ability status of parental lines and cross combinations. A diallel set of crosses involving naked and partially naked parents was used to identify potential combiners and combinations.

Material & Methods

The present study was carried out in the Botanical garden, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, Dharwad during *Kharif* 2018-19. The experimental material comprised of 6 parents DHN-1, DHN-2, DHN-3, DHN-4, DHPN-1 and DHPN-2. In this investigation, these six parents were crossed according to full diallel system of crossing and 30 hybrids were developed. The seeds of 30 hybrids were produced by hand emasculation and hand pollination in a 6 \times 6 diallel mating design and seeds of parents were produced by selfing during *Kharif* 2017-18.

The seeds of 30 hybrids and their six parents were field-planted during June 2018 in randomized complete block design with two replications. Seeds of 36 entries in each replication were planted in two row plot having nineteen plants spaced at the distance of 90 cm between the rows and 60 cm between plants within the rows. All standard agronomic practices *i.e.* hoeing, irrigation and fertilization were followed according to recommended package of practices from sowing to harvest. Observations were recorded for characters number of bolls per plant, boll weight (g) and seed cotton yield per hectare (/ha) from plants of parents and hybrids. For number of bolls, the total number of fully opened bolls were counted on five randomly selected plants and averaged. The boll weight in grams was obtained by taking the average weight of 25 randomly collected bolls per genotype. To record seed cotton yield per hectare, total weight of seed cotton was weighed in grams on plot basis and converted into kilogram per hectare.

Analysis of variance for individual character was carried out on the basis of mean value per entry per replication using randomized block design (RBD) to see whether there are significant differences among genotypes or not (Panse *et al.*, 1961) [16]. The characters showing significant genotypic differences were further analyzed through combining ability technique by adopting Method I with Eisenhart's Model II, since the present study included parents, F_1 's and reciprocals. Analysis was carried out in WINDOSTAT 8.1 software.

Results & Discussion

Simple analysis of variance revealed significant differences ($P \leq 0.01$) among the parents, hybrids, and their reciprocals for seed cotton yield, number of bolls, and boll weight (Table 1). The general combining ability effects of six parents are presented in Table 2, while Table 3 contains estimates for specific combining ability and reciprocal effects for hybrid evaluation. These estimates are explained in the following sections.

Table 1: Mean squares of preliminary analysis of variance and combining ability analysis for seed cotton yield, number of bolls and boll weight of *Gossypium hirsutum* L.

Source of variation	Degrees of freedom	No. of bolls per plant	Boll weight (g)	Seed cotton yield (qtl/ha)
Replicates	1	0.98 ^{ns}	0.012 ^{ns}	17.425 ^{ns}
Treatments	35	98.28**	1.79**	48.53**
Parents	5	49.36**	1.70*	14.11**
Hybrids	29	106.75**	1.89**	54.50**
GCA	5	92.18**	0.75 ^{ns}	27.91**
SCA	15	51.48**	1.12**	29.93**
Reciprocal	15	32.45**	0.72*	17.39**
Error	35	6.38	0.33	6.12
σ^2 GCA		3.51	-0.02	-0.1

σ^2 SCA		26.18	0.45	13.82
σ^2 Reciprocal		13.03	0.19	5.63

*-Significant at 0.05 probability level, **-Significant at 0.01 probability level, ns: non-significant; GCA=general combining ability; SCA=specific combining ability; σ^2 GCA =Variance due to general combining ability; σ^2 SCA=Variance due to specific combining ability; σ^2 Reciprocal=Variance due to reciprocal effects.

The results revealed that the effects of general combining ability, specific combining ability, and reciprocals on seed cotton yield were highly significant ($p \leq 0.01$). The variance due to specific combining ability (13.82) is greater than that due to general combining ability (-0.1). This suggests a stronger influence of non-additive variation in the inheritance of seed cotton yield than that of additive variation (Saifullah

et al., 2014, and Rathore *et al.*, 2004) [17, 18]. The general combining ability of six parents (Table 2) showed that DHN-3 (3.77) was the best general combiner, followed by DHPN-2 (2.9), for seed cotton yield per hectare. The parent, namely DHN-1, with a GCA estimate of -15.72, is considered to be a poor general combiner for this trait.

Table 2: Estimates of general combining ability for seed cotton yield, number of bolls and boll weight in parental lines of naked seeded types of cotton

Source of variation	No. of bolls per plant	Boll weight (g)	Seed cotton yield (qtl/ha)
DHN-1	-3.24 **	0.02	-15.72 *
DHN-2	-1.08	-0.24	10.50
DHN-3	4.77 **	0.44 **	-2.77 **
DHN-4	-0.39	-0.22	-0.52
DHPN-1	-1.39 *	-0.05	3.9**
DHPN-2	1.35	0.05	3.36

* Significant at 0.05 probability level, ** Significant at 0.01 probability level

Among F1 hybrids, crosses, namely DHN-1 \times DHPN-2 (7.17), DHN-2 \times DHPN-1 (5.02), and DHN-3 \times DHPN-1 (3.86), showed significant SCA effects in the positive direction and were identified as the best specific combinations, whereas their reciprocal crosses were non-significant, indicating no reciprocal difference present for seed cotton yield per hectare. Two crosses, namely DHN-1 \times DHN-2 and DHPN-1 \times DHPN-2, have significant SCA effects in the negative direction with poor performance (Table 3). The superior reciprocal combination identified for this trait was DHN-3 \times DHPN-2 (4.57) (Table 3).

Mean squares for general combining ability and specific combining ability were highly significant for the number of bolls per plant (Table 1). The variance due to specific combining ability (26.18) is greater than that due to general combining ability (3.51). This suggests a stronger influence of non-additive variation in the inheritance of the number of

bolls than that of additive variation (Shakeel *et al.*, 2018) [19]. The comparison of general combining ability effects in Table 2 revealed DHN-3 (4.77) as the best general combiner. The two parents, namely DHN-1 (-3.24) and DHPN-1 (-1.39), revealed significant negative general combining ability effects and were poor general combiners for the number of bolls per plant.

The best specific cross combination was DHN-1 \times DHPN-2 (9.50). The hybrids resulting from crosses, namely DHN-3 \times DHPN-1 (4.84), DHN-2 \times DHPN-1 (4.68), and DHN-2 \times DHPN-2 (3.35), performed better regarding the number of bolls (Table 3), and reciprocals of these crosses were found to be non-significant, indicating no reciprocal differences were observed for the character. However, the superior reciprocal combinations identified for this trait were DHN-3 \times DHPN-2 (9.16) and DHN-2 \times DHN-3 (5.06) (Table 3).

Table 3: Estimates of specific combining ability for seed cotton yield, number of bolls and boll weight of crosses developed based on naked seeded types of cotton

Crosses	Character		
	No. of bolls per plant	Boll weight (g)	Seed cotton yield (kg/ha)
DHN-1 \times DHN-2	-5.05 **(-0.56)	-0.91 * (0.27)	-5.54 ** (1.66)
DHN-1 \times DHN-3	-1.28 (-5.25**)	0.07(-0.76 *)	0.71(-2.36)
DHN-1 \times DHN-4	0.95(-9.31**)	-0.58(-0.58)	0.55(-5.39 **)
DHN-1 \times DHPN-1	-2.12(-2.5)	-0.83 *(-0.10)	-2.75(-1.48)
DHN-1 \times DHPN-2	9.50**(-1.37)	1.44**(0.80 *)	7.17**(-1.88)
DHN-2 \times DHN-3	-0.96(5.06 **)	-0.31(0.15)	-2.26(1.24)
DHN-2 \times DHN-4	-2.28(-5.53 **)	-0.07(-0.84 *)	0.69(-4.55 **)
DHN-2 \times DHPN-1	4.68**(-2.3)	0.92 *(-0.63)	5.02 **(-1.96)
DHN-2 \times DHPN-2	3.35 *(0.65)	0.76 *(0.47)	2.90(0.61)
DHN-3 \times DHN-4	-1.58(-5.68 **)	0.27(-0.85 *)	-0.73(-4.53 **)
DHN-3 \times DHPN-1	4.84 ** (0.12)	0.02(0.68)	3.86 *(-3.20 *)
DHN-3 \times DHPN-2	0.42(9.16**)	-0.20(0.47)	-0.14(4.57 **)
DHN-4 \times DHPN-1	2.14(-8.12**)	-0.28(-0.33)	0.35(-4.27 *)
DHN-4 \times DHPN-2	2.73(-3.72 *)	0.25(-1.20 **)	1.11(-4.90 **)
DHPN-1 \times DHPN-2	-7.56**(-3.06)	-0.75 *(-0.487)	-5.52 **(-3.78 *)

* Significant at 0.05 probability level, ** Significant at 0.01 probability level.

(-)-Reciprocal effects are shown in parenthesis

Genetic analysis of boll weight revealed that the effects of specific combining ability and reciprocals were significant, while the general combining ability appeared to be non-significant (Table 1). The magnitude of specific combining ability variance (0.45) was greater than general combining ability variance (-0.02), indicating the role of dominant genes in the expression of boll weight (Reddy *et al.*, 2017, and Simon *et al.*, 2013) [20, 21].

The comparison of general combining ability (Table 2) identified DHN-3 as the best general combiner for this trait. The best specific combination was DHN-1 × DHPN-2 (1.44), while its reciprocal cross, DHPN-2 × DHN-1 (0.8), showed significant SCA effects in the positive direction, indicating the presence of reciprocal differences in the inheritance of the trait.

The hybrids resulting from specific combinations DHN-2 × DHPN-1 (0.92) and DHN-2 × DHPN-2 (0.76) performed better for boll weight, and their reciprocals were non-significant (Table 3). Among reciprocal crosses, one combination, DHPN-2 × DHN-1 (0.80), was found to be superior. The combination DHN-4 × DHPN-2 had the strongest negative reciprocal effect (-1.20) for boll weight.

Effective genetic improvement in seed cotton yield, number of bolls, and boll weight may be achieved by exploiting the genetic basis of variation in different morphological characters (Tariq *et al.*, 2012, and Wankhade *et al.*, 2008) [22, 23]. Quantitative genetic analyses provide reliable information about the type of genetic effects involved in the inheritance of polygenic traits, and they also assist in modifying selection methods to enhance cultivar development besides upgrading germplasm pools (Hallauer, 2007) [24].

From the present data, it was revealed that DHN-3 proved to be the best general combiner due to the highest seed cotton yield and the production of the maximum number of bolls and boll weight. The parental line DHPN-1 was also identified as a good general combiner for seed cotton yield. Therefore, the inclusion of both these parents in crop breeding programs for yield enhancement could be rewarding. The parent DHN-1 appeared to be a poor general combiner for traits such as the number of bolls and seed cotton yield, while the parent DHN-2 exhibited poor general combining ability for boll weight.

In the present study, some unique combinations were identified. For example, DHN-1 did not perform well as a general combiner, but when put in combination with another good combiner (DHPN-2), it exhibited a good response in a specific cross, as parents showing poor general combining ability effects may result in good hybrid combinations (Patel *et al.*, 2009, and Patel *et al.*, 2016). For instance, the specific cross DHN-1 × DHPN-2 performed better for seed cotton yield, similar to findings reported for seed cotton yield.

The best combinations identified for a higher number of bolls were DHN-1 × DHPN-2, DHN-3 × DHPN-1, DHN-2 × DHPN-1, and DHN-2 × DHPN-2, while the crosses DHN-1 × DHPN-2, DHN-2 × DHPN-1, DHN-2 × DHPN-2, and DHPN-2 × DHN-1 were identified as the best specific combinations for boll weight. The studied traits were found to be under the influence of non-additive gene action. Under such circumstances, the selection of segregants in early generations would result in poor-performing genotypes in later segregating generations and make selection ineffective (Rajamani *et al.*, 2015) [33].

Conclusion

The six parents possessed substantial genetic diversity for

seed cotton yield, boll number, and boll weight. Based on the general combining ability (GCA) effects of parents, it was revealed that DHN-3 proved to be the best general combiner due to the highest seed cotton yield and production of the maximum number of bolls and boll weight. Based on specific combining ability (SCA) effects, the specific cross DHN-1 × DHPN-2 performed better for seed cotton yield, and hence, it is expected to exhibit higher heterosis. When there is non-additive gene action (partial dominance, complete dominance, and over-dominance), the population responds to selection in later segregating generations. Hence, selection must be delayed until later generations, as all three traits showed a non-additive type of gene action. It is further suggested that characters showing non-additive inheritance may be improved by employing heterosis breeding.

References

1. ICAR-AICRP (Cotton) Annual Report ICAR - All India Coordinated Research Project on Cotton, Coimbatore. 2018-19;641:003.
2. Musaev DA, Abzalov MM. Some questions concerning the inheritance of fuzz in cotton seeds (*Gossypium hirsutum* L.). *Genetika*. 1972;8:7-16.
3. Turley RB, Kloth RH. Identification of a third fuzzless seed locus in upland cotton (*Gossypium hirsutum* L.). *J Hered*. 2002;93(5):359-364.
4. Ware JO, Nenedict NI, Rolfe WH. A recessive naked-seed character in upland cotton. *J Hered*. 1947;38(10):313-320.
5. Turley RB, Kloth RH. The Inheritance model for the fiberless trait in upland cotton (*Gossypium hirsutum* L.) Line SL1-7-1: Variation on a Theme. *Euphytica*. 2008;64(1):123-132.
6. Ware JO. Relation of fuzz pattern to lint in upland cotton cross. *J Hered*. 1940;31:489-496.
7. Bechere E, Turley RB, Auld DL, Zeng L. A new fuzz less seed locus in an upland cotton (*Gossypium hirsutum* L.) mutant. *American J Plant Sci*. 2012;3:799-804.
8. Zhang TZ, Pan JJ. Genetic analysis of a fuzzless lintless mutant in *Gossypium hirsutum* L. *Jiangsu J Agric. Sci*. 1991;7:13-16.
9. Turley RB, Vaughn KC, Scheffler JA. Lint development and properties of fifteen fuzzless seed lines of upland cotton (*Gossypium hirsutum* L.). *Euphytica*. 2007;156:57-65.
10. Stansfield WD. *Theory and Problems of Genetics*. McCraw Hill Book Co. Inc. New York; c1969. p. 139-150.
11. Sprague GF, Tatum LA. General and specific combining ability in single crosses in corn. *J American Soc. Agron*. 1942;34:923-932.
12. Subramanian A, Ravikesavan R, Iyanar K, Thangaraj K, Vindhyavarman P. Combining ability analysis in upland cotton (*Gossypium hirsutum* L.). *Plant Arch*. 2005;5(1):23-28.
13. Wandhare MR, Patil BR, Ambhore KT, Bhongle SA. Diallel analysis for estimating combining ability of quantitative traits in upland cotton. *Ann. Plant Physiol*. 2010a;24(1):62-64.
14. Wandhare MR, Patil BR, Ambhore KT, Bhongle SA. Combining ability studies for seed cotton yield and fibre quality parameters in *Gossypium hirsutum* L. *Ann. Plant Physiol*. 2010b;24(1):65-67.

15. Griffing B. Concept of general and specific combining ability in relation to diallel crossing systems. *Australian J Biol. Sci.* 1956;9:463-493.
16. Panse VG, Sukhatme VP. *Statistical Methods for Agricultural Workers*, ICAR, New Delhi; c1961. p. 412-432.
17. Saifullah A, Kandhro MM, Laghari S, Arain MA, Deho ZA. Combining ability and heterosis for yield contributing traits in upland cotton (*Gossypium hirsutum* L.). *Pakistan J Bot.* 2014;41(4):1769-1774.
18. Rathore P, Garg HR, Varma PK, Pathak D. Genetics of seed cotton yield and some other traits in American cotton using triple test cross analysis. *J Indian Soc. Crop Improv.* 2004;30(1):67-70.
19. Shakeel A, Khokhar ES, Maqbool MA, Abuzar MK, Zareen S, Aamir SS, *et al.* Studying combining ability and heterosis in different cotton (*Gossypium hirsutum* L.) genotypes for yield and yield contributing traits. *Pakistan J Agric. Res.* 2018;31(1):55-68.
20. Reddy KB, Reddy VC, Ahmed ML, Naidu TCM, Srinivasarao V. Combining ability analysis for seed cotton yield and quality traits in upland cotton (*Gossypium hirsutum* L.). *Electron. J Plant Breed.* 2017;8(1):142-152.
21. Simon SY, Kadams AM, Aliyu B. Combining ability analysis in F₁ hybrids of cotton (*Gossypium hirsutum*) by diallel method in North-eastern Nigeria. *Greener J Agric. Sci.* 2013;3(2):090-096.
22. Tariq MK, Uzair QM. Genetic studies of yield traits in cotton (*Gossypium hirsutum* L.). *J Agric. Res.* 2012;50(1):21-29.
23. Wankhade SN, Patil SP, Kayande NV, Burghate SK. Diallel analysis for estimating combining ability of quantitatively inherited traits in upland cotton. *J Cotton Res. Dev.* 2008;22(2):147-149.
24. Hallauer AR. History, contribution, and future of quantitative genetics in plant breeding; Lessons from maize. In *International Plant Breeding Symposium*, R. Bernardo, (ed.). August 20–26, 2006, Mexico City. ASA, CSSA, and SSSA, Madison, WI; c2007. p. 4-19.
25. Patel AD, Patel UG, Kumar V. Diallel analysis for combining ability for seed cotton yield and its component traits in upland cotton. *J Cotton Res. Dev.* 2009;23(2):222-225.
26. Patel UG, Patel AD, Patel NN, Mehta NP, Patel JC. Heterosis and Combining Ability Studies in Asiatic Cotton. *Indian. J Genet Pl. Br.* 2016;50(3):0975-6906.
27. Imran M, Shakeel A, Azhar FM, Farooq J, Saleem MF, Saeed A, *et al.* Combining ability analysis for within-boll yield components in upland cotton (*Gossypium hirsutum* L.). *Genet. Mol. Res.* 2012;11(3):2790-2800.
28. Inam-ul-Haq, Azhar FM. Genetic basis of varietal differences for seed cotton yield and its components in *Hirsutum* spp. *Int. J Agr. Biol.* 2004;6:904-907.
29. Imran M, Shakeel A, Azhar FM, Farooq J, Saleem MF, Saeed A, *et al.* Combining ability analysis for within-boll yield components in upland cotton (*Gossypium hirsutum* L.). *Genet. Mol. Res.* 2012;11(3):2790-2800.
30. Jatoi WA, Baloch MJ, Veesar NF, Panhwar SA. Combining ability estimates from line × tester analysis for yield and yield components in upland cotton genotypes. *J Agric. Res.* 2011;49(2):165-172.
31. Khan NU, Hassan G, Marwat KB, Farhatullah Batool S, Makhdoom Khan I, Khan IA, *et al.* Genetic variability and heritability in upland cotton. *Pak. J Bot.* 2019;42(4):1695-1705.
32. Mohammad AA, Bhatti MF, Abbas A, Khan IA. Assessment of inheritance pattern of some multigenic characters in cotton (*Gossypium hirsutum* L.). *J Agric. Res.* 2010;48(1):25-35.
33. Rajamani S, Sumalatha T, Gopinath M. Studies on genetic parameters of seed cotton yield in upland cotton (*Gossypium hirsutum* L.). *J Cotton Res. Dev.* 2015;29:36-38.