ISSN: 2458-8989

Natural and Engineering Sciences

NESciences, 2025, 10 (2): 495-509 doi: 10.28978/nesciences.1740074

Nature In Inheritance of Yield and Its Components in Different Mating Designs of Cotton Genotypes (Gossypium Hirsutum L.)

Dawood Salman Madab [1], Hussein Ali Hindi [2], Yaseen Obaid Noori Ahmed Sharif [3*], Tariq Raad Thaer Al-Mafarji [4]

[1] Department of Field Crops, College of Agriculture, Tikrit University, Tikrit, Iraq. E-mail: dawoodobaidy@tu.edu.iq

[2] Department of Field Crops, College of Agriculture, Tikrit University, Tikrit, Iraq. E-mail: husseinali@tu.edu.iq

[3*] Department of Field Crops, College of Agriculture, Kirkuk University, Kirkuk, Iraq. E-mail: yaseenobaidnoori@uokirkuk.edu.iq

[4] Department of Medicinal and Industrial Plants, College of Medicinal and Industrial Plants, University of Kirkuk, Kirkuk, Iraq. E-mail: tariqraad@uokirkuk.edu.iq

Abstract

Eight lines of cotton (IK, Lashata, Pac Kot 189, Ceebro, Coocker310, W888, Dise and Montana) were conducted in a field farm in the Baghdad Governorate using a half-and-partial diallel cross design to examine the genetic behavior of cotton seeds and their constituent features. (33.05N latitude, 44.32E longitude). A randomized Complete Block Design with three replicates was used for a comparison experiment for studying plant height, vegetative branches, fruiting branches, ball numbers, ball weight and single plant yield. Results concise: Significant changes were found in all examined characteristics of the yield of cotton and its constituent parts between parents and hybrids, as well as between parents and hybrids included in the research. Parent Coocker310, and its hybrids Pac Kot189*Coocker310, superior in terms of cotton output per plant, along with additional yield components, in addition to hybrid Dise*Montana Pac Kot189*Dise, W888*Dise, and 7*8, Dise*Montana demonstrating a significant superiority in hybrid vigor for yield trait compared to best parental lines. Partitioning of these differences into their components revealed a significant genetic effect of its components, reflected by the unique combining abilities of the hybrid on cross as well as the general combining capacity of parents. Dise, Cooker310, and Pac Kot189 show strong compatibility in addition to the hybrids' supremacy. Dise*Montana and Packot189*Coocker310 have a unique combination of abilities with lint yield and a few of its additional components. Both general and particular combining skills are important for yield, but specific combining skills are more important. As a result, dominance variances are more significant

*Corresponding Author: Yaseen Obaid Noori Ahmed Sharif, E-mail: yaseenobaidnoori@uokirkuk.edu.iq

compared to additive variances, with a dominance degree greater than one in traits of cotton yield and its components. This was reflected in reduced narrow-sense heritability of studied traits, as determined by the half-diallel crossing system. Even while additive gene effects predominated and narrow-sense heritability was present in both the number of branches that fruit and ball weight, in addition to plant production, the partial diallel technique of estimating genetic parameters revealed the significance of additive and dominant effects. Spearman's correlation estimates demonstrated a negative relationship between half diallel crossing method and partial diallel crossing method in two most important genetic parameters: general combining ability variance and heritability in narrow sense (-0.25 and -0.92 respectively), despite the first's lack of importance, suggesting a variation in the additive form of gene activity that is used to suggest the best breeding strategy. Therefore, the results of the partial diallel crossing method cannot be substituted as an alternative to the half diallel crossing method. Pac Koot 189 parent can be considered as donor parents, which showed superiority in single plant yield and its components in half and partial diallel methods, as well as in their promising hybrid (Pac Koot189*Coocke310), which needs to be evaluated in early segregating generations.

Keywords:

Cotton, genotypes, half diallel, partial diallel.

Article history:

Received: 21/04/2025, Revised: 23/05/2025, Accepted: 05/07/2025, Available online: 30/08/2025

Introduction

Cotton yield contributes about 85% of the natural fiber textile industry and has the best technical properties among other natural fibers. Diallel mating design has made a significant contribution to improving and increasing seed and cotton yields of American cotton cultivars through the utilization and selection of promising genotypes (Bourgou et al., 2022). Crossing among cotton genotypes creates opportunities for diversity existence of new genotypes carrying parental desired traits. Despite the preponderance of nonadditive types of gene action and the fact that other genotypes were better combiners than others, the half diallel pairing-up design is a good technique that is frequently used in the initiation, along with the assessment of new gene combinations. This can be seen through the estimation of genetic parameters (GCA and then SCA effects) on the yield of seed cotton and its quality. (Moiana et al, 2021, and Al-Jubouri & Madab, 2024; Mohammed, 2016). The degree of diversity resulting from different parental lines that might create attractive segregating lines determines the effectiveness of boosting seed cotton production and the components of crosses. (Shaker et al, 2016). Although the majority of nonadditive gene action & many parents and crossings were better for the yield of seed cotton per plant, both additive & nonadditive gene action had a significant impact on seed cotton yield components. (Nimbal et al, 2019;). Despite being a crucial selection process in early segregate generations due to high additive variations in seed cotton production, heritability in the narrow sense is a good signal for additive kinds of gene action, which varied from 0.07 to 0.48 in seed the cotton yield (Nayak & Raghatate, 2024; Far, 2017). one plant and one hundred seed weight (Efe and Gencer, 1998; Krishnan & Iyer, 2024).

Physiological activities controlled by gene expression which differ according to their combinations and independent segregation however, While other characteristics (seed cotton yields, lint yield, and ball weight) were governed by dominant gene activity, lint percentage demonstrated the significance of additive gene action (Queiruz et al, 2017; Kumar et al., 2017) .Except for plant height and the monopodial area, which are regulated by recessive genes, (Khan & Hassan, 2011; Uzakbaeva & Ajiev, 2022) discuss the significance of dominant genes and have high levels of heritability in both wide and narrow senses of the percentage of lint and lint yield. Due to strong GCA and SCA effects, the majority of seed cotton yield characteristics showed both additive and dominant effects. (El-Aref et al., 2019). Aside from partial dominance, breeding value is an insignificant genetic signal in breeding programs that correlates with additive gene action that controls the number of balls and the percentage of lint. Overdominance, on the other hand, controls the yield of seed cotton. (Eknici and Basbag,2018; Vasconcelos et al., 2018; Abo Sen et al, 2022). Significant cotton cross heterosis indicates genetic capacity in production and describes the dominant and additive forms of gene activity that regulate seed cotton output and its constituent parts (Khokhar et al., 2018).

Partial diallel abbreviated fort involves a relatively large number of parents in the mating design, compared to other crossing systems. Comparative study of calculating genetic parameters by different methods for the same crop has a great value in breeding programs (Viana et al., 1999)

In this work, the genetic development of the seed cotton crop and its components half and partial dialed mated design will be examined.

Materials and Methods

To investigate the nature of inheritance, growth, and seed cotton yield features, eight parents (as shown in Table 1) were employed in a half diallel along with a partial mating design (Efe & Gencer, 1998). Then, conducted field comparison studies in the Baghdad Governorate's field farm between parents and their F1s using a complete block design randomized to each participant with three replicates. (33.05N latitude, 44.32E longitude). Cotton seeds were grown in 70 and 15 cm of inter and intra hill distances. Nitrogen and phosphorus fertilizers were added by 150 and 50 kg ha-1 as N (Al-Juheishy & Al-Layla, 2018). and P_2O_5, respectively, with splitting Nitrogen in two doses (Kumbhar et al., 2008; Sharif et al., 2024a). Other agricultural practices are applied according to plant needs. Seed cotton yield is harvested annually at the end of the season. Ten plants of randomly sampled plants were taken to study plant height (cm), vegetative branches, fruiting branches, quantity of balls, ball weight, and cotton production from a single plant seed (Tarek & Abood, 2014). The Griffing methods II approach (fixed model) was used to do statistical and molecular evaluation of a half diallel mating design (Sen et al., 2022). The analysis for the half diallel mating design was conducted by (Singh & Chaudhry, 2017) Genetic parameters: hybrid vigor, GCA effects, SCA effects, GCA variances, SCA variances, variance GCA/SCA, The characteristics that showed significant differences were calculated using the following metrics: average degrees of dominance ($\bar{a}$), phenotypic variance ($\sigma 2P$), environmental variance, dominance variation ($\sigma 2D$), genotypic variation ($\sigma 2G$), additive variance ($\sigma 2A$), and heritability in a limited sense (H2ns). Additionally, the final genetic factors and the parents' GCA impacts were calculated using the partial diallel technique. The correlations among genetic parameters in the half and partial diallel method were compared by using the Spearman correlation coefficient estimated by using the following equation:

$$rs=1-(\sum di^2)/(n(n-1))\text{……………}(1)$$

Based on the rankings of the provided coefficients following ranking is assumed, assuming that the impact does not follow the distribution of normality, as indicated by El-Hashash and Shiekh (2022). SAS V.9 and Excel software were used in the analysis of variance, mean comparison, and other statistical analyses.

The limits of heritability in the narrow sense, according to Al-Adhari (1987), are: less than 20% is low, from 20% to 50% is moderate, and more than 50% is high. The expected genetic advance (E.G.A) is calculated using the one that follows formula as the percentage of the trait's total average (Singh and Chaudhry, 2017).

.E.G.A = (G.A) / (X-) × 100 …………………….. (2)

E.G.A. stands for anticipated genetic improvement expressed as a percentage of the trait's overall average.

G.A.: Stands for the anticipated genetic advancement.

$\bar{X}$: Denotes the trait's average.

The ranges for the anticipated genetic improvement put out by Agarwal & Ahmed (1982) were accepted. (less than 10% low, between 10%-30% moderate, and more than 30% high).

Table 1. Origin of cotton genotypes

No.	Genotypes	Origin
1	IK259	Greece
2	Lashata	Aspain
3	Pac-cot	USA
4	Cebro8886	Greece
5	Cocker310	USA
6	W888	USA
7	Dise	USA
8	Montana	USA

Results and Discussion

The findings of Table 2, which displays the mean squares for the qualities being examined, demonstrate that, for all traits examined, the impact of genetic genotypes was significant at an acceptable probability threshold of 0.01. This means there is variability in the performance of genetic genotypes (36 genotypes) due to differences in their genetic behavior based on genes present in these genotypes. Furthermore, this result allows us to partition genetic differences into their components according to the genetic analysis method used in the study. For all traits under study, the Kruskal-Wallis analysis results in Table 3 also demonstrated the significance as well as the significance of the parents' general combining ability and the hybrids' specific combining ability, highlighting the role of dominance and additive genetic effects in regulating the traits under study. The presence of genetic heterogeneity in the genotypes of cotton under study is shown by the hybrids' higher performance and the parents' capacity to combine. These findings concur with those of (Ekıncı & Basbag, 2018; Sharif et al., 2024b; Alagarsamy, 2024).

Table 2. Mean squares of studied traits

S.O.V.	d.f.	M.S					
		PH	VB	FB	BP	BW	SY
Rep.	2	299.95	10.86	25.98	16.86	2.98	1032.37
Genotypes	35	1198.94**	4.73**	51.64**	81.15**	1.22**	592.52**
Parents	7	947.05**	2.61**	1.53**	11**	1.93**	522.41**
Crosses	27	162.4**	0.35**	2.16**	0.83**	0.32**	79.54**
Crosses vs. Parents	1	328973.2**	371.77**	7092.83**	6903.52**	244.2**	50681.75**
Due to GCA	7	2461.98**	6.12**	20.3**	70.94**	1.75**	562.32**
Due to SCA	27	883.18**	4.38**	59.47**	83.7**	1.09**	600.07**
Error	70	150.42	0.4	1.94	0.7	0.31	64.46

VB: vegetative branches, PH: plant height (cm). FB: fruiting branches, Plant 1 BP: each plant has balls, SY: one plant's yield (g), BW: ball weight (g).

The variation in genotypes is the foundation upon which the analysis of the genetic behaviour of these traits in the lineage is built. The genotype P5 recorded the highest rates for height of the plant (132.49 cm), number of fruits branches (12.45), the amount of balls each plant (11.33 the ball plant-1), mean weight of each ball (5.29 grams), as well particularly high mean yield of cotton per plant (59.77 g), according to Table (3), which shows differences in the parents' averages at a level of significance of 0.05 for all traits examined. In the meantime, the genotype P7 had the largest mean number of vegetative branches (2.96 vegetative branches per plant) compared to other genotypes. This is attributed to differences in genetic genotypes regarding studied traits, based on their genetic variance resulting from the differences in the genes present in these genotypes. Genotype P5 performed the best as it provided the highest means for key traits under study, and it is possible to benefit from this parent in transferring its traits to the following hybrids. These results are in agreement with (Dawod & Al-Guboory, 2012; Sarteb & Mohammed, 2023; Al-Mafarji & Al-Jubouri, 2023).

Table 3. Means of traits in parental lines

Genotypes	PH	VB	FB	BP	BW	SY
P1	92.46	2.3	9.63	9.97	2.73	27.35
P2	77.33	1.763	10.2	8.67	3.84	33.41
P3	98.1	2.877	7.15	5.79	3.48	20.53
P4	78.1	0.7	8.49	6.9	3.25	22.51
P5	132.49	0.71	12.45	11.33	5.29	59.77
P6	85.73	1.11	7.94	6.84	2.88	20.01
P7	82.7	2.96	9.37	6.35	3.43	22.12
P8	92.2	2.53	10.47	8.33	3.1	26.23
LSD(0.05)	18.53	0.942	2.18	0.85	0.84	6.42

It can be seen from Table 4, which displays the arithmetic means of the twenty-eight hybrids for the characteristics under study, that hybrid 1*5 had the greatest mean for the plant height trait (143 cm), while hybrid 3*7 recorded the lowest mean for the same trait (73.6 cm). This is attributed to the compatibility of parent 5 with other parents, which resulted in the highest mean for this trait and its inheritance to its hybrid 1*5. It is noted that the shortest plant was hybrid 3*7, which produced the highest rate of vegetative branches (5.18) per plant and showed no discernible differences between hybrids 1*7 and 4*8. This may be attributed to the segregation effect of growth nature in parents, characterized by taller plants and more vegetative branches. Hybrid 3*5 achieved the highest rate for the trait of fruiting branches (22.46) per plant, while the lowest mean for this trait (7.75) was recorded in hybrid 5*8. This is explained by the fact that parent 5 gave its hybrid 3*5 the greatest average for this characteristic. Additionally, it is observed that the highest rate of balls per plant (25.63 and 26.11) was recorded for hybrids 7*8 and 3*5, respectively. This is attributed to parents 7 and 5 achieving the highest mean in number of balls per plant (Table 3), allowing them to transfer this trait to their hybrids.

The hybrids varied in the trait of ball weight, with their values increasing in hybrids 1*5, 1*7, 2*4, 2*5, 3*8, and 4*7, which were 3.65, 4.04, 4.29, 3.54, 3.59, and 3.37 g, respectively. This is primarily due to the ability of the parents to pass on part of their genetics to the offspring, leading to superiority of some hybrids over their parents. Hybrid 3*5 excelled in the trait of cotton yield per plant, generating 69.69 g plant-1, & showed no discernible differences from the 3*7, 6*7, and 7*8 hybrids. The hybrid's superiority in both secondary yield parameters (number of branches that fruit per plant) and other yield factors (number of pods per plant) (Table 4) is responsible for this improvement in final cotton output. The hybrid 3*5 outperforms the others in terms of plant height and key yield indicators, such as the quantity of branches that fruit and pods per plant. They concur with the findings of (Abo Sena et al., 2022; Al-Guboory, 2016).

Table 4. Half diallel crosses of the studied traits

Genotypes	PH	VB	FB	BP	BW	SY
1*2	101.13	2.167	12.89	8.667	2.703	23.561
1*3	129.5	3.367	12.44	14.6	2.87	42.1
1*4	90.26	2.667	13.067	11.077	3.287	36.485
1*5	143	2.067	8.12	7.357	3.65	26.832
1*6	98.467	3.557	8.627	7.493	2.66	20.065
1*7	108.6	4.417	9.66	5.627	4.047	22.435
1*8	90.933	3.71	16.48	10.72	2.84	30.54
2*3	78.133	1.457	9.973	8.857	2.987	26.659
2*4	105.8	2.807	8.663	6.3	4.293	28.435
2*5	87.133	3.533	13.043	11.333	3.543	40.782
2*6	80.267	3.367	14.047	10.37	2.81	28.932
2*7	96.8	2.967	7.963	12.093	3.29	39.558
2*8	88.8	1.76	15.28	11.8	3.59	42.96
3*4	81.067	2.513	17.197	8.857	2.38	21.14
3*5	135.533	2.05	22.467	25.633	2.72	69.697
3*6	117.667	3.647	16.437	16.48	2.79	46.093
3*7	73.6	5.187	19.43	18.8	3.133	59.38
3*8	113.867	2.26	12.18	10.04	2.14	21.46
4*5	82.933	1.09	8.91	12.26	2.23	27.196
4*6	79.6	3.707	11.88	7.78	2.593	20.264
4*7	77.6	0.91	16.977	12.383	3.377	42.373
4*8	84.533	4.35	8.92	12.13	2.77	33.43
5*6	133.8	0.573	16.617	16.317	2.867	47.149
5*7	79.6	4.553	10.473	8.57	2.833	24.786
5*8	77.6	3.53	7.75	10.38	2.19	22.75
6*7	84.533	4.467	8.347	22.17	2.557	57.089
6*8	125.633	0.95	19.49	17.79	2.51	45.13
7*8	79.6	4.123	20.2	26.11	2.49	64.5
LSD(0.05)	20.91	0.97	2.41	1.49	0.94	14.64

(Table 7) shows hybrid vigor according to the first generation's departure from the finest parents. There was positive and extremely significant hybrid vigor in the 1*3, 2*4, and 6*8 hybrids. (24.24, 26.18, and 26.61 respectively) for the trait of plant height. In contrast, hybrid vigor was negative and highly significant for hybrids 2*5, 3*7, 4*5, 5*7, and 5*8. This indicates that hybrids with positive hybrid vigor can be utilized in suitable varieties for mechanical harvesting, while those with negative hybrid vigor can help reduce plant height, making this trait more suitable for mechanical harvesting. Therefore, stronger genetic composition can be formed over consecutive isolating generations if the attribute corresponds with the plant's development direction, as long as both parents have a generic combining capacity in the same direction. The lack of significance in hybrid vigor for most hybrids highlights importance of certain hybrids, such as 6*8 and 1*3, in direction of increasing plant size and suitability for mechanical harvesting, while most other hybrids tend to be shorter, indicating their suitability for producing shorter varieties more appropriate for mechanical harvesting, The total number of vegetal branches is a desired feature for cotton breeders, and hybrid 2*3, 4*7, and 6*8 showed negative and extremely significant hybrid vigor about this trait. If the majority of these hybrids produce more fruiting branches than vegetative branches, they may be advantageous. While hybrids 1*8 and 2*4 were significant, hybrid (1*6, 1*7, 2*5, 2*6, 3*7, 4*6, 4*8, 5*7, 6*7, and 7*8) demonstrated strong and substantial positive hybrid vigor for the number of vegetative branches in the plant. High and substantial positive hybrid vigor suggests that the cumulative impacts of trait-controlling genes produced the result.

In terms of the quantity of fruiting branches, the majority of hybrids showed positive and extremely significant hybrid vigor (1*8, 2*5, 2*6, 2*8, 3*4, 3*5, 3*6, 3*7, 4*6, 4*7, 4*8, 5*6, 6*7, 6*8, and 7*8), while hybrids 1*5, 1*6, and 1*7 The majority of hybrids that demonstrated significant and beneficial hybrid vigor in number of fruiting branches had more bolls per plant, which is one of the most important traits for cotton breeders because a decrease in this trait leads to a higher in the single yield of cotton plants. The majority of hybrids that displayed significant hybrid vigor in important yield components (the number of producing fruit branches along with the number of bolls per plant) and had lower plant height performed significantly with positive hybrid vigor for cotton yield per plant. Additionally, the positive as well as highly significant hybrid vigor amounts indicate additive effects, which were controlling the desired trait (1*3, 3*6, 3*7, 4*7, 5*7, 6*7, 6*8, and 7*8). The variation and difference in hybrid vigor are due to the variability of parental traits used in the study, as they differ in their morphological characteristics and branching nature. This indicates the efficiency of hybrids in directing their growth towards flowering, which was reflected in increased final yield of cotton flowers. It is possible to benefit from hybrids with high positive significant hybrid vigor in segregation generations through selection techniques for the trait of single plant yield. These findings concur with those of (Ekıncı & Basbag, 2018; Khokhar et al., 2018; Al-Mafarji & Al-Jubouri, 2023; Al-Jubouri & Madab, 2024). Shown in Table 5.

Table 5. Heterbeloties percentage in half diallel crosses

	Traits					
Crosses	**PH**	**VB**	**FB**	**BP**	**BW**	**SY**
1*2	8.57ns	-6.13 ns	3.41 ns	-51.03**	-42.06 **	-41.8 ns
1*3	24.24**	14.55 ns	-0.08 ns	31.71**	-21.25 ns	35.03*
1*4	-2.42 ns	13.76 ns	4.72 ns	9.99 ns	1.12 ns	25.03 ns
1*5	7.34 ns	-11.27 ns	-53.32**	-54**	-44.93**	-122.75**
1*6	6.1 ns	35.33*	-44.31**	-33.05**	-8.27 ns	-36.3 ns
1*7	14.86 ns	32.98**	-28.88**	-77.18**	15.24 ns	-21.9 ns
1*8	-1.67 ns	31.8*	24.45**	6.99 ns	-9.15 ns	10.44 ns
2*3	-2.55 ns	-97.46**	-2.27 ns	2.11 ns	-28.55 ns	-25.32 ns
2*4	26.18**	37.19*	-17.74 ns	-37.61**	10.55 ns	-17.49 ns
2*5	-52.05**	50.09**	21.79**	0.002 ns	-49.3**	-46.55**
2*6	-6.8 ns	47.63**	27.38**	16.39**	-36.65*	-15.47 ns
2*7	14.56 ns	0.7 ns	-28.09	28.8**	-16.71 ns	15.54 ns
2*8	-3.82 ns	-24.85 ns	31.47**	26.52**	-6.96 ns	22.22 ns
3*4	-21.01 ns	-14.48 ns	50.63**	22.09**	-46.21**	-6.48 ns
3*5	2.24 ns	-40.34 ns	57.13**	55.79**	-94.48**	14.24 ns
3*6	16.62 ns	21.11 ns	51.69**	58.49**	-24.73 ns	55.45**
3*7	-33.28**	42.93**	51.77**	66.22**	-11.07 ns	62.74**
3*8	13.84 ns	-27.3 ns	14.03ns	17.03**	-62.61**	-22.22
4*5	-59.75**	34.86 ns	-8.08 ns	7.58 ns	-137.21**	-119.77**
4*6	-7.67 ns	70.05**	28.53**	11.31 ns	-25.33 ns	-11.08 ns
4*7	-6.57 ns	-225.27**	44.8**	44.27**	-1.56 ns	46.87**
4*8	-9 ns	41.83**	-17.37 ns	31.32**	-17.32 ns	21.53 ns
5*6	0.97 ns	-93.71 **	42.04**	30.56**	-84.51**	26.76 ns
5*7	-66.44**	34.98**	8.04 ns	-32.2**	-86.72**	141.14**
5*8	-70.73**	28.32 ns	-35.09**	-9.15 ns	-141.55**	-162.72**
6*7	-1.41 ns	33.73**	-12.25 ns	69.14**	-34.14 ns	61.25**
6*8	26.61**	-166.31**	46.28**	25.07**	-23.5 ns	41.87**
7*8	-15.82ns	28.2**	48.16**	68.09**	-37.75*	59.33**
S.E.	10.01	0.51	1.15	0.68	0.45	6.55

The parents used in study were divided into two groups: first group showed a general positive and significant ability for plant height (8.05 and 5.92 for parents 1 and 3 respectively), while the general ability was negative for other parents (Table 3) This suggests a tendency for kids to inherit the characteristic of shortness, as the majority of parents have genes that diminish plant height. This means that the trait of the height of their plants is controlled by the additive influence of genes. With values of 0.23, 0.20, 0.83, and 0.15, respectively, the parents P1, P3, P7, and P8 showed a positive and substantial effect of general combining ability on the trait of the number of green branches in the plant. For parenting p2 (-0.26), p4 (-0.47), p5 (-0.53), and p6 (-0.16), on the other hand, it was considerably negative, suggesting that the non-additive genetic activity of genes controls the remaining parents (p1, p3, p7, and p8). With respective values of 1.36 and 1.04, parental p3 and p8 had a positive, generally combined effect on the trait of the number of fruiting branches, suggesting that they carried genes that markedly boosted the number of fruiting branches in the plant. However, other parents (p1, p4, and p5) had significantly unfavourable effects, with respective values of -0.85, -0.82, and -0.41. Because the influence of general ability to combine was positive and substantial in parents, the trait of the number of bolls in the plant behaved slightly differently than the trait of the number of fruiting branches p3 (1.08), p5 (1.04), p6 (6.8), p7 (1.44), and p8 (1.16), while it was negative in remaining parents. This indicates the genetic potential of parents to increase the number of flowers in cotton plants, either by increasing the number of fruiting branches that bear flowers or by increasing the flowers on the same fruiting branch under the influence of general combining ability, which signifies the additive effect of genes. As for the trait of boll weight, the parents did not show important effects except in P2 and P7. Table 6 shows single plant yield, significant GCA impacts in p3, p5, and p7 relate to combiner ability brought about by additive gene activity. These findings concur with those of (Moiana et al., 2021; Ekıncı & Basbag, 2018; Nimbal Sagar et al., 2019; Shaker et al., 2016; Al-Mafarji et al., 2024; Bourgou et al., 2022).

Table 6. GCA effects of diallel cross

Genotypes	PH	VB	FB	BP	BW	SY
P1	8.05	0.23	-0.44	-1.85	-0.002	-5.42
P2	-7.35	-0.26	-0.85	-1.72	0.33	-1.32
P3	5.92	0.2	1.36	1.08	-0.15	1.66
P4	-10.82	-0.47	-0.82	-1.94	-0.01	-5.65
P5	-13.83	-0.53	-0.41	1.04	-0.3	6.78
P6	-2.52	-0.16	0.04	0.8	-0.29	-0.61
P7	-10.05	0.83	0.09	1.44	0.1	4.34
P8	-2.09	0.15	1.04	1.16	-0.27	0.23
S.E.(gi)	2.09	0.1	0.24	0.14	0.09	1.37

Table 7 shows that the overall height from hybrid 1*3, 1*4, 1*7, 2*4, 2*7, 3*5, 3*8, 4*8, and 6*8 increased greatly as a result of the specialised combining ability for single hybrids. However, with hybrid 1*3, 2*3, 2*7, 2*8, 3*5, 3*8, 4*7, 5*6, and 6*8, the influence of specialized combining capacity was significantly unfavorable and undesirable for the characteristic of the number of green branches. This indicates the genetic potential of resulting hybrids to reduce both plant height on one hand and green branches on the other, which may drive the plant's energy towards increasing fruiting branches and final yield. In terms of important qualities like the number of fruiting branches, bolls per plant, and yield per plant for the first hybrid, in addition to the number of bolls per plant & yield per plant for the second hybrid, the hybrids 3*5 & 7*8 demonstrated a unique individual capacity. We determined that hybrid 2*8 offered a desirable specific ability to combine in terms of the number of fruit branches, the number of bolls per plant, the mean weight of each boll, as well as single plant yield. In terms of height of the plant, number of fruit and vegetative branches, along with single plant yield, hybrid 3*5 came in second, and hybrid 7*8 came in third, as well as yield per plant. Cotton hybrids' superior specific combining ability is ascribed to the relative performance of cross combinations compared to their parents. This is because specific combining ability indicates a strong influence of the hybridization along with complementary inherited action among superior hybrid parents, reflecting the latent inherited potential of both parents and the resulting hybrid. This implies that these hybrids may be used to assess how well they segregate for crucial yield characteristics. These results are in agreement with Shaker et al., 2016; Ekıncı & Basbag, 2018; Nimbal Sagar et al., 2019; Moiana et al., 2021).

Table 7. SCA effects of diallel cross

Genotypes	**PH**	**VB**	**FB**	**BP**	**BW**	**SY**
1*2	4.179	-0.497	1.879	0.69	-0.691	-4.244
1*3	19.263	0.238	-0.788	3.815	-0.033	11.307
1*4	-3.214	0.215	2.022	3.318	0.238	-13.015
1*5	24.861	-0.321	-3.329	-3.394	0.283	-9.077
1*6	-8.357	0.802	-3.29	-3.015	-0.101	-8.443
1*7	14.346	0.656	-2.304	-5.519	0.884	11.036
1*8	-11.2	0.62	3.57	-0.14	0.06	1.18
2*3	-16.694	-1.176	-2.845	-2.057	-0.253	-8.231
2*4	27.729	0.851	-1.971	-1.587	0.907	0.866
2*5	-15.595	1.641	2.004	0.454	-0.161	0.774
2*6	-11.147	1.108	2.54	-0.267	-0.288	-3.675
2*7	17.956	-0.298	-3.59	0.819	-0.21	1.989
2*8	1.99	-0.81	2.78	0.8	0.47	9.5
3*4	-10.287	0.094	4.345	-1.838	-0.515	-9.417
3*5	19.521	-0.306	9.211	11.946	-0.492	26.701
3*6	12.969	0.923	2.713	3.035	0.184	10.498
3*7	-18.527	1.458	5.659	4.717	0.125	18.823
3*8	13.77	-0.79	-2.53	-3.76	-0.48	14.98
4*5	-16.322	-0.589	-2.162	1.599	-1.129	-8.477
4*6	-8.341	1.66	0.34	-2.639	-0.159	-8.009
4*7	2.229	-2.142	5.39	1.327	0.222	9.138
4*8	1.19	1.98	-3.61	1.35	0.004	4.31
5*6	21.201	-1.41	4.672	2.905	-0.204	6.437
5*7	-20.429	1.565	-1.518	-5.479	-0.639	-20.888
5*8	-30.39	1.22	-5.18	-3.38	-0.9	-18.8
6*7	-4.181	1.111	-4.113	8.364	-0.31	18.816
6*8	28.95	-1.72	6.08	4.27	0.03	10.96
7*8	-4.5	0.44	6.74	11.95	-0.39	25.38
S.E.(sij)	5.58	0.29	0.64	0.38	0.25	3.65

The elements of genetic and phenotypic variations are shown in Table 8. Although both general and specialized combining skills were significant in the qualities under study, the importance of dominant effects on the traits under study was shown by the fact that the specific ability to combine was more significant. The assessment of the degree of dominance, which was larger than one for every feature under study, confirms this and shows that the dominant effects of genes predominate. Low narrow-sense heredity for the amount of fruiting branches, bolls, and seed cotton output was indicative of this (0.18, 0.06, and 16% respectively), besides moderate values in all traits except low estimates in fruiting branches. In contrast, heritability was moderate (20-40) for the number of vegetative branches and mean boll weight (0.26 and 0.31, respectively), and high for plant height (0.57). Based on these genetic data, the method of hybridization followed by selection is important for improving cotton yield traits and their components. These results are in agreement with Ekinci and Basbag (2018); Abdel-Aty et al., 2022; Abdel-Aty et al., 2023; Sharif et al., 2024b)

Table 8. Genetic parameters of studied traits

S.O.V.	**Traits**					
	PH	**VB**	**FB**	**BP**	**BW**	**SY**
GCA Variance	80.39	0.19	0.65	2.35	0.05	18.02
SCA Variance	277.68	1.41	19.6	27.82	0.32	192.86
GCA/SCA	0.28	0.13	0.03	0.08	0.15	0.09
VA	160.78	0.38	1.3	4.7	0.1	36.04
VD	277.68	1.41	19.6	27.82	0.32	192.86
$\sigma^2 g$	438.46	1.79	20.9	32.52	0.42	228.9
$\sigma^2 e$	150.42	0.4	1.94	0.7	0.31	64.46
$\sigma^2 p$	588.88	2.19	22.84	33.22	0.73	293.36
$\bar{a}$	1.85	2.72	5.49	3.44	2.52	3.27
H^2n.s.	0.366	0.212	0.062	0.144	0.238	0.157
G.A%	16.24	20.60	4.23	12.63	11.73	13.7
Mean	96.25	2.68	12.31	11.56	3.05	34.54

Table 9 presents the partial diallel method's illustration of general combining ability effects. It demonstrates that, even though the majority of their effects are negative, parents' general bringing together ability effects are not significant when it comes to having genes that significantly affect plant height or the number of vegetative branches (Table 9). These results did not match exactly of half diallel method, which may be due to the absence of influence of other parents compared to diallel crosses. The significant effects of parents on trait of number of fruiting branches were divided into two sections: first section included negative effects, as seen in parents P1 (-4.62) and P8 (-6.71), In the second segment, parental P3 (6.03) and P4 (4.78) showed favorable general combining ability impacts. Furthermore, the amount of balls per plant characteristic had a major adverse effect on both parents, P1 (-3.27) & P8 (-4.112), although parent P3 (4.201) had a favourable influence on general combining ability. In a series of crosses, the results of the general combination ability for the traits of the amount of balls and number of the vegetative branches in the parents P1 and P8 show that both of these parents lack the genes which enhance these traits, whereas parent P3 stands out due to its genes that increase the number of branches with fruit and the rate of his balls per plant. Additionally, parent P4 has genes that increase the plant's number of fruiting branches. The additive effect of genetic material in this trait for the parents P4 and P5 is demonstrated by the concentration of positive as well as negative general combined effects for the ball weight trait in these parents. This suggests that these parents have significant genes that favorably influence an increase in ball weight. On the other hand, both parents, P6 and P8, had negative and substantial general combining ability effects, indicating that they had genes with additive effects that lower the mean ball weight. The general combining ability of parents P3 and P4 was shown to have a considerable favorable impact on seed cotton output. These findings concur with those of (Al-Jubouri and Madab 2024; El-Aref et al., 2019).

Table 9. GCA effects in partial diallel of cotton parents

Parents	Traits					
	PH	VB	FB	BP	BW	SY
1	21.721	-0.274	-4.62	-4.112	0.089	-11.534
2	-0.279	0.15	-1.061	-1.007	0.246	-0.33
3	15.696	0.396	6.03	4.201	0.141	13.904
4	-12.00	-0.479	4.781	2.359	0.445	11.592
5	2.021	-0.185	1.56	0.826	0.35	5.682
6	-8.646	0.261	0.709	0.091	-0.376	-3.83
7	-13.537	-0.172	-0.674	0.912	0.019	3.86
8	-4.97	0.3	-6.71	-3.27	-0.91	-19.35
S.E.(gi-gj)	29.53	2	3.03	2.89	0.29	9.02

Table 10 displays the estimated value of genetic characteristics using the partial diallel cross approach, showing significant variations for both generic and specialized combining skills in all traits, except specific combination abilities in two variables: single plant yield and ball weight. Additionally, the trait of ball weight was characterized by significant effects in general combining ability only. Genetic differences can be partitioned into their components by estimating the symmetrical genetic value of GCA and SCA, as shown by the calculation of variances for the ratios of general and particular combining skills. Ball weight of fruiting branches and seed cotton output had GCA/SCA variation ratios larger than one. In contrast, the qualities of the plant's height, number of balls, and the number of vegetative branches demonstrated that specific combining ability had the most variance, suggesting that additive gene action predominates in the trait of the yield of cotton and several of its key components. The calculation of the genetic variance component (dominance and additive), the number of balls per plant, the weight of the balls, and the cotton production per plant further supports this. In both plant height and the number of vegetative branches, dominance variances were larger than additive fluctuations. In the major dominance variance components, the average degree of domination is represented by the irrelevant genetic criteria that make up the highest percentage of all genetic variants. Being less than a single for the remainder yield features and their other components, while being closest and more than one for the plant height, number of vegetative subdivisions, and ball plant. Higher narrow-sense heritability ratios for the characteristics of cotton production, number of fruiting branches, and number of balls per plant were found in conjunction with the results (0.385, 0.592, 0.485, 0.354 and 0.481) respectively companied by high percentage ratios of expected genetic advanced in vegetative and fruiting branches and single plant yield traits (56.94, 41.55, and 37.86 respectively) besides moderate values in plant height and ball weight (13.45, 29.06 and 15.42 respectively), that investigates significant additive gene action of the phenotypes under study(EL-FEKI et al., 2009). The absence of many successful parents in a partial diallel led to a state of equilibrium passed on by parents and shifted the narrower meaning from diallel mating design. Additionally, excluding limited mating design on restricted lines compared to half diallel led to the appearance of both additive along dominance kinds of gene action at investigated cotton genotypes (Queiroz et al., 2017). Spearman correlational estimates among the same genetic variables for half and a partial diallel pairing-up design showed significant beneficial effects in both processes for most traits, except inheritance in a narrow sense (Essam et al., 2022). These findings concur with those of (El-Hashash & Shiekh ,2022; Méndez-Natera et al., 2012).

Table 10. Genetic parameters and Spearman correlation of the partial diallel mating design of cotton hybrids

Genetic parameter	**Traits**						**Spearman correlation (rs)**
	PH	**VB**	**FB**	**BP**	**BW**	**SY**	
Due to GCA	951.96**	1.02**	64.26**	40.22**	1.04*	540.79**	0.88**
Due to SCA	1831.54**	8.41**	19.37**	17.64**	0.18ns	171.11ns	0.94**
GCA Var.	114.02	0.95	5.81	2.92	0.11	47.92	-0.25ns
SCA Var.	529.07	2.68	5.68	5.71	0.05	34	0.94**
GCA/ SCA	0.21	0.35	1.02	0.51	2.2	1.40	0.99**
σ2 A	228.04	1.91	11.63	5.85	0.22	95.84	.94**
σ2 D	529.07	2.68	5.68	5.71	0.05	34	0.99**
σ2 g	757.11	4.59	17.31	11.56	0.27	129.84	0.94**
σ2 e	244.32	0.37	2.32	0.5	0.35	69.09	0.98**
σ2 p	1001.43	4.96	19.63	12.06	0.62	198.93	0.94**
$\bar{a}$	2.15	1.67	0.98	1.39	0.67	0.84	0.25ns
H^2ns	0.227	0.385	0.592	0.485	0.354	0.481	-0.92**
G.A %	13.45	56.94	41.55	29.06	15.42	37.86	0.085ns
Mean	93.99	2.65	11.11	10.2	3.18	31.53	0.99**

Conclusion

Both methods are similar in most genetic parameters except heritability in narrow sense that exhibited difference concentrate in additive type of gene action which state absence of jsome parents from other crosses affect in narrow sense heritability estimates though significant additive variances and similarity of dominance variances in both half and partial diallel cross, therefore, each method can't be substituted by other and differences appear in inter and intra of half and partial diallel cross. Genotypes differ significantly in their genetic ability in most studied traits; some of the parents are good combiners, and some of the crosses are superior in single-seed cotton yield and its components.

References

Abdel-Aty, M. S., Sorour, F. A., Yehia, W. M. B., Kotb, H. M. K., Abdelghany, A. M., Lamlom, S. F., ... & Abdelsalam, N. R. (2023). Estimating the combining ability and genetic parameters for growth habit, yield, and fiber quality traits in some Egyptian cotton crosses. *BMC Plant Biology*, *23*(1), 121. https://doi.org/10.1186/s12870-023-04131-z

Abdel-Aty, M. S., Youssef-Soad, A., Yehia, W. M. B., El-Nawsany, R. T. E., Kotb, H. M. K., Ahmed, G. A., ... & Abdelsalam, N. R. (2022). Genetic analysis of yield traits in Egyptian cotton crosses (Gossypium barbdense L.) under normal conditions. *BMC Plant Biology*, *22*(1), 462. https://doi.org/10.1186/s12870-022-03839-8

Alagarsamy, M. (2024). Combining ability studies in desi cotton (Gossypium arboreum L.) genotypes. *Journal of Cotton Research, 7*(1), 37. https://doi.org/10.1186/s42397-024-00200-2

Al-Guboory, K. K. A. (2016). Combining ability and gene action in upland cotton using half diallel crossing among seven varieties. Kirkuk University. *Journal for Agricultural Sciences, 7*(3), 60-75. doi: https://doi.org /10.58928/ku16.07306

Al-Jubouri, A. A. J., & Madab, D. S. (2024, July). Analysis of Combining Ability and Heterosis in Partial Diallel Cross of Cotton. In *IOP Conference Series: Earth and Environmental Science* (Vol. 1371, No. 5, p. 052042). IOP Publishing https://doi.org/10.1088/1755-1315/1371/5/052042

Al-Juheishy, W., & Al-Layla, M. (2018). Effect Of Nitrogen Fertilization And Plant Spaces In Quantitative Characters For Varieties Of Cotton (Gossypium hirsutum L.). *Kirkuk University Journal for Agricultural Sciences*, *9*(2), 59-68. https://doi.org/10.58928/ku18.09210

Al-Mafarji, T. R. T., & Al-Jubouri, J. M. A. (2023). Combining ability and gene action of half diallel crosses in bread wheat (*Triticum aestivum* L.). *IOP Conference Series: Earth and Environmental Science*, *1262*(5), 052027. https://doi.org/10.1088/1755-1315/1262/5/052027

Al-Mafarji, T., Al-Jubouri, D. J. M. A., & Kanbar, A. (2024). Estimate Combining Ability and Gene Action of Yield, and Some Qualitative Traits of Genotypes Bread Wheat.(Triticum aestivum L.) of Half-Diallel Crosses. *Tikrit Journal for Agricultural Sciences*, *24*(3), 182-196. https://doi.org/10.25130/tjas.24.3.15

Bourgou, L., Dever, J. K., Sheehan, M., Kelly, C. M., Diané, S. K., & Sawadogo, M. (2022). Diallel crosses of cotton (Gossypium hirsutum L.) from Burkina Faso and Texas A&M AgriLife Research—1-Analysis of agronomic traits to improve elite varieties from Burkina Faso. *Agronomy*, *12*(4), 939. https://doi.org/10.3390/agronomy12040939

Dawod, M. K., & Al-Guboory, Kh. K. (2012). Estimation of heritability and some genetic parameters in upland cotton. *Kirkuk University Journal for Agricultural Sciences*, *3*(1), 56-66. doi: 10.58928/ku12.03107

Efe, L., & Gencer, O. (1998, September). Inheritance of important properties in Half-Diallel hybrids of some glandless cotton,(Gossypium hirsutum L.) cultivars. In *New Frontiers of Cotton Research, Proc. of World Cotton Research Conference* (Vol. 2, pp. 239-243).

Ekıncı, R., & Basbag, S. (2018). Combining ability analysis and heterotic effects for cotton fiber quality traits. *Ekin Journal of Crop Breeding and Genetics*, *4*(2), 20-25.

El-Aref, K. A., Zaher, A. E., Haridy, M. H., & Shrmokh, H. M. (2019). Genetic analysis for diallel crosses on Egyptian cotton (Gossypium barbadense L.). *Assiut Journal of Agricultural Sciences*, *50*(3), 1-15. https://doi.org/10.21608/ajas.2019.52640

El-Feki, T. A., Harb, R. K., & Sultan, A. M. (2009). Heterosis and Gene Action for Partial Diallel Crosses in Cotton I. Cotton Insect Resistance and Multivariate Analysis for Traits RELATED TO INSECT Resistance. *Egyptian Journal of Agricultural Research*, *87*(4), 1119-1134. https://doi.org/10.21608/ejar.2009.198835

Essam, F., El, H., & Ali, S. R. H. (2022). A comparison of the pearson, spearman rank and kendall tau correlation coefficients using quantitative variables. *Asian J. Probab. Stat*, *20*(3), 36-48. https://doi.org/10.9734/AJPAS/2022/v20i3425

Far, L. M. (2017). Regression Techniques Using Data Mining in Flowering Plant. *International Academic Journal of Science and Engineering*, *4*(2), 190-197.

Khan, N. U., & Hassan, G. (2011). Genetic effects on morphological and yield traits in cotton (Gossypium hirsutum L.). *Spanish Journal of Agricultural Research*, *9*(2), 460-472.

Khokhar, E. S., Shakeel, A., Maqbool, M. A., Abuzar, M. K., Zareen, S., Syeda, S. A., & Asadullah, M. (2018). Studying combining ability and heterosis in different cotton (Gossypium hirsutum L.) genotypes for yield and yield contributing traits. *Pakistan Journal of Agricultural Research*, *31*(1). http://dx.doi.org/10.17582/journal.pjar/2018/31.1.55.68

Krishnan, M., & Iyer, S. R. (2024). Protein Concentration from Plant-Based Sources Using Cross-Flow Filtration. *Engineering Perspectives in Filtration and Separation*, 17-20.

Kumar, T. P., Tharnish, T., Govindaraj, R., & Kumar, K. S. (2017). Design and Fabrication of Cotton Buds Manufacturing Machine. *International Journal of Advances in Engineering and Emerging Technology*, *8*(1), 25-28.

Kumbhar, A. M., Buriro, U. A., Junejo, S., Oad, F. C., Jamro, G. H., Kumbhar, B. A., & Kumbhar, S. A. (2008). Impact of different nitrogen levels on cotton growth, yield and N-uptake planted in legume rotation. *Pak. J. Bot*, *40*(2), 767-778.

Méndez-Natera, J. R., Rondón, A., Hernández, J., & Merazo-Pinto, J. F. (2012). Genetic studies in upland cotton. III. Genetic parameters, correlation and path analysis.

Mohammed I. M. (2016). Estimation of genetic diversity in a number of cotton varieties by using cluster analysis and its relation with gene action in half-diallel crossing. Kirkuk University *Journal for Agricultural Sciences, 7*(4), 120-135. https://doi.org /10.58928/ku16.07412

Moiana, L. D., Filho, P. S. V., Maleia, M. P., Mufambira, S., João, J., Teca, J. O., ... & Artur, C. R. R. (2021). General and specific combining ability of cotton germplasm in Mozambique using circulant dialells. *Australian Journal of Crop Science*, *15*(6), 933-939. https://doi.org /10.21475/ajcs.21.15.06.p3177 ISSN:1835-2707.

Nayak, A., & Raghatate, K. S. (2024). Image segmentation and classification of aquatic plants using convolutional neural network. *International Journal of Aquatic Research and Environmental Studies*, *4*, 14-19.https://doi.org/10.70102/IJARES/V4S1/3

Nimbal Sagar, S., Sangwan, R. S., Kumar, P., Jangid, K., & Bankar, A. H. (2019). Combining ability analysis for different morphological traits in diallel crosses of upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*, *33*(2), 208–213.

Queiroz, D. R., Farias, F. J. C., Vasconcelos, J. J. C., Carvalho, L. P., Neder, D. G., Souza, L. S. S., ... & Teodoro, P. E. (2017). Diallel analysis for agronomic traits in upland cotton in semi-arid zones in Brazil. *Genetics and Molecular Research*, *16*(3), 1-8.

Sarteb, M. M., & Mohammed, M. I. (2023). Performance, Selection indices for six cotton genotypes to yield and some Components. *Journal of Kirkuk University for Agricultural Sciences*, *14*(3). https://doi.org/10.58928/ku23.14327

Sen, E. Z. A., El-Dahan, M. A., Badawy, S. A., Katta, Y. S., Aljuaid, B. S., El-Shehawi, A. M., ... & El-Tahan, A. M. (2022). Evaluation of genetic behavior of some Egyption Cotton genotypes for tolerance to water stress conditions. *Saudi Journal of Biological Sciences*, *29*(3), 1611-1617. https://doi.org/10.1016/j.sjbs.2021.11.001

Shaker, S. A., Darwesh, A. E. I., & Abd El-Salam, M. E. (2016). Combining ability in relation to genetic diversity in cotton (G. barbadense, L.). *J. Agric. Res., Kafr El-Sheikh Univ*, *42*(4), 426-440. https://dx.doi.org/10.21608/jsas.2016.3034

Sharif, Y. O. N. A., Al-Mafrajy, A. S. H., & Albarzenje, Z. M. M. (2024, July). Evaluation of the Effectiveness of 2.4-D 72% Herbicide in Combating Weedy Leaves Associated with Different Varieties of Forage Sorghum (Sorghum bicolor L.) and Its Effect on Growth Characteristics. In *IOP Conference Series: Earth and Environmental Science* (Vol. 1371, No. 5, p. 052020). IOP Publishing. https://doi.org/10.1088/1755-1315/1371/5/052020

Sharif, Y. O. N. A., Madab, D. S., & Hindi, H. A. (2024, July). Estimation of Path Analysis and Genetic Parameters for Sorghum (Sorghum bicolor (L.) Moench) Varieties in Different Environments. In *IOP Conference Series: Earth and Environmental Science* (Vol. 1371, No. 5, p. 052035). IOP Publishing. https://doi.org/10.1088/1755-1315/1371/5/052035

Singh, R.K and Chaudhry, B.D. (2017). Biometrical methods in quantitative genetics. Kalyani publisher. https://www.amazon.com/Biometrical-Methods-Quantitative-Genetics.

Tarek, H., & Abood, Z. A. U. (2014). The impact of human resource development in the strategic objectives of improving the production processes (A study compared to some of the Iraqi dairy plants). *International Academic Journal of Organizational Behavior and Human Resource Management*, *1*(2), 65–87.

Uzakbaeva, G. B., & Ajiev, A. B. (2022). Legal Regulation of the Use and Protection of Wild Relatives of Cultivated Plants in the Republic of Uzbekistan. *Int Acad J Soc Sci*, *9*(1), 43-46. https://doi.org/10.9756/IAJSS/V9I1/IAJSS0905

Vasconcelos, U. A. A., Cavalcanti, J. J. V., Farias, F. J. C., Vasconcelos, W. S., & Santos, R. C. D. (2018). Diallel analysis in cotton (Gossypium hirsutum L.) for water stress tolerance. *Crop Breeding and Applied Biotechnology*, *18*(1), 24-30. https://doi.org/10.1590/1984-70332018v18n1a4

Viana, J. M. S., Cruz, C. D., & Cardoso, A. A. (1999). Theory and analysis of partial diallel crosses. *Genetics and Molecular Biology*, *22*, 591-599. https://doi.org/10.1590/S1415-47571999000400021