Received: 04 Feb 25 | Revised: 12 March 25 | Accepted: 18 March 25
DOI: https://doi.org/10.62460/TBPS/2025.072

RESEARCH ARTICLE

Trends in Biotechnology and Plant Sciences

Assessing Combining Ability for Yield Related Traits in Upland Cotton through Diallel Analysis

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Abstract

The development of high yielding varieties of cotton with high fiber quality highly relies on the selection of genetically diverse and superior parental lines. Estimation of combining ability is a key factor in the selection of parents for hybridization. During crop season 2023, Cotton lines namely Tipo-1, C-1, FH-Super, CIM-600, and FH-444 were crossed by using full Diallel mating design in the greenhouse of Plant Breeding and Genetics Department, University of Agriculture Faisalabad. Twenty-five crosses and five parental genotypes were planted in the field in two replications using a randomized block design. Data was calculated for different yield parameter sympodial branches, monopodial branches, number of bolls per plant, plant height, seed cotton yield, seed index, seed weight, lint index, boll weight, ginning out turn of cotton crop. The recorded data were analyzed statistically using Griffing's approach for the estimation of general and specific combining abilities. The parents FH-444, CIM-600 and Tipo-1 showed superior general combining ability (GCA) for most of the traits. The crosses Tipo-1 × C-1, Tipo-1 × FH-444 and C-1 × FH-444 exhibited high specific combining ability (SCA). The Crosses FH-super × Tipo-1, FH-444 × CIM-600 and FH-444 × CIM-600 showed good reciprocal combining ability (RCA) for most of the traits. Most of the characters were found to be under the control of dominance gene action. This information may be helpful to identify suitable parents and hybrids for future breeding programs.

KEYWORDS
Combining Ability, GCA, SCA, Hybridization, Cotton Breeding, Genetic Variation.

1 |INTRODUCTION

Cotton is a significant fiber crop in the domain and it belongs to the genus *Gossypium* and family *Malvaceae.* Only four out of 50 species in the genus are cultivated for their spinnable fiber (Wendel and Grover, 2015). Cotton is a major source of income and plays a significant role among all the crops (Ahmad et al., 2007). A variety of plant breeders have focused their huge scientific attention on the cotton crop due to its commercial worth. (Sarwar et al., 2021). Cotton is a multipurpose crop that provides an inclusive range of benefits for both humans and animals. Cotton is the best widely produced standard fiber worldwide, providing a source of income for the global agricultural community. In addition to being a major source of income for many farmers, cotton plays a significant role in economic growth (Jans et al., 2021).

Cotton crop requires about 28-35°C for its normal growth but in Pakistan it reaches to 41-45°C and sometime reaches to 50°C that is the main cause of heat stress in the cotton and leads to the favorable environment for the attack of whitefly and other insect pests (Shuli et al, 2018). The current varieties of cotton are not adapting to the constantly changing climatic conditions, which has led to a yearly decline in cotton production. Additionally, it is difficult for researchers to find early maturing and high-yielding good combiners. It was necessary to develop parental combinations that produced high yields and matured early. There is continual fluctuation in seed cotton yield in Pakistan and there are many reasons for this change. In cotton production, Pakistan has been ranked 5th.Cotton contributed 0.3 percent to GDP this year and 1.4 percent to value added in agriculture Government of Pakistan, 2022-23). The growth of high yielding cultivars with improved quality of fiber requires selection of the best parents. These parents must be genetically superior and good general combiners for all traits to produce hybrids with higher yield and resistant to biotic and abiotic stresses (Kumar et al., 2015).

The main goal of cotton breeders is to evaluate new varieties of cotton with high lint yield and fiber quality suitable for the textile industry (Dimitrova et al*.,* 2019). The main factors influencing the choice of selection strategy to boost productivity are heterosis, genetic control of yield-related traits, and the genotypes' capacity to combine for the parameters in question (Khokhar et al., 2018). The development of new varieties of cotton with superior fiber quality and high yields is the key objective of breeders (Kumar et al., 2015). The primary phase in a popular breeding program is choosing suitable parents. The best way select superior lines for this is through diallel analysis. It is suitable biometric technique for determining suitable crosses and parents by calculating general and specific combining ability. Diallel mating is a method for recognizing potential genotypes and identifying promising recombination methods by combining parental genotypes using general combining ability and specific combining ability.

While there are several approaches to the diallel analysis, Griffing's (1956) approach allows for the estimation of both the general and specific combining abilities. Breeders can determine genetic parameters, such as specific combining ability and general combining ability, about how well the parental varieties perform in relation to one another using the Griffing methodology. Genes exhibiting additive genetic effects are referred to as having general combiner ability, whereas dominant genetic effects are linked to specific combiner ability. The evidence regarding combining ability for the yield of seed cotton and its attributing traits helps in selecting suitable parents and promising cross combinations for a breeding program (Reddy et al., 2022). The researcher's efforts to identify parents for the creation of high-yielding hybrids are helped by studies on combining ability. Quantitative genetics is well aware of two types of combining ability specific and general. Breeders commonly utilize the ability to combine to identify and select suitable parental genotypes in order to large producer offspring of new combinations through hybridization. The objective of the study was the estimation of general and specific combining ability effect in upland cotton.

2 METERIAL AND METHOD

The study was conducted at the Department of Plant Breeding and Genetics at the University of Agriculture, Faisalabad, during the 2023 crop season. Five cotton lines (Tipo-1, C-1, FH-Super, CIM-600 and FH-444) were sown in pots in November 2022 in a controlled glasshouse environment. A 5 x 5 full diallel crossing was performed through hand emasculation in the evening and pollination the next morning. Self-pollination was also carried out for pure seed collection. Seeds from all crosses and parents were harvested separately and ginned for the next season's planting.

The following year, 25 crosses were sown in a randomized complete block design (RCBD) with two replications. Five plants per line were selected for data collection, with row-to-row distance of almost 75 cm and 30 cm of plant-to-plant spacing. Throughout the crop cycle, standard agronomic practices were followed.

Parents used in study

Tipo-1
C-1
FH-super
CIM-600
FH-444

Data were recorded for each individual plant when they reached maturity.

Morphological traits

The following methodology was used to collect and analyze the data for each character.

Plant height (cm)

Measured the height of five plants using a measuring tape. The plants were selected based on a standard criterion and their heights were recorded in centimeters from first node to apex when they had reached their final height.

Number of Monopodial Branches

From a row, a random sample of five mature plants were taken, and indirect fruit-bearing branches was recorded for each plant. The mean value was calculated for monopodial branches for data analysis.

Number of Sympodial Branches

Sympodial branches are the cotton plant's direct fruiting branches. When the selected plants matured, the sympodial branches on each plant were determined. For each replication, we calculated the average sympodial branches per plant.

Number of Bolls

The total number of bolls on five mature plants were counted at harvest. The mean value for number of bolls was calculated for data analysis.

Number of seeds per boll

The total seeds of five separately collected bolls were counted manually after ginning and the divided by 5. This was done for five plants from each row then average was taken to get single value from each row.

Seed Cotton Yield

An electric balance was used to measure the yield of seed cotton on an individual plant basis. Seed cotton was picked from five guarded plants and placed in separate bags. The average yield was calculated for further analysis.

Seed Index

From every plant, 100 seeds were selected at random. A balance was used to weigh the seeds, and the mean weight was computed. Then, additional analysis was conducted using this mean weight.

Boll Weight

By dividing the number of picked bolls from the total quantity of yield of seed, the average weight of the bolls was determined. For statistical analysis, the average boll weight from each plant in a row in each replication was determined.

Ginning out-turn Percentage (%)

Each genotype's seed cotton yield was processed at the ginnery using a single roller electrical ginning machine. Each sample's yielded lint weight was measured, and the supplied formula was used to calculate the lint percentage.

$$GOT\ \% = \frac{weight\ of\ lint}{weight\ of\ seed\ cotton} \times 100$$

Lint Index

The lint index is a metric used to determine the quantity of cotton fiber (known as lint) that can be obtained from a cottonseed. The higher the lint index, the more fiber can be extracted from the seed cotton, and the better the quality of the cotton. Lint index was calculated by using following formula.

$$lint\ index = \frac{seed\ index\ \times\ lint\%}{100 - lint\ \%}$$

Statistical Analysis

Collected data were subjected to statistical analysis for further examination (Steel et al. 1997), The diallel approach proposed by Griffing (Griffling, 1956) was used the estimation of combining ability effect.

3 RESULTS & DISCUSSION

To estimate the combining ability effects, analyses were performed on the data for all traits.

1: Number of Monopodial Branches

The analysis of variance for monopodial branches per plant revealed significant differences in general combining ability (GCA), specific combining ability (SCA), and reciprocal effects (RCA), indicating the influence of both additive and non-additive genetic interactions Table 1). The higher SCA variance compared to GCA suggests that non-additive gene action primarily drives genetic variability in this trait. Among the parents, C-1 and CIM-600 exhibited strong GCA, while the crosses Tipo-1 × C-1 and Tipo-1 × FH-super showed superior SCA effects (Table 2). Additionally, FH-444 × Tipo-1 demonstrated notable RCA effects. These findings align with previous research by Imran et al. (2011) and Khan et al. (2015), which also emphasized the role of gene interactions in determining monopodial branching.

2: Number of Sympodial Branches

This study highlights the significant influence of both general combining ability (GCA) and specific combining ability (SCA) on the number of sympodial branches in cotton, which are critical for flower and boll production. The predominance of SCA variance over GCA suggests that gene interactions play a more substantial role than individual gene effects (Table 2). Among the parent lines, Tipo-1 and FH-444 exhibited strong GCA, while the crosses C-1 × FH-super, FH-super × CIM-600, and CIM-600 × FH-444 demonstrated superior SCA effects. Additionally, reciprocal effects (REC) were notable in C-1 × Tipo-1 and FH-444 × CIM-600 (Table 1). These findings emphasize the importance of selecting parents with desirable GCA and identifying crosses with strong SCA effects to enhance cotton yield. The results align with previous studies, such as those by Raza et al. (2013).

Table 1: ANOVA for Combining Ability

SOV	MBPP	SBPP	NBPP	PH	BW	GOT	SPB	SCY	LI	SI
GCA	0.5607	4.2497	18.4823	306.7527	0.0763	5.9797	2.6136	79.6424	0.0589	0.259
SCA	0.5168	4.5874	8.5207	147.0276	0.1964	9.8783	1.881	21.939	0.1161	0.1337
REC	0.4506	2.5389	7.2958	92.5963	0.0744	8.6101	1.8191	28.9917	0.1406	0.2886

Table 2: The GCA, SCA and RCA effects of different cotton genotypes for various traits

Genotypes	Monopodial BPP	SBPP	No. BPP	Plant Height	Boll Weight	GOT%	SPB	SCY	LI	SI
Parents	GCA effect	GCA effect	GCA effect	GCA effect	GCA effect	GCA effect	GCA effect	GCA effect	GCA effect	GCA effect
Tipo-1	0.009 ns	0.687**	0.149*	1.323**	0.001^{ns}	-0.464**	0.537*	1.967**	-0.008 ns	0.219**
C-1	-0.286**	-0.893**	-1.686**	-6.697**	0.051^{ns}	0.241**	0.372 ns	-2.518**	0.002 ns	0.109*
FH-super	0.144 ns	0.197*	0.994**	0.893**	0.071^{ns}	-0.814*	-0.493*	0.857**	-0.113 *	-0.101 ns
CIM-600	-0.171 *	-0.438**	-1.031**	-3.472**	0.026^{ns}	1.196**	-0.588*	-3.383**	0.102 *	-0.051 ns
FH-444	0.304**	0.447**	1.574**	7.953**	-0.149**	-0.159^{ns}	0.172 ns	3.077**	0.017 ns	-0.176**
Direct crosses	SCA effect	SCA effect	SCA effect	SCA effect	SCA effect	SCA effect	SCA effect	SCA effect	SCA effect	SCA effect
Tipo-1 × C-1	-0.429*	-1.207**	-1.614**	-7.668**	-0.091^{ns}	-1.751**	-0.287 ns	-1.932**	0.233 *	-0.349**
Tipo-1 × FH-super	-0.209*	-1.297**	-0.969**	-2.533**	-0.286**	1.129**	1.253**	-0.232 ns	-0.277**	0.336**
Tipo-1 × CIM-600	-0.369 ns	-1.612**	-3.394**	-14.168**	-0.241**	-1.306**	-0.627 ns	-5.567**	-0.017 ns	0.211 ns
Tipo-1 × FH-444	0.681**	0.328 ns	1.401**	5.907**	0.234**	-2.076**	-1.587**	4.123**	0.343**	-0.164 ns
C-1 × FH-super	0.436**	1.233**	1.791**	4.687**	0.014^{ns}	0.999**	0.443 ns	1.753**	0.138 ns	-0.179 ns
C-1 × CIM-600	-0.274 ns	-0.057 ns	0.166 ns	1.877**	-0.091^{ns}	-0.461*	0.388 ns	0.068 ns	-0.127 ns	-0.054 ns
C-1 × FH-444	0.351*	0.983**	0.461**	3.252**	0.284**	1.619**	0.478 ns	1.083**	-0.142 ns	-0.104 ns
FH-super × CIM-600	0.396*	1.103**	2.336**	10.137**	0.214**	0.669**	-0.397 ns	2.318**	0.413 **	-0.244*
FH-super × FH-444	-0.079 ns	0.143 ns	-0.494**	-0.113 ns	-0.386**	-4.101**	-0.507 ns	-1.217**	-0.052 ns	0.081 ns
CIM-600 × FH-444	0.361*	1.178**	0.506**	0.652*	0.384**	0.414^{ns}	-0.262 ns	3.223**	-0.167 ns	0.031 ns
Indirect crosses	Reciprocal effects	Reciprocal effects	Reciprocal effects	Reciprocal effects	Reciprocal effects	Reciprocal effects	Reciprocal effects	Reciprocal effects	Reciprocal effects	Reciprocal effects
C-1 × Tipo-1	-0.15 ns	1.525**	2.025**	3.4**	-0.075^{ns}	2.05**	0 ns	4.475**	-0.225 ns	-0.475**
FH-super × Tipo-1	0.05 ns	-0.525*	-1.1**	-0.625 ns	-0.1^{ns}	2.025**	-1.625**	0.8**	-0.6 **	0.45**
CIM-600 × Tipo-1	0.375 ns	0.075 ns	0.05 ns	-0.925**	-0.05^{ns}	-2.45**	-0.2 ns	2.025**	-0.125 ns	0.475**
FH-444 × Tipo-1	-1.1**	-2.45**	-4.2**	-12.575**	0^{ns}	-2.875**	0 ns	-8.325**	0.3 *	-0.575**
FH-super × C-1	-0.25 ns	-0.525*	-1.025**	3.125**	0.05^{ns}	1.45**	2.1**	-2.5**	0.025 ns	-0.025 ns
CIM-600 × C-1	0.175 ns	0.25 ns	-0.125 ns	-0.6 ns	-0.1^{ns}	1.95**	0.25 ns	1.925**	-0.225 ns	-0.5**
FH-444 × C-1	-0.375 ns	-0.725**	-1.825**	-8.1**	0^{ns}	2.875**	-0.7 ns	-2.75**	-0.175 ns	0.075 ns
CIM-600 × FH-super	-0.075 ns	-0.2 ns	0.375*	0.05 ns	0.275**	1.875**	-0.8 ns	3.85**	0.05 ns	0.4**
FH-444 × FH-super	-0.275 ns	-0.175 ns	-1.25**	-6.225**	0.4**	0.95**	0.05 ns	-2.675**	0.2 ns	-0.2 ns
FH-444 × CIM-600	0.75**	1.775**	2.725**	13.325**	0.325**	1.375**	-0.9 ns	3.375**	-0.25 *	0.05 ns

3: Number of bolls per Plant

The analysis of variance for the number of bolls per plant revealed highly significant effects for general combining ability (GCA), specific combining ability (SCA), and reciprocal effects (RCA), highlighting the importance of both additive and non-additive genetic influences (Table 1). However, the predominance of SCA variance over GCA variance indicates that non-additive gene action plays a more significant role in determining this trait. Among the parent lines, FH-444 and FH-super exhibited strong GCA, while the crosses C-1 × FH-super and Tipo-1 × FH-444 demonstrated superior SCA effects (Table 2). Additionally, the hybrids C-1 × Tipo-1 and FH-444 × CIM-600 showed notable RCA effects. The mean value graph identified FH-444 × Tipo-1 as the cross with the highest number of bolls per plant. These findings suggest that breeding programs should focus on selecting specific parental combinations to exploit significant SCA effects for yield improvement. The results align with previous studies by Cicek and Kanyak (2007) and Deosarkar et al. (2014), which also emphasized the role of genetic interactions in boll production.

4: Plant Height

The analysis of variance for plant height revealed significant effects of general combining ability (GCA), specific combining ability (SCA), and reciprocal effects (RCA), indicating strong genetic control and interaction effects. The predominance of SCA variance over GCA variance suggests that non-additive gene action plays a key role in plant height variability (Table 2). Among the parents, FH-444 and Tipo-1 exhibited strong GCA, while the crosses FH-super × CIM-600, Tipo-1 × FH-444, and C-1 × FH-super demonstrated superior SCA effects. Additionally, FH-444 × CIM-600 and C-1 × Tipo-1 showed significant RCA effects. The mean value graph identified FH-444 × Tipo-1 as the tallest cross (Table. 1).

Variations in plant height among genotypes and crosses were attributed to genetic differences and genotype-environment interactions. While taller plants may enhance boll production, a moderate plant height is generally preferred in breeding to prevent lodging and ensure timely maturity. These findings align with previous studies by Ekıncı and Basbag (2018) and Islam et al. (2001), which also emphasized the genetic significance of plant height.

5: Boll Weight

The analysis indicates that boll weight is significantly influenced by both additive (GCA) and non-additive (SCA) genetic effects, along with reciprocal effects (RCA) (Table 1). However, the dominance of SCA variance over GCA variance suggests that non-additive gene action plays a more crucial role in determining boll weight. This implies that breeders should focus on specific hybrid combinations rather than solely selecting high-performing parental lines (Table 2). Among the parents, FH-444 exhibited a negatively significant GCA for boll weight. The crosses Tipo-1 × FH-444, C-1 × FH-444, and CIM-600 × FH-444 demonstrated strong SCA effects, while FH-444 × FH-super and FH-444 × CIM-600 showed significant RCA effects. The mean value graph identified FH-super × CIM-600 as the cross with the highest boll weight. These findings align with the conclusions of Javaid et al. (2014), reinforcing the importance of non-additive genetic interactions in breeding programs aimed at improving boll weight.

6: Ginning out turn%

The analysis reveals that ginning out turn percentage (GOT%) is significantly influenced by general combining ability (GCA), specific combining ability (SCA), and reciprocal effects (RCA), indicating strong genetic control and interaction effects (Table 1). The predominance of SCA variance over GCA variance suggests that non-additive gene interactions play a more significant role in determining GOT% in this cotton diallel population. Among the parents, CIM-600 and C-1 exhibited favorable GCA, while the crosses Tipo-1 × FH-super and C-1 × FH-444 demonstrated strong SCA effects. Significant RCA effects were observed in C-1 × Tipo-1, FH-super × Tipo-1, and FH-444 × CIM-600 (Table 2). The mean value graph identified C-1 × FH-444 as the cross with the highest GOT%. While genetic factors predominantly influenced GOT%, environmental conditions may also play a role in the observed variations. These findings align with previous studies by Lakho et al. (2016) and Kaleem et al. (2016), which similarly highlighted the importance of genetic interactions in determining GOT%.

7: Number of Seeds per Boll

The study identified significant variation in the number of seeds per boll among different cotton varieties, prompting a combining ability analysis. The results showed highly significant effects for general combining ability (GCA), specific combining ability (SCA), and reciprocal combining ability (RCA), indicating strong genetic control over this trait (Table 1). The dominance of SCA variance over GCA variance suggests that non-additive gene interactions play a more substantial role in determining seed number per boll. Among the parent lines, Tipo-1 exhibited strong GCA, while the cross Tipo-1 × FH-super demonstrated superior SCA effects (Table 2). Additionally, FH-super × C-1 showed significant RCA effects. The mean value graph identified FH-super × Tipo-1 as the cross with the highest number of seeds per boll. While environmental factors may influence these results, the observed genetic variability highlights the importance of selecting appropriate parental lines and hybrids for breeding programs. These findings align with previous research on seed cotton yield components, including boll weight and seed index, as reported by Khakwani et al. (2022).

8: Seed Cotton Yield

The study identified significant differences in seed cotton yield among the evaluated varieties, leading to a detailed combining ability analysis. The results highlighted the substantial influence of general combining ability (GCA), specific combining ability (SCA), and reciprocal combining ability (RCA), confirming strong genetic control over yield (Table 1). The predominance of SCA variance over GCA variance suggests that non-additive gene interactions play a more critical role in determining seed cotton yield. Among the parents, FH-444 and Tipo-1 exhibited strong GCA effects, while the crosses Tipo-1 × FH-444, FH-super × CIM-600, and CIM-600 × FH-444 demonstrated superior SCA effects (Table 2). Significant RCA effects were observed in C-1 × Tipo-1, CIM-600 × FH-444, and FH-super × CIM-600. The mean value graph identified FH-444 × Tipo-1 as the highest-yielding cross. While environmental factors may influence yield performance, the genetic aptitude of each parent and cross, as indicated by GCA and SCA values, plays a crucial role in breeding programs. These findings are consistent with those of Cicek and Kanyak (2007), further validating the observed genetic trends.

9: Lint Index

The study identified significant variations in lint index among the evaluated varieties, leading to a comprehensive combining ability analysis. The results demonstrated the substantial influence of general combining ability (GCA), specific combining ability (SCA), and reciprocal combining ability (RCA), indicating strong genetic control over lint index (Table. 1). The predominance of SCA variance over GCA variance suggests that non-additive gene interactions play a more significant role in determining this trait. Among the parents, CIM-600 exhibited strong GCA effects, while the crosses FH-super × CIM-600 and Tipo-1 × FH-444 showed superior SCA effects (Table 2). Significant RCA effects were observed in FH-444 × Tipo-1. The mean value graph identified Tipo-1 × FH-444 as the highest-performing cross for lint index. These findings suggest that selecting specific hybrid combinations may be more effective in improving lint index than relying solely on parental performance. The results are consistent with those reported by Huangjun et al. (2011), further validating the observed genetic trends.

10: Seed Index

The higher SCA variance compared to GCA variance suggests that hybrid combinations are more influential in determining seed index than the parental lines themselves (Table 1). Among the parental genotypes, Tipo-1 and C-1 exhibited strong general combining ability (GCA) for seed index, whereas the cross Tipo-1 × FH-super demonstrated superior specific combining ability (SCA). Reciprocal combining ability (RCA) was significantly observed in the hybrids FH-super × Tipo-1 and CIM-600 × Tipo-1 (Table. 2). These findings align with the results reported by Kumar et al. (2014), reinforcing the genetic basis of seed index and its predominantly non-additive inheritance. Breeding programs aiming to improve seed index should focus on hybrid combinations with strong SCA effects rather than solely on the parental performance.

Conclusion

Cotton (*Gossypium hirsutum* L.) is a globally important fiber crop that contributes significantly to the agricultural economy and livelihoods of farmers. The selection of superior parents and their hybrid combinations is crucial for breeding programs aimed at improving cotton productivity. Diallel analysis has been extensively used to evaluate parental genotypes and hybrid crosses, enabling breeders to select the best-performing combinations for yield and fiber quality enhancement. A 5×5 full diallel mating design was used to generate 25 crosses during this research which, along with the parental genotypes, were evaluated and data were recorded for various agronomic traits. The data were analyzed using Griffing's approach, which estimated general combining ability (GCA), specific combining ability (SCA), and reciprocal combining ability (RCA). The findings revealed that the parental genotypes FH-444, CIM-600, and Tipo-1 exhibited superior GCA, indicating their potential as good combiners for hybrid development. Crosses such as Tipo-1 × C-1, Tipo-1 × FH-444, and C-1 × FH-444 displayed high SCA, highlighting their hybrid vigor for yield traits. Additionally, reciprocal effects were significant for crosses like FH-Super × Tipo-1, FH-444 × CIM-600, and FH-444 × CIM-600, suggesting the influence of maternal inheritance. The results demonstrated that dominance gene action played a major role in controlling most traits, emphasizing the importance of non-additive genetic effects in hybrid breeding. These findings provide valuable insights for cotton breeders, helping those select high-performing parental lines and hybrid combinations for future breeding programs aimed at enhancing cotton yield and fiber quality.

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