



Genetics of seed yield and related traits in biparental crosses of okra (*Abelmoschus esculentus* (L.) Moench)

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Abstract

The yield of okra is consistently hampered by several problems, including outdated cultivars. This usually results in lower quality and yielding pods. Therefore, in order to meet the needs of consumers, it is essential to develop genotypes of okra that are both high-yielding and adaptable. The randomized complete block design experiment was carried out in 2022 at the Agricultural Research Farm, Bacha Khan University, Charsadda. The results showed highly significant differences observed for nearly all of these variables under investigation except primary branches plant⁻¹ and seeds pods⁻¹. The best genotypes were found to be P5×P2 for internode length (3.59 cm), P4×P1 for individual fruit weight (9.65 g), P3×P1 for maximum plant height (102 cm), and P2×P3 for the largest number of internodes plant⁻¹ that were recorded (22.5). The highest reported pods plant⁻¹ (33.5) and seeds pod⁻¹ (48.5) for P4×P5 and P1×P2 were found, respectively. All features were controlled by non-additive gene action, according to combing ability analysis. In a similar vein, parental lines P2 and P3 demonstrated strong general combiners for several characteristics. Due to their strong SCA effects and good performance per se, P2×P3 and P3×P4 were also exceptional crosses. Heritability studies cautioned against relying solely on phenotypic performance for trait selection. Most crossings surpassed the checks in heterosis, suggesting their suitability for future okra breeding programs. Additionally, inbreeding depression estimates indicated negative effects due to selfing, yet self-pollinated crops like okra demonstrated resilience to inbreeding depression. Based on our findings, the top crosses for yield and associated traits were identified as P2×P3, P3×P4, and P5×P3. We recommend further breeding programs utilizing these genotypes to enhance the quantitative traits of *A. esculentus*.

Keywords: Combining ability, Diallel mating, Heritability, Heterosis, Inbreeding depression

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Introduction

Okra (*A. esculentus*) is one among 130–150 species that make up the genus *Abelmoschus*. Its easy cultivation, steady production, tolerance to changes in rainfall, and adaptability to different soil types and moisture conditions make this crop highly valued (Gopalan et al., 2007). Due to its wide range of uses and nutritive value, it has been successfully cultivated in Pakistan, India, China, Thailand, Egypt, Nigeria, Sudan, South Africa, Brazil, and the Caribbean, among other nations (Farinde et al., 2007). Okra is a fruit-vegetable crop that is grown annually and is said to have its origins in Southeast Asia. The crop suggests that the best places to cultivate it are tropical and subtropical areas. (Reddy et al., 2012), and in these regions, it has great significance as a vegetable (Odedara et al., 2011). Depending on the cultivar, it can live for 60–120 days, and the primary propagules are seeds. Depending on the species, the crop can grow up to 4 m in height and has varying branching on an erect, sturdy stem. It has single blooms that are borne on the axils of its alternating,

often palmately five-lobed leaves (Maldonado-Peralta et al., 2021).

Farmers start farming in January and take advantage of increased pricing by growing the off-season Kharif crop, which thrives in warm weather (Zareen et al., 2017). In order to get maximum efficiency, higher soil and nighttime temperatures are necessary. Two months (February to November) are viable for harvesting, with summer being the busiest (Anonymous, 2016). Pods can be collected every day during fruiting (Ali et al., 2013). Okra varieties fall into two main categories: those that are native to a particular area and those that originate from other places. Farmers should choose okra varieties that suit their local environment and soil properties in order to optimize profitability (Kumar et al., 2016). An acre of crops will normally yield 400–600 kg of seed. First harvesting is done for seed collecting when viral infections are a threat. When the pods mature and change color, indicating that they have separated from the plant, it is time to harvest (Madisa et al., 2015).

Pakistan's okra yields are only 7-12 tonnes per hectare, far less than those of the US and Cyprus, which produce 20

tonnes. Reduced yields are caused by factors like poor soil, poor planting techniques, poor seed, and scarce resources (Alam et al., 2020). In order to overcome these obstacles and increase yield, despite land and fertilizer availability limitations, farmers increase plant density. Okra output is continuously limited by a number of issues, such as outdated cultivars. These frequently lead to lower yields and lower-quality pods. Thus, it is important to create genotypes of okra that are both adaptive and high-yielding in order to suit the needs of the general public. Okra yield is influenced by environment, genotype, and their combined effects. Generating better genotypes that will satisfy the public should therefore be the primary goal of any okra improvement plan (Oyetunde & Ariyo, 2014).

The expression of genes when they work independently or collectively is referred to as gene activity. The selection of appropriate breeding procedures is made easier by the knowledge of the gene effect within a population. The degree to which a gene affect dominated determined considerably regarding the way to handle a certain character. The ratio of additive to non-additive variance demonstrates the proportionate significance of the gene activity governing the character judgments. Additive variance predominates when the ratio is above unity (>1), but non-additive variance predominates when the ratio is below unity (<1) (Mackay et al., 2019). Additionally, it has been consistently determined the weight and number of pods per plant are important determinants influencing pod yield (Arvind et al., 2021). Furthermore, choosing parents who are best suited is essential for hybridization to produce better genotypes (Falconer, 1996). The aim of this study

was to investigate the relationship between yield parameters and morphological differences in okra genotypes derived from diallel crosses. The objective of the study was to develop a high yielding Okra cultivar for the Charsadda district based on the performance of biparental crosses for yield and yield related attributes.

Materials and Methods

In the year March 2021, field experiments were carried out at the Bacha Khan University Agriculture Research Farm. Different superior genotypes of okra, collected from the farmers of Charsadda vicinity, were sown in a replicated study (Table 1). The same material was also sown in a crossing block. Data were gathered for various yield related characteristics usually preferred by the local farmers. To save time, crossings between the genotypes were made in a full diallel pattern in the meantime. After the parental lines were analyzed for yield related traits, only crosses with better parental performance were kept for additional testing. In the agricultural area close to the Agriculture block, selected diallel crosses were sown together with standard commercial varieties available in the market (checks) for comparison purpose during March 2022. The genotype was assigned in replicated trials. The standard distance between plants and rows was kept at 25 and 75 cm, respectively. Throughout the growth season, standard agricultural techniques were followed (Anyaocha et al., 2022).

Table 1 List of the parental genotypes, F₁, and checks that were used in the study

Parents		F ₁ 's		F ₁ 's	
i.	BKUC-2 (P1)	i.	P1 × P1 (G1) (S)	xiv.	P3 × P4 (G14)
ii.	BKUC-3 (P2)	ii.	P1 × P2 (G2)	xv.	P3 × P5 (G15)
iii.	BKUC-4 (P3)	iii.	P1 × P3 (G3)	xvi.	P4 × P1 (G16)
iv.	BKUC-7 (P4)	iv.	P1 × P4 (G4)	xvii.	P4 × P2 (G17)
v.	BKUC-8 (P5)	v.	P1 × P5 (G5)	xviii.	P4 × P3 (G18)
		vi.	P2 × P1 (G6)	xix.	P4 × P4 (G19) (S)
Checks		vii.	P2 × P2 (G7) (S)	xx.	P4 × P5 (G20)
i	C-1 (G26)	viii.	P2 × P3 (G8)	xxi.	P5 × P1 (G21)
ii	C-2 (G27)	ix.	P2 × P4 (G9)	xxii.	P5 × P2 (G22)
iii	C-3 (G28)	x.	P2 × P5 (G10)	xxiii.	P5 × P3 (G23)
		xi.	P3 × P1 (G11)	xxiv.	P5 × P4 (G24)
		xii.	P3 × P2 (G12)	xxv.	P5 × P5 (G25) (S)
		xiii.	P3 × P3 (G13) (S)		

At maturity, five plants from each line in each plot were selected at random to collect data on F₁ plants for a number of agronomic factors (Vekariya et al. 2020)

Data collection

Data gathering focused on the following parameters: Internode length (IL) (cm), Individual Fruit weight (IFW)

(g), Primary branches plant⁻¹ (PBP) (Keerthana et al., 2021), pods on primary branches (PPB), plant height (cm) (PH), internodes plant⁻¹ (IP), pods plant⁻¹(PP), and, and seeds pod⁻¹ (SP) (Kerure & Pitchaimuthu, 2019).

Statistical analysis

The statistical tool M Stat C was used to do an adequate RCB analysis of variance on the experimental data. The information was additionally sent to a diallel analysis employing (Griffing, 1956), Model (fixed effect) and Heterosis (Falconer, 1996) after significant F-value ($F \leq 0.05$).

Results and Discussion

Analysis of variance

Data for various traits demonstrated a significant variation in the diallel crosses and checks' performance, with the exception of primary branches plant^{-1} and seeds pod^{-1} (Table 2). The maximum internode length for genotype G4 was 3.59 cm, while the highest internode length for genotype G22 was 6.45 cm. The average fruit weight varied between 5.59 and 9.65 g, with genotypes G23 and G16 obtaining these values, respectively. Table 3 demonstrates that Check III had the most primary branches (2.50), despite the fact that other genotypes only had one primary branch. On the other hand, genotype G5 has a minimum plant height of 81.50 cm and genotype G11 has a maximum average plant height of 102.0 cm. Table 4 made it clear that genotype G8 had highest 22.50 internodes plant^{-1} , whereas genotype G4 had least 12.00 internodes plant^{-1} . The data regarding the quantity of pods produced by each plant varied from 18.00 (G12) to 36.00 (G20). While genotype G2 had the largest average number of seeds pod^{-1} (48.50), followed by genotype G23 (47.50), genotype G2 had the fewest seeds pod^{-1} (35.50) (Table 4).

Combining ability analysis

A study of combining abilities was only performed on those attributes that displayed significant variations. After the data were analyzed, Table 5 makes it clear that there were significant variations in the genotypes (crosses) for internode lengths. Replication showed that no statistically significant difference was observed. GCA and reciprocal impacts yielded significant mean squares for the internode length, but SCA did not provide any significant changes (Table 5). P5 demonstrated a pretty significant positive value for this trait, making it an outstanding general combiner. P1xP4 showed significant favorable changes for the SCA impact after P1xP2. The reciprocal effects of highly significant differences were seen when P5 was crossed with P1, P2, and P3.

For internode length, the genotypic variance was remarkably low, suggesting that the majority of the variation was not heritable (Table 6) (Priyanka et al., 2018). The variance ratio of GCA to SCA related to this parameter has a value less than one (0.136). No significant variations were found for replication; nevertheless, an analysis of variance indicated that there were highly significant differences in mean squares ($P < 0.01$) across

crosses concerning the weight of each individual fruit (Table 5). A substantial difference was found in the combining ability analysis for GCA, SCA, and RE. A better general combiner for this character was evident for parental line P1. The cross combination of P1xP4 was good for this parameter. The cross between P4 and P1 showed significant differences that could have reciprocal consequences (Table 7). The ratio of the two variances is less than one, as Table 5 demonstrates, the SCA variance is greater than the GCA variance. This implies that the majority of effects are non-additive (Punia & Garg, 2019) (Patel et al., 2021). The genotypes (crosses) displayed highly significant differences for pods on primary branches, as shown by Table 5 (Ranga et al., 2021). While there were no significant differences for SCA or RE, the ANOVA for combining ability (Table 5) showed highly significant differences for GCA. With regard to this feature, P1 has a significant negative combining ability. Despite the non-significant differences between the parental lines, P5 showed to be a competent combiner.

P1 x P3 was the best cross combination for pods primary branches $^{-1}$ based on SCA effects. For this trait, Table 8 demonstrates that P5's cross with P1, P2, and P4 was a successful combiner with discernible reciprocal effects. A significantly reduced ratio of GCA variation to SCA variance than one (0.002) was seen in Pods primary branches $^{-1}$. This was consistent with the results of (Devi et al., 2020) and (Satish et al., 2017) suggested that non-additive gene activity was involved in regulating the feature. (Vekariya et al., 2020) proposed that heterosis breeding programs or recurrent selection for particular combining ability can be used to increase such features. The analysis's findings demonstrated that the crossings (genotypes) differences in plant height were substantial. All the three components of genetic variances that i.e. general and specific combining ability and reciprocal effects were found to be highly significant (Table 9). The strongest GCA estimations were found for P4 x P5, demonstrating the lines' strong propensity to merge throughout many years. The combinations that produced the highest SCA estimations, P1 x P3 and P4 x P5, were likely the most ideal for this specific character (Table 9) (Pithiya et al., 2020). Plant height was the only characteristic for which P3xP1 and P3xP2 displayed non-significant positive and negative reciprocal effects, respectively. The prevalence of non-additive gene activity was indicated by a higher SCA variance relative to GCA variation, as shown by the GCA/SCA variance of 0.190. A similar conclusion was reached by (Satish et al., 2017) and (Mundhe et al., 2023).

Genotypes (crosses) showed highly significant differences for internodes plant^{-1} . Significant genetic variability was shown among the crosses in Table 5. It was consistent with (Raju & Selvam, 2017) findings. Combining ability analysis indicated extremely significant differences for GCA (Chaudhary et al., 2023), the parental lines P5 and P3 attained considerable negative values for this traits. Significant variations were observed for the SCA effect, the combination of cross between P2xP3 revealed significant differences. Additionally, highly significant variations were seen for the reciprocal influence. (Setu, 2023). P3 x P2 combinations have

a significant effect on this attribute. Table 10 displays the highly significant reciprocal negative impacts of P5's cross with P1, P2, and P3. The lower ratio of variance of GCA to SCA (0.499) disclosed additive dominant gene effects (0.499) (Table 5). Additionally, this demonstrated the increased environmental stability of genotypes (Reddy et al., 2013; Suganthi et al., 2020) (Table 5).

For pods plant⁻¹, there were non-significant differences in genotypes ($P < 0.01$), suggesting statistical similarity between the crossings. Replications, however, showed that genotype performance varied significantly (Table 5). It was distinguished from other parental lines by the relevance of the GCA and the comparatively tiny negative value of P4. Table 11 displays the GCA values that were found to be

the most negative for P5. Not to be overlooked were the SCA values. For specific combinations, the greatest value of 2.61 was evident for the cross of P1xP3 while P4 x P5 followed it with value of 2.51 (Table 11). Conversely, the P1 x P4 combination yielded the lowest SCA value. Significant genetic variations are also shown by the reciprocal effects. The reciprocal effects with the highest significant values were P3 x P2 and P5 x P4, while the reciprocal effects with the lowest significant negative values were P4 x P2. For this trait, the GCA/SCA ratio showed a prevalence of non-additive gene action, which is consistent with the findings of (Demta & Surin, 2019) (Javiya et al., 2020). In contrast, our findings (Rathava et al., 2019) showed that additive gene action plays a major a role in this trait's inheritance.

Table 2 Mean sum of squares for various characteristics of the parents, checks, and diallel crosses studied during 2022

TRAITS	IL	IFW	PBP	PPB	PH	IP	PP	SP
MS	1.19 *	2.15 **	0.35 ^{ns}	3.19 *	55.86 **	10.79 **	36.29 *	23.80 ^{ns}
CV %	15.34	23.50	35.48	27.32	3.36	10.13	17.49	17.22

Table 3 Average values of diallel crosses and checks for various traits

Genotypes	IL (cm)	IFW (g)	PBP	PPB
G1	5.59	7.77	1.00	4.50
G2	6.37	7.72	1.00	6.83
G3	5.23	6.20	1.33	6.67
G4	6.45	5.76	1.17	6.50
G5	5.84	6.60	1.33	7.67
G6	6.02	6.43	2.00	7.17
G7	5.62	8.00	1.00	6.17
G8	4.54	8.29	1.50	5.00
G9	5.78	7.97	1.00	6.50
G10	5.67	5.77	1.67	6.50
G11	6.37	5.60	1.33	7.17
G12	6.08	6.23	1.00	5.00
G13	4.62	6.43	1.00	4.34
G14	6.28	8.25	1.84	6.00
G15	5.84	6.67	1.84	5.67
G16	6.03	9.65	1.84	4.67
G17	6.00	6.70	2.00	5.50
G18	5.53	6.45	1.00	4.84
G19	5.08	5.70	1.84	4.50
G20	4.80	7.95	2.00	8.17
G21	4.08	6.40	1.34	5.67
G22	3.59	7.40	1.84	3.84
G23	3.80	5.59	1.50	4.34
G24	5.25	6.17	1.84	3.84
G25	5.03	7.50	1.50	6.34
Check I	4.80	6.25	1.84	5.67
Check II	5.37	6.97	2.00	8.00
Check III	5.09	8.30	2.50	7.50

Table 4 Average values of diallel crosses and checks for various traits

Genotypes	PH (cm)	IP	PP	SP
G1	83.5	14.5	18.5	41.5
G2	85.5	13	19.5	48.5
G3	88.5	14.5	23	44.5
G4	83.5	12	20	40
G5	81.5	13	23.5	46.5
G6	94	14.5	27.5	35.5
G7	93	16.5	23	41
G8	101.5	22.5	28	36.5
G9	91	14	21	40
G10	92	15	26.5	43
G11	102	16	25	43
G12	91	14	18	42
G13	86.5	14	18.5	41
G14	91.5	15	24	43.5
G15	93	14.5	23.5	43
G16	88	13.5	22.5	43
G17	94	15	26.5	37.5
G18	90.5	14.5	22.5	40.5
G19	89.5	15.5	23.5	38.5
G20	98	18.5	33.5	39
G21	94.5	18	26	44.5
G22	88.5	19	26	36
G23	95.5	20.5	26.5	47.5
G24	99.5	16.5	23.5	38
G25	87	14.5	24	42.5
Check I	92	16	25.5	44
Check II	96.5	16	31.5	38.5
Check III	96.5	17	36	36

Table 5 Mean squares of combining ability for various traits studied during 2022

SoV	Internode length	Individual fruit weight	Pods on primary branches	Plant height	Internode on plant	Pods on plant
Crosses	1.300 *	2.229569**	2.956*	58.73**	11.936**	24.505
Replication	0.129	1.414562	5.122*	100.82**	7.99	42.32*
GCA	2.306 *	1.234544*	2.010**	57.11**	13.99**	33.68*
SCA	0.567	1.526578*	2.521*	59.65**	7.10 *	13.113*
Reciprocal	1.632 *	3.330571*	3.770*	58.47**	15.95 **	32.22*
Error	0.604	2.505	2.005	8.44	2.5	13.77
H ²	0.16	0.52	0.04	0.45	0.28	0.09
GCA/SCA variance	0.1363	0.61	0.002	0.190	0.499	0.762

Table 6 Combining ability estimates of 5x5 okra diallel crosses for internode length

Genotypes	P1	P2	P3	P4	P5
P1	-0.50	0.33**	0.17	0.27*	-0.27
P2	0.17	-0.02	-0.09	0.16	-0.37
P3	-0.56 *	-0.77 **	-0.54	0.41	0.06
P4	0.20	-0.11	0.37	-0.76	-0.08
P5	0.87 **	1.04**	1.02 **	-0.222	0.66*

GCA values = diagonal; SCA values = above diagonal; RE values = below diagonal

Table 7 Combining ability estimates of 5x5 okra diallel crosses for individual fruit weight

Genotypes	P1	P2	P3	P4	P5
P1	0.72*	-0.24	-0.77	0.61*	-0.32
P2	0.64	0.42	0.32	-0.02	-0.49
P3	0.29	1.03	0.13	0.63	-0.31
P4	-1.95**	0.63	0.89*	-1.43	0.20
P5	0.09	-0.82	0.54	0.89*	0.92

GCA values = diagonal; SCA values = above diagonal; RE values = below diagonal

Table 8 Combining ability estimates of 5x5 okra diallel crosses for Pods on primary branches.

Genotypes	P1	P2	P3	P4	P5
P1	-2.03*	0.73	1.18*	-0.31	0.43
P2	-0.16	0.16	-0.46	0.36	-0.79
P3	-0.24	-0.00	-0.60	0.31	-0.43
P4	0.91*	0.50	0.58	-0.76	0.40
P5	0.99*	1.33**	0.66	2.16**	0.39

GCA values = diagonal; SCA values = above diagonal; RE values = below diagonal

Table 9 Combining ability estimates of 5x5 okra diallel crosses for Plant height

Genotypes	P1	P2	P3	P4	P5
P1	-2.06	0.19	5.49**	-2.86*	-0.76
P2	-4.25	-0.06	2.49	-0.11	-2.51
P3	-6.75	5.25	-7.46**	-1.81	1.29
P4	-2.25	-1.5	0.5	-2.16	6.94**
P5	-6.5	1.75	-1.25	-0.75	-4.96*

GCA values = diagonal; SCA values = above diagonal; RE values = below diagonal

Table 10 Combining ability estimates of 5x5 okra diallel crosses for Internodes plant⁻¹

Genotypes	P1	P2	P3	P4	P5
P1	1.32	-1.08	0.47	-1.03	0.32
P2	-0.75	0.02	1.82*	-0.93	0.17
P3	-0.75	4.25**	-2.38*	-0.63	0.72
P4	-0.75	-0.5	0.25	1.12	1.47*
P5	-2.5**	-2**	-3**	0.75	-2.68*

GCA values = diagonal; SCA values = above diagonal; RE values = below diagonal

Table 11 Combining ability estimates of 5x5 okra diallel crosses for Pods plant⁻¹

Genotypes	P1	P2	P3	P4	P5
P1	-2.54	0.96	2.61	-1.44	0.41
P2	-4.00**	-1.04	0.11	-0.44	0.41
P3	-1	5.00**	-3.24	0.21	0.31
P4	-1.25	-2.75*	0.75	-0.84	2.51
P5	-1.25	0.25	-1.5	5.00**	-3.64

GCA values = diagonal; SCA values = above diagonal; RE values = below diagonal

Heritability estimates

The estimates of heritability for individual fruit length varied from 52% to 4% for pods per primary branch. Individual fruit weight showed the highest heritability, followed by fruit length (47%) and plant height (45%). However, it was extremely low for internode length (16%) and pods per primary branch (9%) and pods per plant (9%). For these qualities, very low heritability indicates that direct selection is not effective (AdeOluwa and Kehinde, 2011) (Table 5). This implies that direct selection for these qualities cannot improve the genotypes. Since

heredity is a single numerical expression based on the ratio of the two variances, selection based only on heritability estimates may not be successful. Accordingly, Johnson et al. (1955) found that high heritability combined with high genetic advancement as a percentage of mean was more useful in forecasting the effect of selection. Heritability shows that a trait's expression is under genetic control, and phenotypic reliability allows us to estimate a trait's breeding value. Additionally, it predicts the genetic progress that a breeder could expect through selection and the best breeding technique to use (Singh et al. 2017).

Inbreeding depression for different traits

Negative inbreeding is especially advantageous for internode length since it boosts yield. Table 12 shows that P3 had the least degree of positive inbreeding (2.86) and the highest percentage of negative inbreeding (-22.74). (Zate et al., 2021) recorded internode length values as high as 25.81%, a substantial increase beyond our inbreeding

depression findings. The significance of positive inbreeding for fruit weight variation in relation to yield cannot be overstated. The self P4 and self P5 inbreeding ranges are -11.63 to 22.75, in line with earlier trends (Singh et al., 2009) for those that showed signs of favorable inbreeding. Similar findings for fruit weight, with a 30.1% inbreeding depression, were found by Samindre et al. (2022).

Table 12 Estimates of inbreeding depression (ID%) for morphological traits due to selfing

Parental Genotypes	Internode length	Individual fruit weight	Primary branches	Pods primary branches ⁻¹
P1	-1.76	10.68	-16.67	-19.79
P2	-3.44	9.29	-23.08	-2.37
P3	-22.74	1.90	-16.67	-26.57
P4	-7.30	-11.63	22.67	-34.88
P5	2.86	22.75	-6.25	21.92

Productive primary branches were required to increase the number of fruits plant⁻¹; self P4 demonstrated the highest value of (22.67%), while self P2 showed the lowest inbreeding depression (-23.08). The range of IDs for the pods on primary branches was 21.92 to -34.88. P5 (self) gave a favorable response (21.92), while P4 self-demonstrated a negative response (-34.88) (Table 12). According to (Sabesan et al., 2016) high-performing hybrids had considerable levels of inbreeding depression, which may have contributed to the poor performance of significant-yielding F1 hybrids in subsequent generations. For pods in the plant, negative ID is absolutely necessary. Only P5 (9.09%) demonstrated positive inbreeding during the experiment; the other genotypes showed negative ID, with P3 showing the highest result (-11.90). (Zate et al.,

2021) demonstrated maximum 12.45% inbreeding depression for this characteristic (Table 13). The analysis of genotypes for internode plant⁻¹ revealed that P1(2.11) had the highest level of inbreeding, while P5 had the lowest level of inbreeding depression (-14.71) for this feature. (Chavan et al., 2018) observed that inbreeding depression was maximum for nodes plant⁻¹. Regarding plant height, P1 and P3 showed the most and least levels of inbreeding depression, with values of -1.18 and -8.27, respectively. There was no positive inbreeding depression found in any genotype. According to (Mahajan et al., 2017) plant height showed the lowest level of inbreeding depression whereas pods plant⁻¹ displayed the greatest heterosis. For seeds pod⁻¹, the inbreeding depression rating varied from 2.50 to -8.33. P4 showed the least ID (-8.33), while P2 showed the most inbreeding depression (2.50%).

Table 13 Estimates of inbreeding depression (ID%) for yield traits due to selfing

Parental genotypes	Pods plant ⁻¹	Internode plant ⁻¹	Plant height	Seeds pods ⁻¹
P1	-9.76	2.11	-1.18	-8.19
P2	-4.17	-5.71	-2.72	2.50
P3	-11.90	0.00	-8.27	-3.07
P4	-6.00	-6.06	-4.28	-8.33
P5	9.09	-14.71	-3.87	-3.41

Heterotic study of diallel crosses

Heterosis occurs when a cross performs better than either of its parents. Not all cases of positive heterosis are more significant than those of negative heterosis based on the objectives of the study. Negative heterosis is necessary for a breeder who wants early maturity. To boost yield, though, positive heterosis is required. Considering heterobeltiosis for internode length, the values ranged from

(-7.86) to (39.97) for G4 and G22, respectively (Table 14). In order to maximize the amount of fruits produced by a plant, breeders were more interested in plants with shorter internodes. As a result, smaller internode length plants are preferred over larger ones. Considering negative heterosis in favor of internode length, our results are in line with findings of Mundhe et al. (2022) who reported up to 9% heterosis for internode length.

Table 14 Heterotic study of okra diallel crosses for various traits during 2022

Genotypes	Internode length	Individual fruit weight	Primary branches	Pods primary branches ⁻¹
G1	6.52	-6.15	37.50	34.78
G2	-6.52	-5.46	37.50	1.01
G3	12.54	15.30	16.88	3.33
G4	-7.86	21.31	26.88	5.80
G5	2.34	9.84	16.88	-11.16
G6	-0.67	12.16	-25.00	-3.91
G7	6.02	-9.29	37.50	10.58
G8	24.08	-13.25	6.25	27.54
G9	3.34	-8.88	37.50	5.80
G10	5.18	21.17	-4.37	5.80
G11	-6.52	23.50	16.88	-3.91
G12	-1.67	14.89	37.50	27.54
G13	22.74	12.16	37.50	37.10
G14	-5.02	-12.70	-15.00	13.04
G15	2.34	8.88	-15.00	17.83
G16	-0.84	-31.83	-15.00	32.32
G17	-0.33	8.47	-25.00	20.29
G18	7.53	11.89	37.50	29.86
G19	15.05	22.13	-15.00	34.78
G20	19.73	-8.61	-25.00	-18.41
G21	31.77	12.57	16.25	17.83
G22	39.97	-1.09	-15.00	44.35
G23	36.45	23.63	6.25	37.10
G24	12.21	15.71	-15.00	44.35
G25	15.89	-2.46	6.25	8.12

Mankind thrived from positive heterosis since it directly increased yield. G23 showed the highest heterosis (23.63), while G11 showed the lowest heterosis (23.50). On the other hand, G16 clearly had a negative value (-31.83) (Table 14). When compared to the best parents and the industry standard for fruit weight, the genotype G23 displayed the highest level of heterosis. This implies that this cross will serve you well in the future. For primary branches plant⁻¹, there were slight variations amongst the genotypes. The parameter's maximum and minimum heterosis values varied from 37.50 to -25.00. The heterosis values for the pods on the main branches of G24 and G20 ranged from 44.35 to -18.41, respectively. Increased fruit production on the plant depends on positive heterosis for plant height. G1 and G4 had maximum heterosis reported at 12.66%, while G11 had least heterosis reported at -6.69% (Table 15). (Aware et al., 2014) demonstrated similar positive heterosis for plant height, although his heterosis figure was larger in comparison (28.46 %). For internodes plant⁻¹, G2 and G5 showed positive heterobeltiosis (25.71). For the G8, a negative heterotic value of -28.57 was observed. G12 (28.00) shown positive heterobeltiosis for pods plant⁻¹, while G20 (-34.00) demonstrated negative heterobeltiosis (Table 15). (Singh et al., 2009) also noted similar outcomes, registering a

significantly larger (185%) heterosis for this measure. On the other hand, 13.68% heterosis for pods per plant was discovered by (Srikanth et al., 2019) which contradicts our findings. Table 15 demonstrated that while G2 displayed a negative value (-7.30) for seeds pod⁻¹, G6 displayed positive heterosis (21.46). Another significant characteristic is the amount of seeds per pod, particularly when breeders are trying to produce more seeds. High heterosis genotypes that produce more seeds per pod are regarded as superior.

Conclusion

The study found that parental lines P2 and P3 were good general combiners for attributes like days to flowering, fruit weight, and marketable fruit length, while G8 and G14 were superior crosses. With the exception of plant height and individual fruit weight, most traits showed less than 50% heritability. This implies that selection of the investigated features must not to be predicated exclusively on phenotypic performance. Most qualities displayed negative inbreeding depression due to selfing, suggesting they were least influenced by selfing. Thus, it has been practically demonstrated once more that self-pollinated crops are less affected by the inbreeding depression.

Table 15 Heterotic study of okra diallel crosses for various traits during 2022

Genotypes	Internode plant ⁻¹	Plant height	Seeds pods ⁻¹	Pods plant ⁻¹
G1	17.1	12.7	8.2	26.0
G2	25.7	10.6	-7.3	22.0
G3	17.1	7.4	1.5	8.0
G4	31.4	12.7	11.5	20.0
G5	25.7	14.8	-2.9	6.0
G6	17.1	1.7	21.5	-10.0
G7	5.7	2.7	9.3	8.0
G8	-28.6	-6.2	19.2	-12.0
G9	20.0	4.8	11.5	16.0
G10	14.3	3.8	4.9	-6.0
G11	8.6	-6.7	4.9	0.0
G12	20.0	4.8	7.1	28.0
G13	20.0	9.5	9.3	26.0
G14	14.3	4.3	3.8	4.0
G15	17.1	2.7	4.9	6.0
G16	22.9	7.9	4.9	10.0
G17	14.3	1.7	17.0	-6.0
G18	17.1	5.3	10.4	10.0
G19	11.4	6.4	14.8	6.0
G20	-5.7	-2.5	13.7	-34.0
G21	-2.9	1.2	1.5	-4.0
G22	-8.6	7.4	20.4	-4.0
G23	-17.1	0.1	-5.1	-6.0
G24	5.7	-4.1	15.9	6.0
G25	17.1	9.0	6.0	4.0

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