

MEAN PERFORMANCE EVALUATION OF OKRA PARENTS AND CROSSES BASED ON MORPHOLOGICAL AND BIOCHEMICAL PARAMETERS

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(Received, 24th March 2024, Revised 8th June 2024, Published 20th June 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 i.e. plant height, pod length, number of fruits, number of ridges per pod, fruit diameter, fresh fruit weight, number of fruit-bearing nodes, leaf length, and leaf breadth was collected and analyzed statistically through analysis of variance and used to assess mean performance. Correlation analysis was also performed for various plant traits to check the association of characters. Characters' plant height, fruit length, fruit weight, leaf length, and ADF are significantly associated with the number of fruits at the genotypic level. Fruit length exhibited a significant positive association with plant height, fruit weight, and number of fruits at the genotypic level.

Keywords: Okara; mean performance; phenotypic correlation; genotypic correlation; path coefficient

Introduction

Okra (*Abelmoschus esculentus* L. Moench) is a member of the family Malvaceae, an important vegetable of the tropics and subtropics (Armand et al., 2021). Its chromosome number is $2n=8x=72$ or 144 (Aminu et al., 2016). It is an often-cross-pollinated crop, cross-pollination by insects ranges from 5-9% (Sandeep et al., 2022). It can grow in a variety of soil types, but sandy loam is best for healthy growth of okra and less insect-pest attack on okra (Hayati, 2020). Its high nutritional value and low cost of production make it a significant vegetable (Hayati, 2020). It is grown in many parts of the world because of its nutritional importance. Okra is a rich source of essential nutrients and fiber. It also contains vitamins A, B, and C as well as a rich source of oil (18-20%) and protein (20-30%) (HASAN, 2015). Okra has a higher average nutritive value (AVN) than other vegetables like tomatoes,

and brinjal which is 3.21% (Medagam et al., 2012). The root and stem of okra are used for cleaning canned juices (KIRAN et al., 2024) and are also used as a spreading agent in paper manufacturing. It originated in Ethiopia, in the 12th (B.C) century. Egypt people used to cultivate it, and then it spread to North Africa and the Middle East (AHMED, 2017). It is cultivated throughout the year in the tropics. The area under cultivation for this crop was 0.43 million hectares and production is 4.54 million tons in the world (Kenaw et al., 2023). Okra yield in Pakistan is 7.4 tons per hectare; there is a yield gap of 9.6 tons per hectare. Reasons for low yield are the unavailability of quality seeds of high-yielding varieties and contracted choice for cultivars (Yamuna, 2012). Lack of approved varieties and hybrids for specific areas is a problem in its farming

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that's why there is a need to select genotypes that are location-specific (Ranga et al., 2021).

Hybrid breeding is a tool that is being used to enhance crop yield, better adaptation, reproductive ability, and resistance to diseases (Ahmed and El-Sayed, 2021). Hybrid vigor has been reported in okra in 1946 (Alemu Bayu, 2020). Despite the availability of open-pollinated varieties (OPVs) in okra, the importance of hybrids cannot be denied due to their desirable characteristics like low agricultural inputs, and short life span along higher, uniform, and stable yield (Vani et al., 2020). The magnitude of a peculiar trait can increase dramatically when genotypes are brought together in a specific pattern (Naveed et al., 2012). Due to the unfavorable interaction of genes, heterosis may not increase yield but can reduce or loss of yield (RASUL, 2017). Identification of genetically superior and appropriate genotypes and their selection is an important stage for breeding programs (Kumar and Reddy, 2016). Evaluation of genotypes and knowledge of genetic variability are the basic steps in improving any crop (Das et al., 2022).

Enhancement in yield is a major goal of okra breeders. There is an association between traits, and knowledge of this association is important in the selection of genotypes in the breeding program. Correlation analysis is fundamental for the selection and improvement of any character. It helps to identify yield components and superior lines from the population. It tells about the association of one trait with another (Bhardwaj et al., 2021). Yield is a product of many traits that are inter-related, hence knowledge of interrelationship is important in improvement. For measuring the mutual relationship between two traits and identifying component traits in selection correlation analysis is used. It helps in the direct and indirect selection of traits (Abed et al., 2020). All breeding activities aim at boosting the potential of plants for yield (Youssef). Understanding of Genotypic and phenotypic correlation is helpful in breeding programs. Traits can be selected by indirect means. For directly correlated traits, one trait can be enhanced by enhancing the other. The selection of primary traits can be used to improve secondary traits with the help of the coefficient of correlation (Abd El-Aziz et al., 2016). Fruit yield is a complex trait that depends upon other traits, knowledge of the association of plant character helps determine the influence of characters on yield. Successfully breeding program depends upon genetic diversity and knowledge of inter-relationships and their effects. As goal of plant breeders is to achieve more productive varieties by selecting desirable parents and knowledge of interrelationships (Bagadiya et al., 2023).

Objectives

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- Association analysis of different okra traits using statistical approach.
- Mean performance of parents and crosses.

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

The experimental material consisted of okra genotypes collected from the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Line \times 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 F₁S. Genotypes are given below in Table 1.

Table 1: List of parents and 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 \times 1	Patel \times IQRA-III
1 \times 2	Patel \times Perbhani Karanti
1 \times 3	Patel \times Sabz Pari
2 \times 1	Selection Super Green \times IQRA-III
2 \times 2	Selection Super Green \times Perbhani Karanti
2 \times 3	Selection Super Green \times Sabz Pari
3 \times 1	19234 \times IQRA-III
3 \times 2	19234 \times Perbhani Karanti
3 \times 3	19234 \times Sabz Pari

Crossing technique in okra

Okra is often a cross-pollinated crop. The 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 parent were collected and dusted on the emasculated flower. Pollination was performed at 8-10 A.M. Crossed fruit was removed, and 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

PH= plant height, *FL*= fruit length, *FW*= fruit weight, *FD*= fruit diameter, *NR*= no of ridges, *LL*= leaf length, *LB*=leaf breadth, *NF* = node at which first fruit is present, *NOF*= number of fruits, *MO*= moisture contents, *PR*= protein contents, *ASH*= ash contents, *CF*= crude fat, *ADF*= acid detergent fiber, *NDF*= neutral detergent fiber

Statistical analysis

Analysis of variance (Statistix 8.1) was performed to check out the significance of treatments. Genotypic and phenotypic correlation coefficients were estimated to check the association of characters (R Software).

Results and discussion

An increase in productivity is an important goal in any breeding program. The study of genetic architecture plays a vital role as knowledge of genetic components of yield-related traits is essential for the improvement of existing varieties as well as for the development of new varieties. Selection of genotypes with desirable traits is the basic step in breeding.

Mean performances of parents and crosses

The highest plant height was observed in cross Patel × Perbhani Karanti (130.8 cm) followed by Patel × IQRA-III (128.4cm), Patel× Sabz Pari (117.2 cm) and Selection Super Green × Perbhani Karanti (107.5 cm) as shown in figure 1. The lowest value for crosses was exhibited by cross 19234 × Sabz Pari (100.5 cm). Mean values for fruit length showed a range from 11.4 cm (Sabz Pari) to 19.5 cm (19234). Maximum fruit length (19.5 cm) was exhibited by line 19234 and minimum length (14.2 cm) was observed by Selection Super Green. Among testers maximum and minimum observed values i.e. 19.1 and 11.4 cm were exhibited by Perbhani Karanti and Sabz Pari, respectively. Mean values for crosses ranged from 13.4 to 18.7 cm. The highest values for fruit length were observed by cross 19234 × Sabz Pari (18.7 cm) (Figure 2). Mean values for fruit weight ranged from 13.6 to 33.2 g. Among lines maximum fruit weight was observed by line 19234 (32.9 g) and among testers Perbhani Karanti showed the highest value for fruit weight i.e. 27.9 g. Among lines minimum observed value for fruit weight was 23.1 g, exhibited by Selection Super Green, and among testers minimum value exhibited by Sabz Pari (13.6 g). Mean values varied from 33.2 to 17.5 g for

crosses (figure 3). Maximum value for fruit diameter was exhibited by Selection Super Green × Perbhani Karanti (21.5mm) followed by Patel × IQRA-III (20.1 mm), Patel × Perbhani Karanti (18.9 mm), Selection Super Green × Sabz Pari (18.7 mm) and Patel × Sabz Pari (18.5 mm). Among crosses, minimum values for fruit diameter were observed for 19234 × Perbhani Karanti (16.7 mm) and 19234 × IQRA-III (16.9 mm) (figure 4). For leaf length, mean values ranged from 12.1 to 28.1 cm (figure 7). The mean value for the crosses' maximum observed leaf breadth was 34.8 cm, as exhibited by Patel × Perbhani Karanti (figure 8). Mean values for the number of fruits per plant varied from 9.1 to 34.5 (figure 9). Mean values for moisture contents varied from 9.4 to 39.5%. Among crosses, Patel × Sabz Pari showed the maximum mean value (39.5%) followed by Selection 19234 × Perbhani Karanti (37.4%) and Super Green × IQRA-III (34.5%) (figure 10). For protein contents in fruit, mean values ranged from 14.5 to 20.2%. In lines, it varied from 15.5 to 20.2 % (figure 11). Mean values for ash contents showed the broad range of expression among lines, testers, and crosses, it ranged from 3.4 to 56.7 %. Among lines, it varied from 7.2 to 41.5 % (figure 12). The maximum mean value for crosses for crude fat exhibited by Selection Super Green × IQRA-III (4.7 %) followed by 19234 × Perbhani Karanti (4.4 %) and Patel × Sabz Pari (4.1 %). Crosses Selection Super Green × Sabz Pari, 19234 × IQRA-III and Patel × IQRA-III showed a mean value of 1.5, 1.5, and 1.6 % respectively. Selection Super Green × Perbhani Karanti exhibited a minimum value of mean (1.2 %) among all crosses (figure 13). Mean values for ADF ranged from 13.7 to 37.63 %. Among lines, it varied from 27.5 to 31.6 %. Among lines maximum mean value for ADF was exhibited by Patel (31.6 %) and the minimum value was exhibited by 19234 (27.5 %). Among testers, values ranged from 24.2 to 25.4 %. Maximum ADF value was shown by Sabz Pari (25.4 %) followed by IQRA-III (24.2 %) and Perbhani Karanti (23.3 %). Mostly crosses showed higher mean values than parents. Among crosses, maximum value was observed by Selection Super Green × Perbhani Karanti (37.6 %) and the minimum value was observed by 19234 × Sabz Pari (13.7 %). Crosses Selection Super Green × IQRA-III, Selection Super Green × Sabz Pari, and 19234 × IQRA-III showed mean values of 36.7, 35.1 and 33.8 % respectively (figure 14). Among testers mean values for NDF varied from 40.2 % to 38.4 %. Perbhani Karanti depicted the highest value of 40.2 % followed by IQRA-III and Sabz Pari with mean values of 39.1 and 38.4 % respectively. Among crosses, it fluctuated from 54.8 to 18.5 %. Maximum mean value exhibited by Selection Super Green × Perbhani Karanti (54.8 %) followed by Selection

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Super Green × Sabz Pari (54.7 %). The minimum value observed among crosses was 18.5 %, exhibited by 19234 × Sabz Pari. Crosses Patel × Perbhani

Karanti and 19234 × Perbhani Karanti showed mean values of 48.6 % and 48.2 %, respectively (figure 15).

Figure 1: Mean performance of lines, testers and crosses for plant height

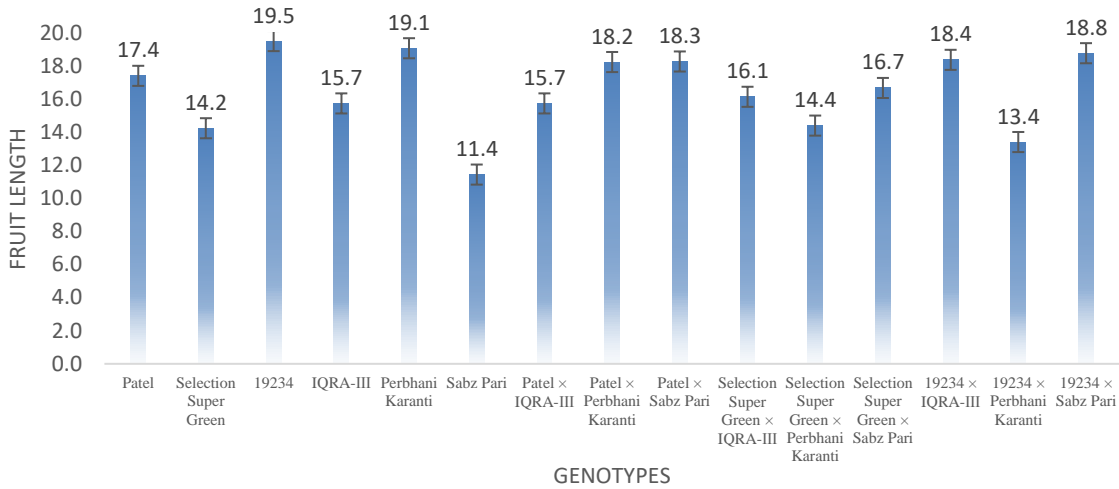


Figure 2: Mean performance of lines, testers and crosses for fruit length

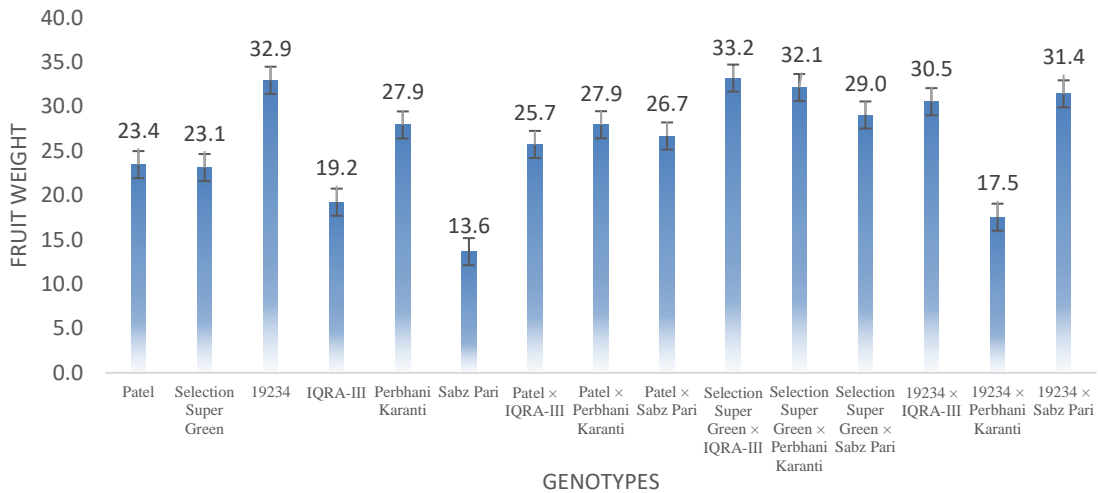
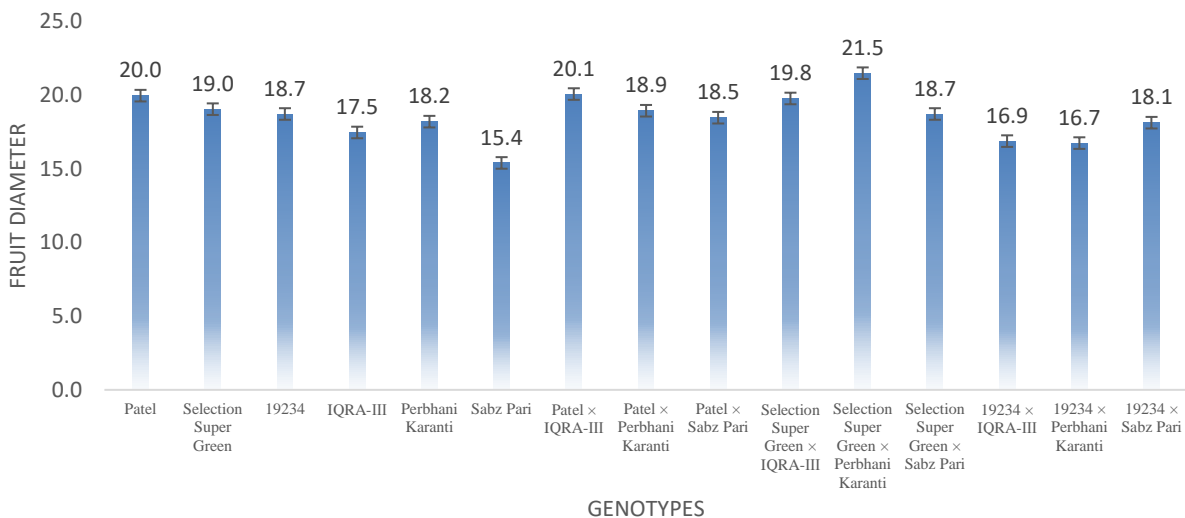


Figure 3: Mean performance of lines, testers and crosses for fruit weight



[Citation: Khan, F., Saeed, A., Fatima, N., Ullah, I., Iqbal, R.A., Khan, Z.A., Rabnawaz, Toor, S., Arshad, M., Siddiq, M.A., Ahmad, M.I (2024). Mean performance evaluation of okra parents and crosses based on morphological and biochemical parameters. *Biol. Clin. Sci. Res. J.*, 2024: 968. doi: <https://doi.org/10.54112/bcsrj.v2024i1.968>]

Figure 4: Mean performance of lines, testers and crosses for fruit diameter

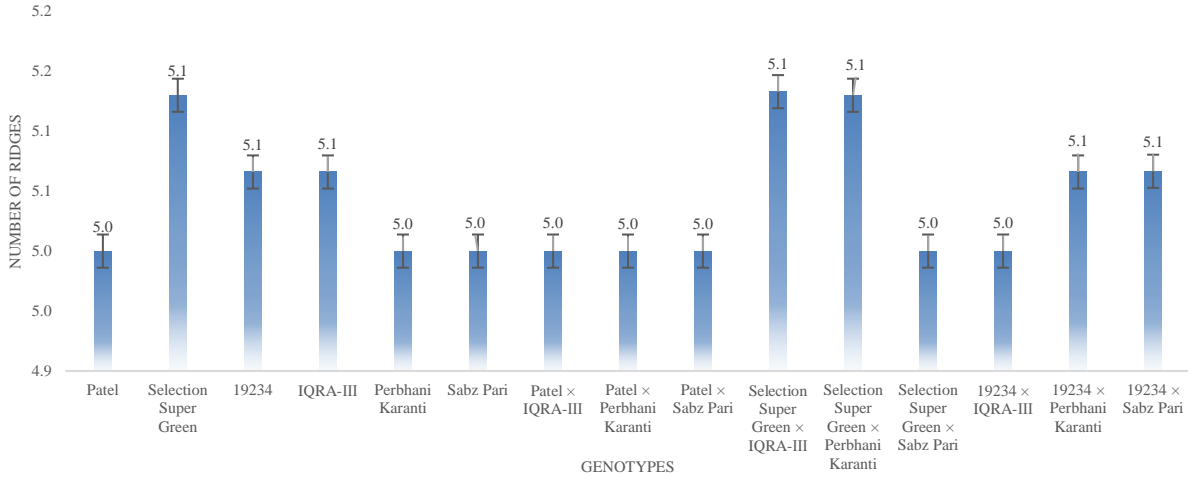


Figure 5: Mean performance of lines, testers and crosses for number of ridges on fruit

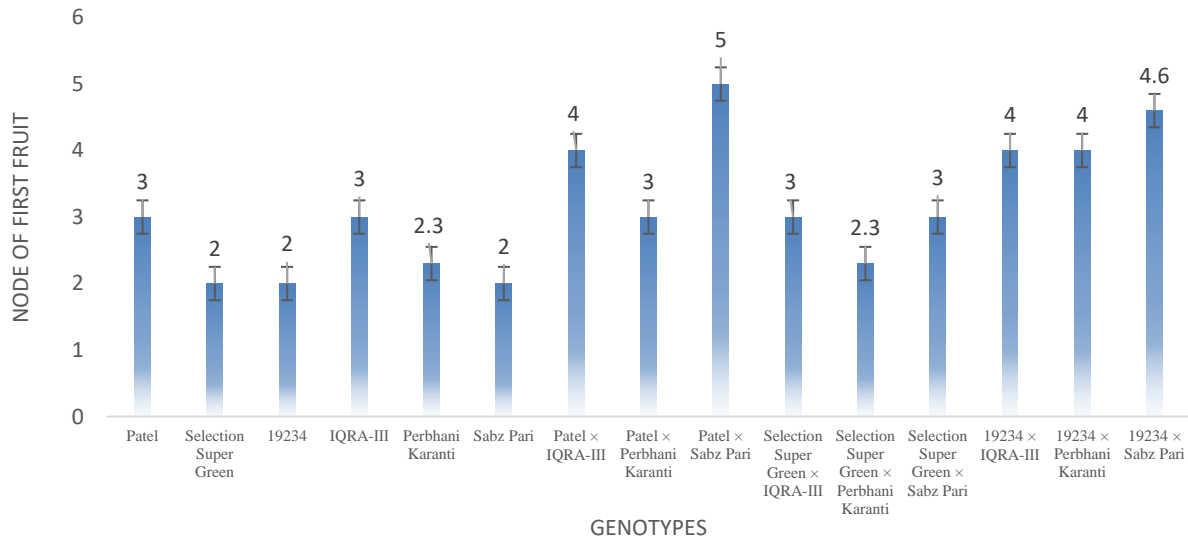
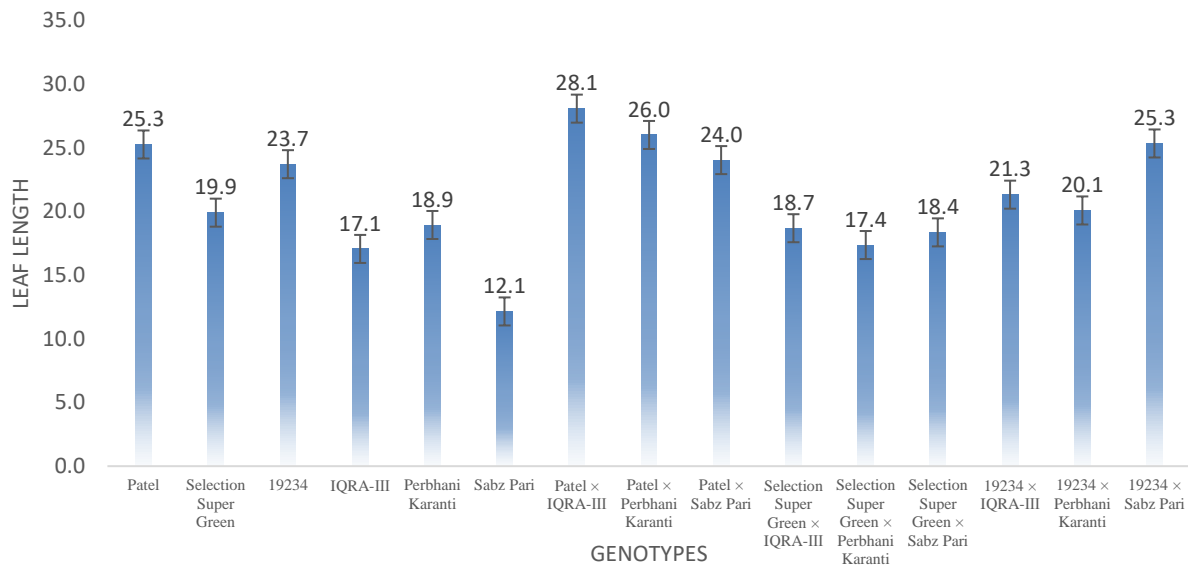


Figure 6: Mean performance of lines, testers and crosses for node at which first fruit is present



[Citation: Khan, F., Saeed, A., Fatima, N., Ullah, I., Iqbal, R.A., Khan, Z.A., Rabnawaz, Toor, S., Arshad, M., Siddiq, M.A., Ahmad, M.I (2024). Mean performance evaluation of okra parents and crosses based on morphological and biochemical parameters. *Biol. Clin. Sci. Res. J.*, 2024: 968. doi: <https://doi.org/10.54112/bcsrj.v2024i1.968>]

Figure 7: Mean performance of lines, testers and crosses for leaf length

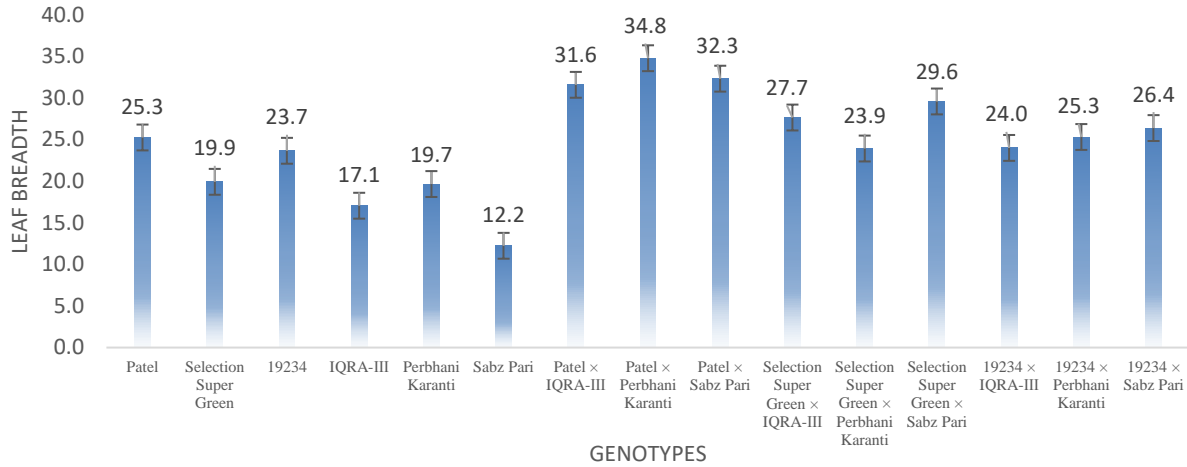


Figure 8: Mean performance of lines, testers and crosses for leaf breadth

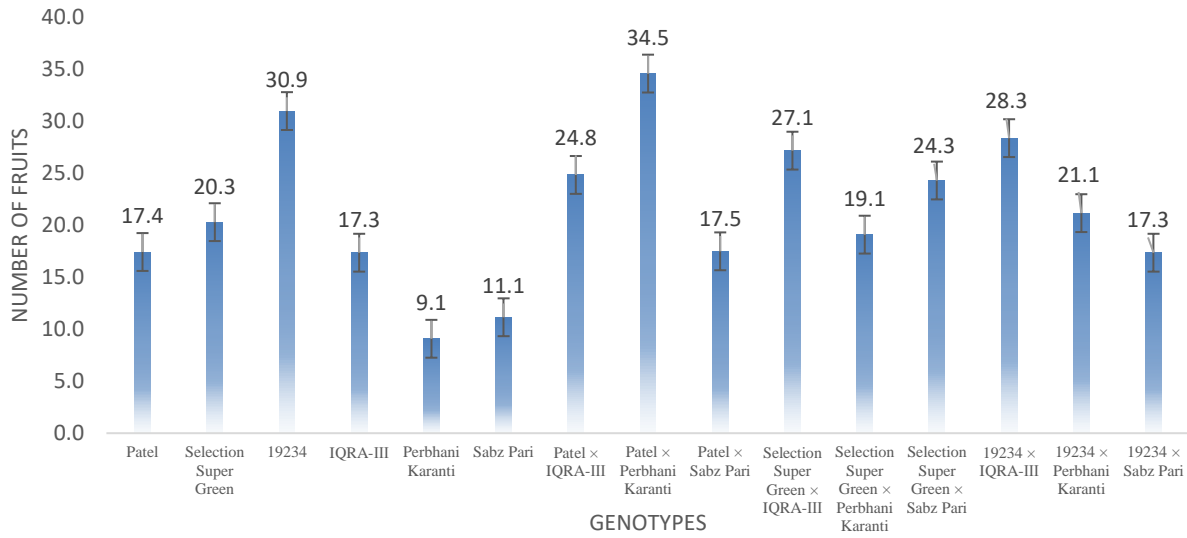
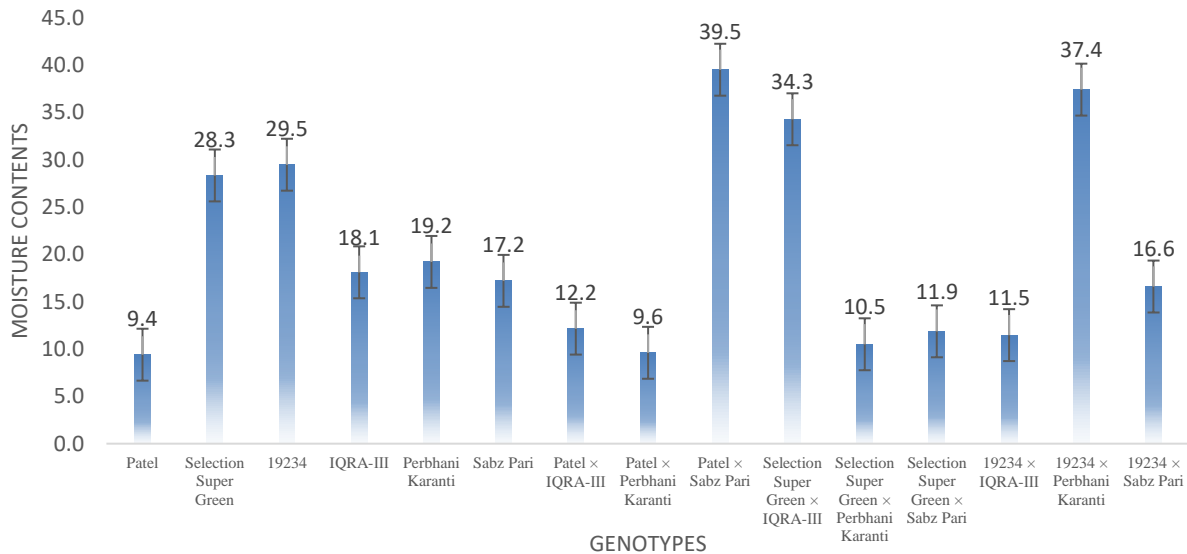


Figure 9: Mean performance of lines, testers and crosses for number of fruits per plant



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Figure 10: Mean performance of lines, testers and crosses for moisture contents

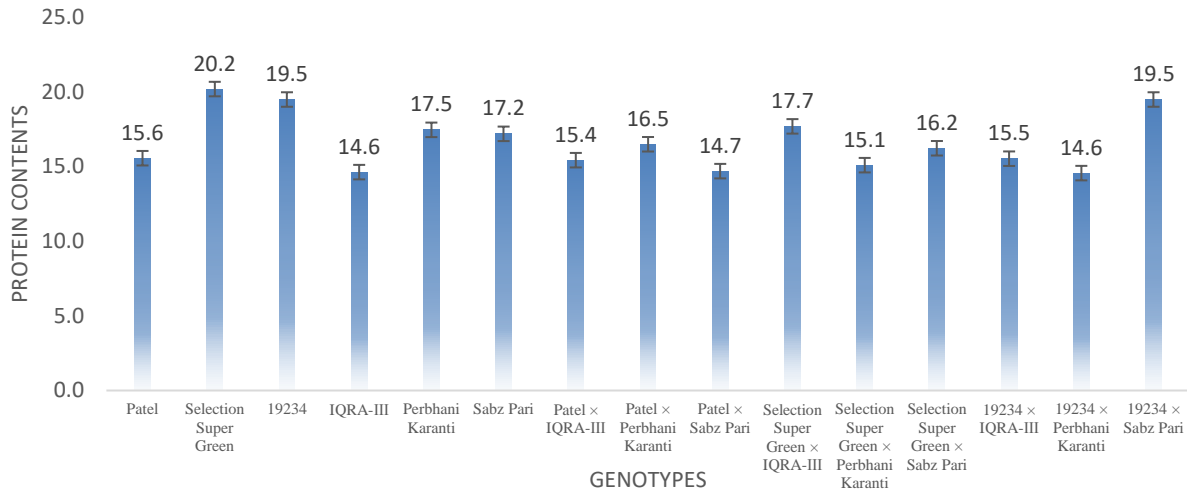


Figure 11: Mean performance of lines, testers and crosses for protein contents

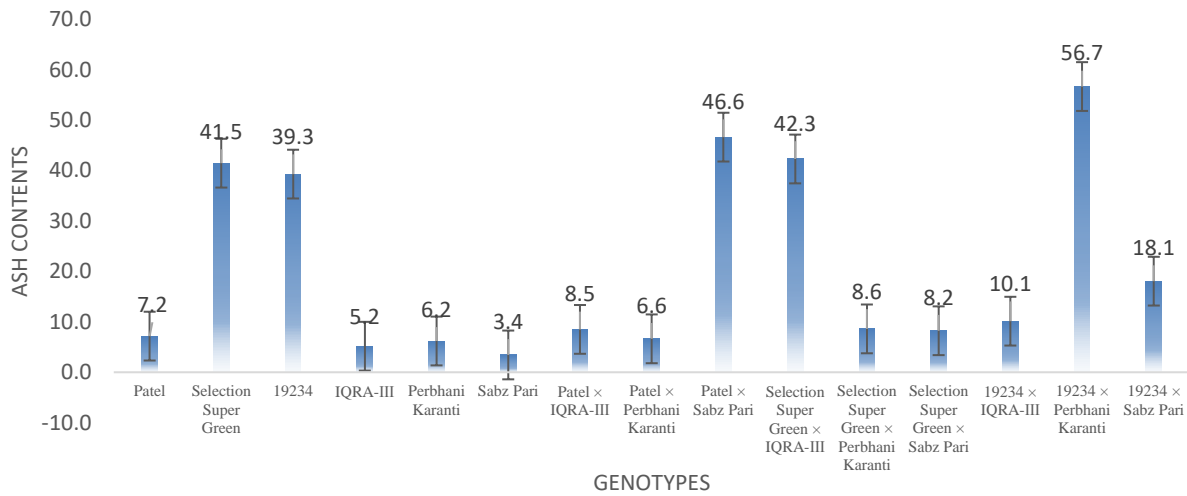
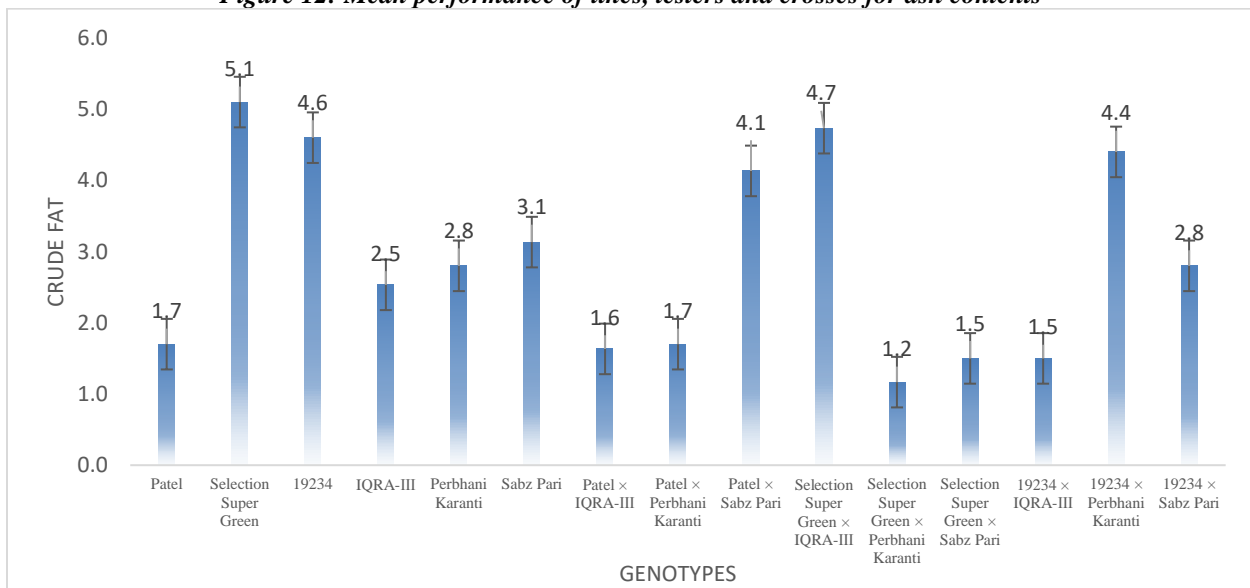


Figure 12: Mean performance of lines, testers and crosses for ash contents



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Figure 13: Mean performance of lines, testers and crosses for crude fat

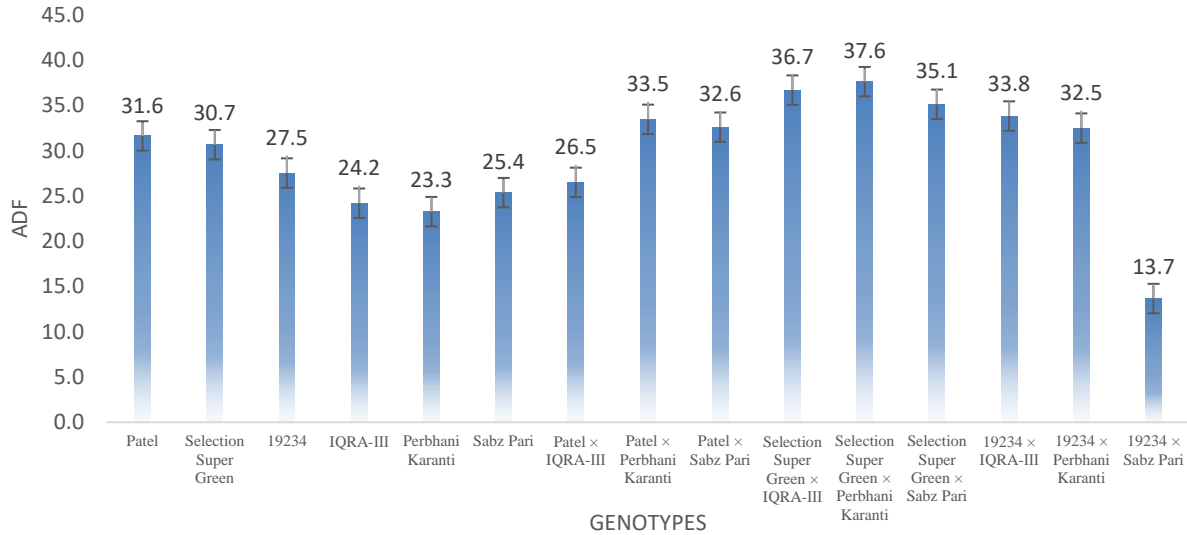


Figure 14: Mean performance of lines, testers and crosses for ADF (acid detergent fiber)

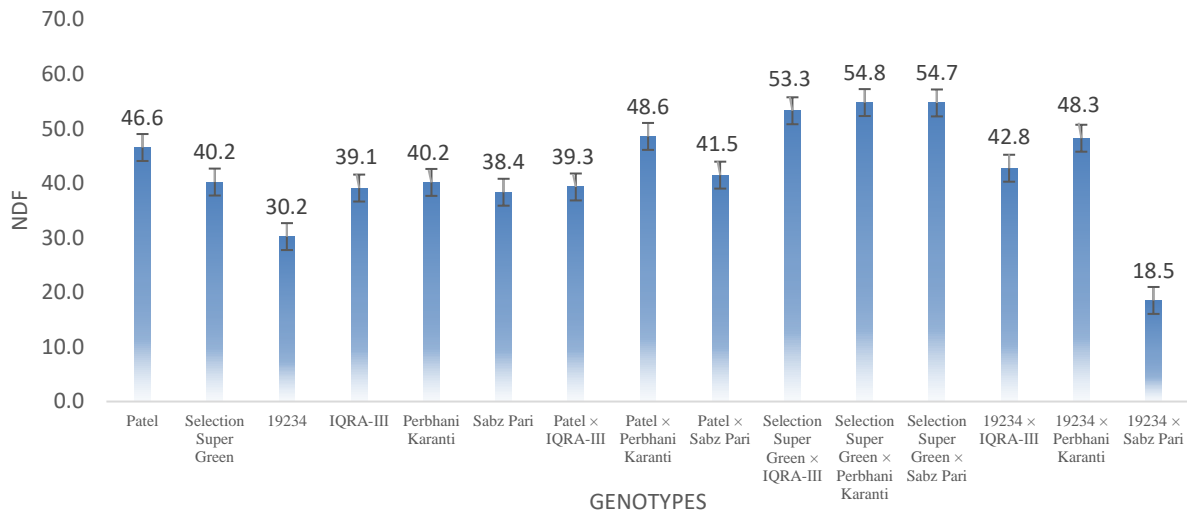


Figure 15: Mean performance of lines, testers and crosses for NDF (neutral detergent fiber)

Correlation analysis (genotypic and phenotypic correlations)

Genotypic and phenotypic correlation coefficients were calculated to check the association of characters. Correlation analysis is used to estimate the relationship between traits. Knowledge of interrelations between traits helps in the selection of genotypes. Association analysis was performed on both genotypic and phenotypic basis.

Genotypic correlation

Correlation analysis revealed that plant height had a significant positive association with fruit length, fruit weight, fruit diameter, leaf length, number of fruits, ADF, NDF, and number of ridges. Plant height showed a negative association with protein contents and crude fat. It exhibited a significant negative association with the node at which the first fruit is present. Similar results were reported by (Ashraf et al., 2020). Fruit length showed a significant positive

association with plant height, fruit weight, leaf length, leaf breadth, number of fruits, and node at which the first fruit is present. The correlation matrix indicated a negative significant association of fruit length with NDF and the number of ridges. A positive significant correlation of fruit length with the number of fruits per plant was also reported by (Singh et al., 2006). Similar results were reported by (Aminu et al., 2016). Results showed close similarity with (Simon et al., 2013). Correlation analysis displayed a positive significant association of fruit weight with plant height, fruit length, fruit diameter, leaf length, leaf breadth, number of ridges, node of first fruit, and number of fruits. It showed a negative significant correlation with NDF. (Ahamed et al., 2015) reported a significant association of fruit weight with plant height and fruit length. Results

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showed close similarity with (Shivaramgowda et al., 2016). Fruit diameter showed a significant positive association with plant height, fruit weight, leaf length, leaf breadth, ADF, NDF, and number of ridges. A significant positive association was observed for fruit weight, fruit diameter, leaf breadth, moisture contents protein contents, ash contents, and crude fat with the number of ridges. The correlation matrix exhibited a negative significant association with plant height, fruit length, and leaf length. The correlation index showed a positive significant association of leaf length with plant height, fruit length, fruit weight, fruit diameter, leaf breadth, NDF, number of ridges, and node of the first fruit. It showed a non-significant association with other parameters. A positive significant association was observed for leaf breadth with fruit length, fruit weight, fruit diameter, leaf length, number of ridges, the node at which the first fruit is present, ADF, and NDF. Plant height, fruit length, fruit weight, leaf length, and leaf breadth showed significant correlations with the node at which the first fruit is present. It exhibited a negative association with protein contents. The number of fruits per plant positively correlated with plant height, fruit length, fruit weight, leaf length, and ADF. (Singh et al., 2007) also found that the number of fruits was positively correlated with plant height and fruit diameter. Moisture content had a positive significant linkage with ash, crude fat, and the number of ridges. It had a non-significant negative association with fruit length, fruit weight, fruit diameter, leaf length, and number of fruits. The correlation matrix showed that protein contents had a positive significant correlation with crude fat, number of ridges, and node of the first fruit. It showed a negative significant association with NDF. Ash contents showed a positive significant association with moisture contents, crude fat, and the number of ridges. Crude fat depicted a positive significant correlation with moisture contents, protein contents, ash contents, and the number of ridges on fruit. (Ranga et al., 2021) also observed a non-significant correlation of crude fat with the number of fruits. ADF showed a positive significant correlation with plant height, fruit diameter, leaf breadth, number of fruits, and NDF. It showed a negative non-significant association with fruit length, leaf length, and protein contents. The correlation matrix showed that NDF positively correlated with plant height, fruit diameter, and ADF. Correlation analysis also indicated that NDF had negative significant association with fruit length, fruit diameter and protein contents.

Phenotypic Correlation

The correlation matrix showed that plant height had a significant positive correlation with fruit weight,

fruit diameter, leaf length, leaf breadth, number of fruits, ADF, and node at which the first fruit is present. Similar results were reported by (YADAV et al., 2017). Fruit length exhibited a positive significant association with fruit weight, fruit diameter, and leaf length. It showed a negative but non-significant association with moisture contents, ash contents, crude fat, ADF, and NDF. A non-significant positive association was observed for leaf breadth number of fruits and protein contents. (Yadav et al., 2010) reported a significant association of fruit length with plant height and fruit weight. Fruit weight exhibited a significant positive relationship with plant height, fruit length, fruit diameter, leaf breadth, and number of fruits. It showed a non-significant positive association with leaf length, protein contents, ash contents, and ADF. A non-significant but negative relationship was observed for moisture, crude fat, and NDF. Similar results were reported by (Yadav et al., 2010). (Alam et al., 2020) reported a significant association between fruit weight and fruit length. The correlation matrix depicted a significant positive association of fruit diameter with plant height, fruit length, fruit weight, leaf breadth, NDF, and number of ridges. A non-significant correlation was observed between fruit diameter and leaf length, number of fruits, protein content, and ADF. (Alam et al., 2020) also reported a significant association of fruit diameter with plant height, fruit length, first flowering node and number of fruits per plant. Number of ridges on fruit showed a positive significant association with fruit diameter, ash, and crude fat. A non-significant but negative association was observed for plant height, fruit length, fruit weight, leaf length, moisture contents, and node of the first fruit. (Mishra et al., 2015) reported similar non-significant results for the number of ridges. Leaf length is significantly correlated with plant height, fruit length, leaf breadth, number of fruits, and node at which the first fruit is present. It showed a non-significant (positive) correlation with fruit weight, fruit diameter, protein contents, and ash contents. A negative significant correlation was observed for ADF while negative non-significant results were observed for moisture contents and crude fat. The correlation matrix depicted that leaf breadth significantly (positive) correlated with plant height, fruit weight, fruit diameter, leaf length, number of fruits, ADF, and node of first fruit. Fruit length, moisture, and ash contents showed a non-significant correlation with leaf breadth. The correlation matrix exhibited a significant correlation between the node of the first fruit with plant height, leaf length, and leaf breadth. A significant negative association was observed for protein contents (-0.3081). Correlation analysis revealed that the number of fruits per plant had a

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positive significant correlation with plant height, fruit weight, leaf length, leaf breadth, and ADF. The high value of the coefficient of correlation (0.6663) was observed for plant height. Fruit length and fruit diameter had a non-significant correlation with the number of fruits. (Das et al., 2022) found number of fruits positively correlated with plant height and fruit length at the phenotypic level. (Kenaw et al., 2023) obtained similar results. A positive significant correlation was observed for moisture contents with ash contents and crude fat. 0.926 value for the phenotypic coefficient of correlation was observed for ash contents. It had a non-significant association with all other indices. Protein contents showed a significant positive association with crude fats while it showed a negative significant association with ADF, NDF, and node of the first fruit. A non-significant negative relationship was observed with plant height. The correlation matrix exhibited a positive significant correlation of ash contents with moisture contents, crude fat, and number of ridges. Non-significant relationship was observed with all other parameters. Crude fat had positive significant association with moisture contents with coefficient value of 0.9098. It also showed significant positive

association with protein, ash and number of ridges. Negative but non-significant association was observed for crude fat with plant height, fruit length, fruit weight, fruit diameter, leaf length, leaf breadth and number of fruits. Similar results were indicated by (Hayati, 2020). Correlation analysis revealed positive significant relationship of ADF with plant height, leaf breadth, number of fruits and NDF. It had negative significant association with leaf length (-0.1153) and protein contents. Non-significant association was observed for other traits. Negative non-significant relationship was observed with fruit length. Correlation matrix depicted that NDF had positive significant correlation with fruit diameter and ADF. Negative significant correlation was observed between NDF and protein contents (-0.528). All other indices showed non-significant results.

Conclusion

Parent 19234 performed overall best and in cross-combination Selection Super Green × Perbhani Karanti performed well in overall attributes.

Table 2: Genotypic correlation

	PH	FL	FW	FD	NR	LL	LB	NF	NOF	MO	PR	ASH	CF	ADF
FL	0.357*													
FW	0.563*	0.689**												
FD	0.564**	0.124	0.58**											
NR	-0.15*	-0.677**	0.301*	0.514**										
LL	0.746*	0.855**	0.487**	0.522**	-0.432*									
LB	0.99	0.624**	0.630**	0.589**	0.297*	0.761**								
NF	0.375*	0.338*	0.115*	-0.099	-0.49	0.58**	0.616**							
NOF	0.685*	0.354*	0.496**	0.277	0.107	0.526**	0.667	0.082						
MO	0.001	-0.089	-0.089	-0.201	0.59**	0.093	0.045	0.178	-0.035					
PR	-0.099	0.198	0.29	0.0023	0.55**	0.037	-0.174	-0.39**	0.063	0.141				
ASH	0.221	-0.058	0.043	-0.034	0.736**	0.116	0.238	0.22	0.19	0.93**	0.19			
CF	-0.144	-0.145	-0.130	-0.234	0.765**	-0.148	-0.166	0.22	-0.04	0.911**	0.48**	0.855**		
ADF	0.472*	-0.209	0.175	0.379*	0.266	-0.149	0.38*	-0.146	0.440**	0.092	-0.40	0.215	-0.062	
NDF	0.320*	-0.347*	-0.065	0.353*	0.129	-0.321*	0.242*	-0.20	0.198	-0.069	-0.53**	-0.018	-0.232	0.89**

Table 3: Phenotypic correlation

	PH	FL	FW	FD	NR	LL	LB	NF	NOF	MO	PR	ASH	CF	ADF
FL	0.274													
FW	0.517**	0.705**												
FD	0.493**	0.342*	0.621*											
NR	-0.113	-0.073	0.193	0.298*										
LL	0.531**	0.343*	0.262	0.250	-0.172									
LB	0.787**	0.230	0.419*	0.311*	-0.111	0.654**								
NF	0.341*	0.226	0.085	0.095	-0.168	0.456**	0.472**							
NOF	0.666**	0.265	0.461*	0.233	0.057	0.399**	0.555**	0.08						
MO	0.002	-0.068	-0.083	-0.174	0.244	-0.074	0.036	0.171	-0.035					
PR	-0.102	0.160	0.275	0.011	0.252	0.026	-0.144	-0.308*	0.065	0.1407				
ASH	0.217	-0.044	0.040	-0.03	0.310*	0.086	0.196	0.216	0.190	0.926**	0.18945			
CF	-0.137	-0.105	-0.121	-0.206	0.304*	-0.118	-0.14	-0.094	-0.036	0.908**	0.479**	0.853*		
ADF	0.458*	-0.158	0.166	0.336	0.304*	-0.115*	0.304*	-0.144	0.433**	0.091	-0.404**	0.214	-0.064	
NDF	0.313	-0.269	-0.007	0.309*	0.049	-0.246	0.202	-0.20	0.197	-0.069	-0.528**	-0.018	-0.232	0.89**

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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

All authors contributed equally.



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