Biological and Clinical Sciences Research Journal
eISSN: 2708-2261; pISSN: 2958-4728
www.bcsrj.com
DOI: https://doi.org/10.54112/bcsrj.v2024i1.848
Biol. Clin. Sci. Res. J., Volume, ***2024****: 848*
Orignial Research Article

GENETIC STUDIES FOR SOME YIELD-RELATED TRAITS IN OKRA (*ABELMOSCHUS ESCULENTUS* L.)

KHAN F[1], KAYNAT A[2], *SAEED A[1], JAVAID T[3], IQBAL RA[3], LATIF A[4], NAWAZ MS[5], LATIF A[5], SIDDIQUI GM[6], HASSAN A[7], JAVED HM[8]

[1]Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan
[2]Institute of Horticultural Sciences, University of Agriculture Faisalabad, Pakistan
[3]Potato Research Institute, Sahiwal, Pakistan
[4]Vegetable Research Institute, AARI Faisalabad, Pakistan
[5]Vegetable Research Station Karor, Pakistan
[6]Vegetable Research Station Raiwind, Pakistan
[7]Oilseeds Research Institute AARI Faisalabad, Pakistan
[8]Rice Research Institute, Kala Shah Kaku, Pakistan
**Corresponding author email address: drasifpbg@gmail.com*

(Received, 17th February 2024, Revised 10th May 2024, Published 18th May 2024)

Abstract *Okra is a traditional vegetable famous for its nutritional value. It is a perfect villager's vegetable due to its robust nature, dietary fiber, and seed protein balance of both tryptophan and lysine. The research was carried out in the research area of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Cross combinations among 3 lines (Patel, Selection Super Green, and 19234) and 3 testers (IQRA-III, Perbhani Karanti, and Sabz Pari) were developed by using line × tester design. Crossed seeds along with parents were grown in the field under Randomized Complete Block Design (RCBD) with three replications. Data for various morphological traits was collected and analyzed statistically through analysis of variance and used to assess GCA, SCA, and gene action. Genotype 19234 exhibited maximum significant GCA (-11.4) for plant height in the negative direction and genotype Selection super Green proved a good general combiner for fruit weight, fruit diameter, and first flowering node, exhibiting values of 3.21, 1.191, and -0.89. IQRA-III (3.00), Patel (2.00), and Perbhani Karanti (1.11) exhibited significant GCA for number of fruits per plant. Line 19234 observed a good general combiner for crude fat (0.28), ash (5.43), and protein (0.39). Cross combination Patel × Perbhani exhibited the highest SCA for the number of fruits (7.78) followed by Selection Super Green × Sabz Pari (4.78) hence can be exploited for heterosis breeding. Cross combination Selection Super Green × Perbhani Karanti exhibited the highest significant SCA for plant height (-7.60) and Selection Super Green × IQRA-III displayed the maximum significant SCA value (2.26) for crude fat. Line Patel proved a good general combiner for most of the yield-related traits. Based on GCA and SCA, line 19234 can be used to enhance quality traits and cross combination Patel × Perbhani Karanti can be used to increase the number of fruits per plant.*

Keywords*:* *variation; line × tester analysis; GCA; SCA*

Introduction

There is a dire need to develop high-yielding okra cultivars because of the yield barrier in existing verities (Kishor *et al.*, 2013b). Despite its importance both in terms of nutrients and benefits, it is an under-estimated crop. There is no access for farmers to its high-yielding varieties. Many of them use local cultivars and others use open-pollinated varieties (Kamble & Rani, 2020). That's why okra breeding has its value for overcoming yield barriers. For this purpose, appropriate breeding methods are useful for achieving yield goals (Joshi *et.al.*,2019). Combining ability assists in the selection of appropriate parents and the identification of suitable crosses for the utilization of heterosis (Lyngdoh *et al.*, 2013). Combining ability is defined as the crossing of lines in such a manner that desirable genes will be transmitted to their progeny (Fasahat *et al.*, 2016). Various techniques are used for combining ability analysis, line × tester crossing is a technique, which is used to estimate the combining ability of the parents that can be selected for heterosis breeding (Dempta and Surin 2019). Combining ability is very important because knowledge about the mean performance of genotype is not enough to indicate the best combiners (Seth *et al.*, 2016). Breeders can indirectly select parent genotypes with characters

[Citation: Khan, F., Kaynat, A., Saeed, A., Javaid, T., Iqbal, R.A., Latif, A., Nawaz, M.S., Latif, A., Siddiqui, G.M., Hassan, A., Javed, H.M. (2024). Genetic studies for some yield-related traits in okra (*Abelmoschus esculentus* L.). *Biol. Clin. Sci. Res. J.*, **2024***:* 848. doi: https://doi.org/10.54112/bcsrj.v2024i1.848]

that are high-yielding and have high heritability (Gangashetty *et al*., 2013). Genetic diversity in the population is base for crop improvement. For hybrid development combining ability analysis is important (Feng et al., 2021).

Different designs are used for combining ability analysis but line × tester which is primarily a top cross has been proven the best for analysis. It estimates the GCA of lines, the GCA of testers, and the SCA of crosses. General combining ability can be defined as the average performance of a line in a specific order of crosses while specific combining ability is a better accomplishment of a hybrid than other crosses (Rahman et al., 2021). Low GCA shows that the mean of parents does not fluctuate largely from the mean of crosses while high GCA shows that parental mean fluctuates from the general mean and shows that required genes flow from parents to generation. It also indicates the presence of additive gene action. high SCA indicates both parents combine well to combine desirable genes (Fasahat *et al*., 2016). The significance of the interaction between lines and testers (line × tester) gives information about the significance of dominance variance, while the significance of lines and testers gives direction that additive variance is significant (Nduwumuremyi *et al*., 2013). Line × tester analysis is a valuable tool for preliminary evaluation of genetic stock for use as a population with favorable fixable genes for effective yield improvement (Sapavadiya *et al*., 2019). The success of our breeding strategy depends upon the potential and magnitude of the re-combinations present in the gene pool and the presence of variability in the population (Sujata et.al.,2019). The effectiveness of heterosis breeding is highly dependent upon germplasm availability, its selection, and the screening process (Vekariya *et al*., 2019). Line × tester analysis is an important and useful tool used to find out the strength of the interrelation of yield-related traits. The analysis also gives insight into the successful selection and combinations of the plants to develop superior kinds of genotypes (Sujata *et al*., 2019). The objective of the current study was to estimate the combining abilities and genetic variances of okra genotypes with the help of line × tester analysis.

Materials and Methods

The experiment was conducted in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad.

Experimental material

Experimental material consisted of okra genotypes collected from the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Line × tester mating design was used. For this purpose, three lines (Patel, Selection Super Green, and 19234) and three testers (IQRA-III, Perbhani Karanti, and Sabz Pari) were used and crossed to develop nine F_1S (table 1).

Table 1: Lines, testers and their crosses used in the experiment

Lines	
1	Patel
2	Selection Super Green
3	19234
testers	
1	IQRA-III
2	Perbhani Karanti
3	Sabz Pari
Crosses	
1 × 1	Patel × IQRA-III
1 × 2	Patel × Perbhani Karanti
1 × 3	Patel × Sabz Pari
2 × 1	Selection Super Green × IQRA-III
2 × 2	Selection Super Green × Perbhani Karanti
2 × 3	Selection Super Green × Sabz Pari
3 × 1	19234 × IQRA-III
3 × 2	19234 × Perbhani Karanti
3 × 3	19234 × Sabz Pari

Crossing technique in okra

Okra is often a cross-pollinated crop. A flower that was just opened or near to opening was selected for emasculation. Emasculation was done in the evening from 3-6 P.M. Androecium was removed along with corolla and bud was enclosed in butter paper bags. Pollens from the required male parents were collected and dusted on emasculated flowers. Pollination was performed at 8-10 A.M. Crossed fruit was removed, seeds were collected after drying the fruit.

Experimental design

The parental genotypes (Patel, Selection Super Green, 19234, IQRA-III, Perbhani Karanti, and Sabz Pari) were grown in crossing blocks at a distance of 60 × 30 cm. All agronomic and cultural practices were performed to raise crops. Genotypes were crossed according to line × tester design. Crossed seed dried, collected, and stored. In the next season, parental genotypes along with crossed genotypes were sown in a Randomized Complete Block Design. All cultural practices were performed and data of five random plants from each replication was taken. Data on the following traits was recorded

1. Plant height (cm): PH
2. Fruit length (cm): FL
3. Fruit weight (grams): FW
4. Fruit diameter (mm): FD
5. Number of ridges on fruit: NR
6. Leaf length (cm): LL
7. Leaf breadth (cm): LB
8. Node at which first fruit is present: NF
9. Number of fruits: NOF

[Citation: Khan, F., Kaynat, A., Saeed, A., Javaid, T., Iqbal, R.A., Latif, A., Nawaz, M.S., Latif, A., Siddiqui, G.M., Hassan, A., Javed, H.M. (2024). Genetic studies for some yield-related traits in okra (*Abelmoschus esculentus* L.). *Biol. Clin. Sci. Res. J.*, **2024***:* 848. doi: https://doi.org/10.54112/bcsrj.v2024i1.848]

10. Moisture content in fruit %: MO
11. Protein %: PR
12. Ash %: ASH
13. Crude fat %:CF
14. ADF (acid detergent fiber) %: ADF
15. NDF (neutral detergent fiber) %: NDF

Statistical analysis:

Analysis of variance (Steel *et al.,* 1997) was performed to check out the significance of treatments. Crosses were evaluated for estimation GCA and SCA by line × tester mating design (Kempthorne, 1957).

Results and Discussion

Analysis of variance showed that significant variation is present in all genotypes and crosses for all traits except several ridges on fruit. All lines were highly significant for all traits under study except for fruit length and number of ridges on fruit. Testers and line × tester showed non-significant results for the number of ridges on fruit, lea length, and leaf breadth (table 2).

Table 2: ANOVA of line × *tester (including parents)* for all attributes

SOV	*PH*	*FL*	*FW*	*FD*	*NR*	*LL*	*LB*	*NF*	*NOF*	*MO*	*PR*	*ASH*	*CF*	ADF	NDF
REP	24.68^{ns}	1.13^{ns}	0.029^{ns}	0.0007^{ns}	0.0169^{ns}	11.8291^{ns}	199.17^{**}	0.089^{ns}	0.09^{ns}	0.0780^{ns}	0.0069^{ns}	0.04^{ns}	0.0002^{ns}	0.80^{ns}	0.0696^{ns}
GENO	1204.59^{**}	16.57^{**}	104.67^{**}	6.93^{**}	0.0089^{ns}	54.4778^{**}	112.75^{**}	2.85^{**}	150.55^{**}	338.1653^{**}	10.6346^{**}	1052.06^{**}	5.67^{**}	119.15^{**}	274.1778^{**}
CROSS	360.81^{**}	10.99^{*}	67.25^{**}	6.85^{**}	0.010^{ns}	44.2106^{*}	42.78^{*}	2.33^{**}	97.75^{**}	485.6408^{**}	7.6348^{**}	1184.15^{**}	6.15^{**}	162.06^{**}	387.0068^{**}
LINE (C)	1132.58^{**}	6.57^{ns}	69.77^{**}	17.77^{**}	0.018^{ns}	140.4982^{**}	134.48^{**}	5.44^{**}	29.78^{**}	19.5278^{**}	2.4804^{**}	200.46^{**}	0.54^{**}	218.64^{**}	724.5970^{**}
TESTER (C)	72.98^{*}	14.77^{*}	39.50^{**}	0.94^{ns}	0.0044^{ns}	6.6408^{ns}	13.55^{ns}	2.78^{**}	122.11^{**}	35.0678^{**}	4.5959^{**}	44.22^{**}	0.34^{**}	130.06^{**}	341.9915^{**}
L × T (C)	118.84^{*}	11.31^{*}	79.86^{**}	4.35^{**}	0.0089^{ns}	14.8517^{ns}	11.55^{ns}	0.56^{**}	119.56^{**}	943.9839^{**}	11.7315^{**}	2245.95^{**}	11.86^{**}	149.78^{**}	240.7193^{**}
PARENT	1149.70^{**}	28.41^{**}	134.5^{**}	7.47^{**}	0.0089^{ns}	66.8014^{**}	62.85^{*}	0.72^{**}	182.99^{**}	169.8183^{**}	13.9832^{**}	979.94^{**}	5.01^{**}	35.74^{**}	82.3970^{**}
LINE (P)	416.88^{**}	21.09^{*}	93.48^{**}	1.24^{ns}	0.013^{ns}	22.7705^{ns}	9.77^{ns}	1.00^{**}	154.78^{**}	381.2133^{**}	18.7144^{**}	1106.87^{**}	10.11^{**}	13.78^{**}	203.4444^{**}
TESTER (P)	417.33^{**}	43.93^{**}	155.10^{**}	6.32^{**}	0.0044^{ns}	36.8343^{ns}	36.04^{*}	0.78^{**}	52.00^{**}	3.0100^{**}	7.3433^{**}	5.86^{**}	0.27^{**}	3.32^{*}	2.4478^{**}
L (P) vs. T (P)	4080.06^{**}	12.005^{ns}	175.32^{**}	22.21^{**}	0.0089^{ns}	214.7973^{ns}	222.63^{**}	0.056^{ns}	501.39^{**}	80.6450^{**}	17.8006^{**}	2674.24^{**}	4.30^{**}	144.50^{**}	0.2006^{*}
CROSS vs. PARENT	8229.22^{**}	2.039^{ns}	254.88^{**}	4.83^{*}	0.0000^{ns}	74.9974^{*}	921.97^{**}	17.63^{*}	410.70^{**}	0.0963^{ns}	17.8898^{**}	355.93^{**}	5.18^{**}	192.87^{**}	330.4508^{**}
Error	18.45	3.01	4.38	0.6603	0.0055	10.6	15.07	0.07	0.14	0.0849	0.0276	0.06	0.0093	0.53	0.0427

* *significant at 5% probability;* ** *significant at 1% probability;* ^{ns} *non-significant*

Contribution of lines, testers and their interaction

The percentage contribution of lines, testers, and their interaction were also calculated (Table 3). Plant height lines showed the most contribution i.e. 78.47 percent while testers and interaction contributions were 5.05 and 16.46 percent respectively. While for fruit length lines, testers, and interaction contribution were 14.95, 33.58 and 51.45% respectively. In the case of fruit weight interaction value was high (59.37%). For fruit diameter and line value were high (64.83%) while testers showed very little contribution of 3.42%. Similar results for leaf length and breadth were observed where lines contribution was 79.45% and 78.59% respectively while tester's contribution was 3.42% and 3.76% percent respectively and interaction was 31.75 and 16.8 percent respectively for both traits. 44.44% for lines and interaction and 11.11 percent for tester contribution was observed for the number of ridges on fruits. In the case of the first fruiting node, interaction has less contribution of 11.90% while lines and testers contributions were 58.33% and 29.76%, respectively. For number of fruits and interactions had the most contribution (61.15%) while lines showed 7.62% and testers showed a 31.23% contribution. For moisture and protein contents, interaction contribution was high (61.91% and 97.19 % respectively) while lines and testers showed less contribution i.e. 5.58 and 1.01% for lines and 32.50 and 1.81% for testers respectively. For crude fat and ash, interaction values were 94.83 and 96.44 percent respectively while lines and testers had very little contribution. For ADF lines, testers, and interaction contributions were 33.73, 20.06, and 46.21% and for NDF it was 46.81, 22.09, and 31.10% respectively.

Table 3: Percent contribution of lines, testers and their interaction to total variance

Traits	Lines	Testers	L × T
PH	78.47	5.05	16.46
FL	14.95	33.58	51.45
FW	25.93	14.68	59.37
FD	64.83	3.42	31.75
NR	44.44	11.11	44.44

[Citation: Khan, F., Kaynat, A., Saeed, A., Javaid, T., Iqbal, R.A., Latif, A., Nawaz, M.S., Latif, A., Siddiqui, G.M., Hassan, A., Javed, H.M. (2024). Genetic studies for some yield-related traits in okra (*Abelmoschus esculentus* L.). *Biol. Clin. Sci. Res. J.*, **2024***:* 848. doi: https://doi.org/10.54112/bcsrj.v2024i1.848]

LL	79.45	3.76	16.8
LB	78.59	7.92	13.49
NF	58.33	29.76	11.90
NOF	7.62	31.23	61.15
MO	5.58	32.5	61.91
PR	1.01	1.81	97.19
ASH	4.23	0.93	94.83
CF	2.18	1.38	96.44
ADF	33.73	20.06	46.21
NDF	46.81	22.09	31.1

General and Specific combining ability effects for various yield-related traits

Plant height

Line 19234 showed maximum significant GCA (-11.44) effects but in a negative direction while Patel showed significant positive GCA (10.99). Selection Super Green was found to show non-significant GCA effects (10.99) for plant height. Line Selection Super Green showed a high GCA value of 10.99 in a positive direction. All testers exhibited non-significant results for GCA * significant at 5% probability; ** significant at 1% probability; ^{ns} non-significant (table 4). Genotypes with high GCA can be used for variety development. Cross combination Selection Super Green × Perbhani Karanti showed maximum significant SCA (-7.61) for plant height while all other crosses showed non-significant results. Line 19234 and cross Selection Super Green × Perbhani Karanti can be exploited for a reduction in height (table 5).

Fruit length

Non-significant GCA and SCA were observed for fruit length (table 4,5). Sabz Pari and Perbhani Karanti exhibited high values of GCA as compared to other parental genotypes i.e. 1.24 and -1.32 respectively. Bhatt et al. (2015) and (Guimarães et al., 2020) also reported non-significant GCA for fruit length.

Fruit weight

GCA effects were significant and positive for line Selection Super Green (3.21) and tester Perbhani Karanti exhibited significant negative GCA effects (-3.28). Among lines, Patel and 19234 showed non-significant results for GCA (table 4). Among testers IQRA-III and Sabz Pari showed non-significant results for GCA. Cross combination19234 × Perbhani karanti showed highly significant results for SCA (-6.59) but in a negative direction. Cross combinations Patel × Perbhani Karanti (3.54) and 19234 × Sabz Pari (4.12) also showed positive significant results for SCA can be used to exploit heterosis for fruit weight. All other crosses showed non-significant results for SCA (table 5).

Fruit diameter

Line Patel showed non-significant GCA effects while line 19234 and Selection Super Green exhibited highly significant GCA for fruit diameter representing their ability as good general combiners (table 4). Line selection Super Green exhibited positive GCA effects (1.19) while 19234 exhibited negative GCA effects (-1.55). All testers showed non-significant GCA value. Crosses Selection Super Green × Perbhani Karanti and 19234 × Sabz Pari showed positive SCA effects and proved good specific combiners for fruit diameter. All other crosses showed non-significant results for SCA (table 5).

Number of ridges on fruit

For the number of ridges on fruit, all lines and testers exhibited non-significant GCA effects. All crosses also exhibited non-significant results for SCA (table 4,5).

Leaf length

Lines Selection Super Green and Patel showed highly significant GCA effects for leaf length but Patel showed results in a negative direction (-4.002) and Selection Super Green in a positive direction (3.89), hence were good general combiners, while all other lines, testers, and crosses showed non-significant results (table 4,5).

Leaf breadth

Lines Selection Super Green and Patel showed highly significant GCA effects while all other lines, testers, and crosses showed non-significant results. Patel depicted a maximum value of GCA (4.50) in a positive direction but Selection Super Green showed significant GCA but in a negative direction (table 4,5).

Node at which first fruit is present

Lines showed highly significant results for GCA, testers also showed significant results for GCA except for IQRA-III. Selection Super Green depicted the highest GCA value (-0.89) but in a negative direction and desirable for this trait. Patel and 19234 showed a positive GCA effect. These lines proved good general combiners (table 4). The same value of GCA (0.56) was observed by Perbhani Karanti and Sabz Pari but Perbhani Karanti showed results in negative direction and Sabz Pari in positive direction. Highly significant SCA effects were observed for crosses Patel × Parbhani Karanti (-0.44) and Patel × Sabz Pari (-0.44). Selection Super Green × Sabz Pari and 19234 × Perbhani Karanti showed the same negative significant value (-0.33) for SCA. Line selection Super proved a good general combiner for this trait in the required direction (table 5).

Number of fruits per plant

Line Patel exhibited positive significant GCA effects while lines Selection Super Green and 19234 exhibited significant but negative GCA effects (table 4). Genotypes IQRA-III (3.0) and Parbhani Karanti (1.11) showed positive significant GCA effects while Sabz Pari depicted negative significant GCA effects (-4.1). Akotkar and Dubey (2014) reported

[Citation: Khan, F., Kaynat, A., Saeed, A., Javaid, T., Iqbal, R.A., Latif, A., Nawaz, M.S., Latif, A., Siddiqui, G.M., Hassan, A., Javed, H.M. (2024). Genetic studies for some yield-related traits in okra (*Abelmoschus esculentus* L.). *Biol. Clin. Sci. Res. J.*, **2024***:* 848. doi: https://doi.org/10.54112/bcsrj.v2024i1.848]

significant GCA effects by Perbhani Karanti for the number of fruits per plant. IQRA-III observed a good general combiner for the number of fruits. Significant positive SCA effects were observed for cross combinations Patel × Perbhani Karanti (7.78), Selection Super Green × IQRA-III (0.67), Selection Super Green × Sabz Pari (4.78) and 19234 × IQRA-III (3.11) while other five crosses i.e. Patel × IQRA-III, Patel × Sabz Pari, Selection Super Green × Perbhani Karanti, 19234 × Perbhani Karanti, and 19234 × Sabz Pari showed significant SCA but in the negative direction. Crosses with significant SCA can be exploited for heterosis breeding as dominance is present.

Moisture contents

Line 19234 and tester Sabz Pari showed highly significant positive GCA effects i.e 1.44 and 2.28, proved to be good general combiners for this parameter (table 4). Testers IQRA-III and Parbhani Karanti showed negative significant GCA effects. Significant SCA effects were observed for all crosses. Cross combinations Patel × IQRA-III (-7.17), Patel × Perbhani Karanti, (-9.62), Selection Super Green × Perbhani Karanti, (-7.17) Selection Super Green × Sabz Pari (-9.29), 19234 × IQRA-III (-9.29) and 19234 × Sabz Pari (-7.50) displayed highly significant negative SCA. While Patel × Sabz Pari (16.79), Selection Super Green × IQRA-III (16.46), and 19234 × Perbhani Karanti (16.79) exhibited highly significant positive SCA effects. Hence IQRA-III and Parbhani Karanti observed good general combiners for moisture contents (table 4,5).

Protein contents

Among lines 19234 showed maximum GCA effects (0.39), Selection Super Green and 19234 were observed to be good general combiners as highly significant GCA was displayed by them (table 4). Among testers IQRA-III and Sabz Pari showed significant positive GCA effects while Perbhani Karanti displayed negative significant GCA. All crosses showed highly significant SCA except Patel × IQRA-III, Patel × Perbhani Karanti, Selection Super Green × IQRA-III, and 19234× Sabz Pari showed positive SCA effects while all other crosses showed negative SCA effects. Xavier et al. (2019) reported similar results for protein contents (table 5).

Ash contents

GCA effects were significant for all parents, Selection Super Green and Patel showed highly significant positive GCA while line 19234 observed with negative significant GCA (table 4). Testers Sabz Pari and Parbhani Karanti were observed to have significant positive GCA effects. While tester IQRA-III showed highly significant negative GCA effects. All crosses showed significant SCA (table 5).

Crude fat

For crude fat line 19234 tester Sabz Pari showed highly significant positive GCA effects while Selection Super Green, Patel, and Perbhani Karanti showed negative significant GCA effects (table 4). 19234 exhibited the highest value for crude fat which is 0.28 hence can be used to increase crude fat in fruit. Highly significant SCA was observed for all crosses. Selection Super Green × IQRA-III showed the highest SCA (2.26) followed by 19234 × Perbhani Karanti (1.69) and Selection Super Green × IQRA-III (1.45) with highly significant SCA in a positive direction, all other crosses disclosed negative SCA (table 5).

ADF (acid detergent fiber)

Significant GCA was observed for all parents except Patel (table 4). Among testers, IQRA-III (1) and Pabhani Karanti showed highly significant positive GCA effects while highly significant negative SCA was observed by 19234 and Sabz Pari. Among lines Selection, Super Green showed significant GCA in the positive direction (5.15) while 19234 in a negative direction. All Crosses depicted significant SCA except Patel × Perbhani Karanti. Maximum SCA value observed as (6.15) by 19234 × IQRA-III, followed by 19234 × IQRA-III (6.16) (table 5).

NDF (neutral detergent fiber)

All parents and crosses showed significant results for general and specific combining abilities. Among lines, Patel and 19234 showed negative significant GCA while Selection Super Green showed positive significant results (table 4). Line19234 exhibited the highest negative value (-8.13 for GCA followed by Sabz Pari (-6.39) hence desirable for this character Among testers IQRA-III and Perbjani Karanti showed positive while Sabz Pari showed negative GCA. Cross 19234 × Sabz Pari depicted maximum SCA (-11.60) followed by 19234 × Perbhani Karanti (6.85) (table 5).

Table 4: General combining ability effects of lines and testers for yield related traits in okra

	PH	FL	FW	FD	NOR	LL	LB	NF	NOF	MO	PR	ASH	CF	ADF	NDF
Patel	10.99^{**}	0.75^{ns}	-1.46^{ns}	0.35^{ns}	-0.04^{ns}	3.9^{**}	4.31^{**}	0.33^{**}	2.00^{**}	0.06^{ns}	-0.60^{**}	-2.27^{**}	-0.13^{**}	-0.48^{ns}	-1.50^{**}
Selection Super Green	0.45^{ns}	-0.93^{ns}	3.21^{**}	1.19^{**}	0.04^{ns}	-4.00^{**}	-1.13^{**}	-0.89^{**}	-0.44^{**}	-1.50^{**}	0.20^{**}	-3.15^{**}	-0.15^{**}	5.15^{**}	9.63^{**}

[Citation: Khan, F., Kaynat, A., Saeed, A., Javaid, T., Iqbal, R.A., Latif, A., Nawaz, M.S., Latif, A., Siddiqui, G.M., Hassan, A., Javed, H.M. (2024). Genetic studies for some yield-related traits in okra (*Abelmoschus esculentus* L.). *Biol. Clin. Sci. Res. J.*, **2024***:* 848. doi: https://doi.org/10.54112/bcsrj.v2024i1.848]

19234	-11.44^{**}	0.18^{ns}	-1.75^{ns}	-1.55^{**}	0^{ns}	0.11^{ns}	-3.17^{ns}	0.56^{**}	-1.56^{**}	1.44^{**}	0.39^{**}	5.44^{**}	0.28^{**}	-4.67^{**}	-8.13^{**}
IQRA-III	2.76^{ns}	0.08^{ns}	1.58^{ns}	0.11^{ns}	0^{ns}	0.55^{ns}	-0.57^{ns}	0.00^{ns}	3.00^{**}	-1.07^{**}	0.08^{**}	-2.55^{**}	0.003^{ns}	1.007^{**}	0.49^{**}
Perbhani Karanti	0.16^{ns}	-1.32^{ns}	-2.38^{*}	0.26^{ns}	0.02^{ns}	-0.99^{ns}	-0.83^{ns}	-0.56^{**}	1.11^{**}	-1.21^{**}	-0.75^{**}	1.10^{**}	-0.20^{**}	3.20^{**}	5.91^{**}
Sabz Pari	-2.93^{ns}	1.24^{ns}	0.80^{ns}	-0.36^{ns}	-0.02^{ns}	0.44^{ns}	1.41^{ns}	0.56^{**}	-4.1^{**}	2.28^{**}	0.67^{**}	1.45^{**}	0.19^{**}	-4.20^{**}	-6.39^{**}

* significant at 5% probability; ** significant at 1% probability; ^{ns} non-significant

Table 5: Specific combining ability effects of crosses for yield related traits in okra

Crosses	PH	FL	FW	FD	NOR	LL	LB	NF	NOF	MO	PR	ASH	CF	ADF	NDF
Patel×*IQRA-III*	0.19^{ns}	-1.76^{ns}	-2.63^{ns}	0.81^{ns}	0^{ns}	1.48^{ns}	-0.68^{ns}	0.00^{ns}	-3.78^{**}	-7.17^{**}	-0.19^{ns}	-9.54^{**}	-0.86^{**}	-5.36^{**}	-4.30^{**}
Patel×Perbhani Karanti	5.13^{ns}	2.14^{ns}	3.54^{*}	-0.48^{ns}	-0.02^{ns}	0.96^{ns}	1.99^{ns}	-0.44^{**}	7.78^{**}	-9.62^{**}	1.71^{**}	-15.06^{**}	-0.59^{**}	-0.59^{ns}	-0.45^{**}
Patel×Sabz Pari	-5.32^{ns}	-0.38^{ns}	-0.91^{ns}	-0.33^{ns}	0.02^{ns}	-2.44^{ns}	-1.31^{ns}	-0.44^{**}	-4.00^{**}	16.79^{**}	-1.51^{**}	24.6^{**}	1.45^{**}	5.95^{**}	4.75^{**}
Selection Super Green×*IQRA-III*	2.66^{ns}	0.32^{ns}	0.16^{ns}	-0.33^{ns}	0.04^{ns}	-0.003^{ns}	0.82^{ns}	0.22^{ns}	0.67^{**}	16.46^{**}	1.27^{**}	25.14^{**}	2.26^{**}	-0.80^{ns}	-1.46^{**}
Selection Super Green×Perbhani Karanti	-7.61^{*}	-0.02^{ns}	3.05^{ns}	1.24^{*}	0.02^{ns}	0.22^{ns}	-2.4^{ns}	0.11^{ns}	-5.44^{**}	-7.17^{**}	-0.49^{**}	-12.21^{**}	-1.10^{**}	-2.05^{**}	-5.39^{**}
Selection Super Green×Sabz Pari	4.95^{ns}	-0.30^{ns}	-3.21^{ns}	-0.91^{ns}	-0.07^{ns}	-0.21^{ns}	1.59^{ns}	-0.33^{*}	4.78^{**}	-9.29^{**}	-0.78^{**}	-12.93^{**}	-1.16^{**}	2.85^{**}	6.85^{**}
19234×*IQRA-III*	-2.85^{ns}	1.44^{ns}	2.46^{ns}	-0.48^{ns}	-0.04^{ns}	-1.48^{ns}	-0.13^{ns}	-0.22^{ns}	3.11^{**}	-9.29^{**}	-1.08^{**}	-15.60^{**}	-1.40^{**}	6.16^{**}	5.76^{**}
19234×Perbhani Karanti	2.48^{ns}	-2.12^{ns}	-6.59^{**}	-0.76^{ns}	0^{ns}	-1.18^{ns}	0.41^{ns}	-0.33^{*}	-2.33^{**}	16.79^{**}	-1.21^{**}	27.27^{**}	1.67^{**}	2.64^{**}	5.84^{**}
19234×Sabz Pari	0.37^{ns}	0.68^{ns}	4.12^{*}	1.24^{*}	0.04^{ns}	2.66^{ns}	0.28^{ns}	0.11^{ns}	-0.78^{**}	-7.50^{**}	2.30^{**}	-11.67^{**}	-0.29^{**}	-8.80^{**}	-11.60^{**}

* significant at 5% probability; ** significant at 1% probability; ^{ns} non-significant

[Citation: Khan, F., Kaynat, A., Saeed, A., Javaid, T., Iqbal, R.A., Latif, A., Nawaz, M.S., Latif, A., Siddiqui, G.M., Hassan, A., Javed, H.M. (2024). Genetic studies for some yield-related traits in okra (*Abelmoschus esculentus* L.). *Biol. Clin. Sci. Res. J.*, **2024***:* 848. doi: https://doi.org/10.54112/bcsrj.v2024i1.848]

Genetic variance

Variance due to GCA and variance due to SCA predicts possible gene action as GCA variance indicates additive gene action and SCA variance indicates non-additive gene action (table 6). Higher values of SCA variance than GCA variance for all traits represented a preponderance of non-additive gene action. Wammanda et al. (2010) described the importance of non-additive gene action for yield-attributing traits.

Table 6: Genetic variances

	б^{2}GCA	б^{2}SCA	б^{2}GCA/б^{2}SCA	IF F= 0; A	IF F=1; A	IF F=0; D	IF F=1; D
PH	13.40	30.10	0.45	53.77	26.89	120.78	30.20
FL	0.01	2.21	0.00	-0.07	-0.04	8.87	2.22
FW	0.70	24.10	0.03	-2.80	-1.40	96.65	24.16
F. D	0.13	1.11	0.12	0.56	0.28	4.44	1.11
NOR	0.00	0.00	0.11	0.00	0.00	0.00	0.00
LL	1.63	1.71	0.95	6.52	3.26	6.86	1.72
LB	1.70	2.50	0.68	6.94	3.47	-10.18	-2.54
NF	0.09	0.16	0.56	0.40	0.20	0.65	0.16
NOF	1.20	39.70	0.03	-4.85	-2.42	159.19	159.19
MO	25.40	314.60	0.08	-101.85	-50.93	1258.57	314.64
PR	0.20	3.80	0.05	-0.91	-0.46	15.60	3.90
ASH	58.90	748.60	0.08	-235.96	-117.98	2994.57	748.64
CF	0.30	3.90	0.08	-1.27	-0.63	15.80	3.95
ADF	0.60	49.60	0.01	2.73	1.36	198.53	49.63
NDF	8.10	80.20	0.10	32.51	16.25	320.87	80.22

Conclusion

SCA variance was higher than GCA variance for all traits suggesting non-additive gene action for inheritance. A significant association of the number of fruits per plant was present with plant height, fruit length, fruit weight, and leaf length. It could be concluded that significant variation is present among genotypes that can be exploited for yield increase.

References

Bhatt, J., Kathiria, K., Christian, S., & Acharya, R. (2015). Combining ability studies in okra (Abelmoschus esculentus (L.) Moench) for yield and its component characters. *Electronic Journal of Plant Breeding* **6**, 479-485.

Fasahat, P., Rajabi, A., Rad, J. M., & Derera, J. (2016). Principles and utilization of combining ability in plant breeding. *Biometrics & Biostatistics International Journal* **4**, 1-24.

Feng, J.-Y., Wang, R., Thakur, K., Ni, Z.-J., Zhu, Y.-Y., Hu, F., Zhang, J.-G., & Wei, Z.-J. (2021). Evolution of okara from waste to value added food ingredient: An account of its bio-valorization for improved nutritional and functional effects. *Trends in Food Science & Technology* **116**, 669-680.

Guimarães, R. M., Ida, E. I., Falcão, H. G., de Rezende, T. A. M., de Santana Silva, J., Alves, C. C. F., da Silva, M. A. P., & Egea, M. B. (2020). Evaluating technological quality of okara flours obtained by different drying processes. *LWT* **123**, 109062.

Joshi, J., Rajan, R. E. B., & Kumar, C. P. S. (2019). Heterosis for earliness and fruit yield components in bhendi [Abelmoschus esculentus (L.) Moench].

Kamble, D. B., & Rani, S. (2020). Bioactive components, in vitro digestibility, microstructure and application of soybean residue (okara): A review. *Legume Science* **2**, e32.

Kempthorne, O. (1957). An introduction to genetic statistics, John wily and Nordskog. *Inc. London: Chapman and Hall. Ltd*.

Kishor, D., Arya, K., Duggi, S., Magadum, S., Raghavendra, N., Venkateshwaralu, C., & Reddy, P. S. (2013). Studies on heterosis for yield and yield contributing traits in okra (Abelmoschus esculentus (L.) Moench). *Molecular Plant Breeding* **4**.

Lyngdoh, Y. A. (2011). Heterosis and combining ability studies in near homozygous lines of okra *[Abelmoschus esculentus (L.) Moench]* UNIVERSITY OF HORTICULTURAL SCIENCES, BAGALKOT].

Nduwumuremyi, A., Tongoona, P., & Habimana, S. (2013). Mating designs: helpful tool for quantitative plant breeding analysis. *Journal of Plant Breeding and Genetics* **1**, 117-129.

Prem Sagar, S., Dushyanthakumar, B., Kalleshwaraswamy, C., Satish, K., Diwan, J., Raghavendra, V., Swathy, V., & Channabasava. (2023). Diallel approach for estimating hybrid superiority and combining ability of indigenous advanced breeding lines in okra [Abelmoschus esculentus (L.)]. *Genetic Resources and Crop Evolution*, 1-13.

Rahman, M. M., Mat, K., Ishigaki, G., & Akashi, R. (2021). A review of okara (soybean curd residue) utilization as animal feed: Nutritive value and animal performance aspects. *Animal Science Journal* **92**, e13594.

Steel, R. G., Torrie, J. H., & Dickey, D. A. (1997). *Principles and procedures of statistics: a biometrical approach*.

Sujata, P., Satish, D., Babu, A., Chittapur, R., Prabhuling, G., & Peerjade, D. (2019). Studies of character association and path analysis for productivity and quality traits in okra (Abelmoschus esculentus (L.) Moench). *Journal of Pharmacognosy and Phytochemistry* **8**, 1513-1516.

Vekariya, R., Patel, A., Modha, K., & Mali, S. (2019). Study of heterosis over environments for fruit yield and its related traits in okra [Abelmoschus esculentus (L.) Moench]. *International journal of chemical studies* **7**, 484-490.

Wammanda, D., Kadams, A., & Jonah, P. (2010). Combining ability analysis and heterosis in a diallel cross of okra (Abelmoschus esculentus (L.) Moench). *African Journal of Agricultural Research* **5**, 2108-2115.

Xavier, F., Kumar, R., Yadav, R., Behera, T., & Khade, Y. P. (2019). Studies on combining ability of okra genotypes for protein, total dietary fibre and mineral content. *Indian Journal of Horticulture* **76**, 672-677.

Declaration

Ethics Approval and Consent to Participate

Not applicable.

Consent for Publication

The study was approved by authors.

Funding Statement

Not applicable

Conflict of Interest

There is no conflict of interest among the authors regarding this case study.

Authors Contribution

Khan F conducted this research. Saeed A supervised this research. Kaynat A helped during research activities. Remaining all authors contributed in proof reading, editing, data analysis and revision.

[Citation: Khan, F., Kaynat, A., Saeed, A., Javaid, T., Iqbal, R.A., Latif, A., Nawaz, M.S., Latif, A., Siddiqui, G.M., Hassan, A., Javed, H.M. (2024). Genetic studies for some yield-related traits in okra (*Abelmoschus esculentus* L.). *Biol. Clin. Sci. Res. J.*, **2024***:* 848. doi: https://doi.org/10.54112/bcsrj.v2024i1.848]