



# Phenotypic plasticity of okra for yield and associated traits



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**Background:** The genetic improvement of okra for the agro-ecological conditions requires adequate genetic background for understanding the inheritance of the traits and genetic control.

**Aim:** To evaluate collection of okra accessions for their phenotypic plasticity and their relationships among tested accession.

**Setting:** Field trail laid in a randomised complete block design of three replication.

**Methods:** A total of 24 okra accessions were planted at Loskop Research Station in Limpopo province, South Africa, during the 2020 and 2021 cropping seasons.

**Results:** The analysis of variance showed significant differences among the accessions for yield and related traits measured. The principal components analysis revealed 68.85% total variation. The genotypic coefficient of variance (GCV) was higher than phenotypic coefficient of variance (PCV) for all the measured parameters. The study revealed medium heritability for yield (33%), high ( $\geq 60\%$ ), for hundred-seed weight and number of fruits per plant. A positive significant correlation between grain yield and fruit yield per plant ( $r = 0.39$ ) was observed.

**Conclusion:** The study recommended accessions Acc No. 1859.2.3.1, Acc No. 1181.2.1.1 and Acc No. 1900.2.3.1 to be used as breeding lines in future okra breeding programme.

**Contribution:** The accessions identified as potential parents for okra improvement programme, based on complementary agronomic traits could be used for direct cultivation by small-scale farmers and parental lines for breeding population.

**Keywords:** association; food security; genetic variance; heritability; okra.

## Introduction

Okra, as an underutilised fruit vegetable crop, plays a huge role in food security, income generation and nutrition for the ever-growing population, especially for resource-poor farmers. The crop has ample vitamin C, vitamin A and antioxidants, which play an important role in fighting health conditions including stroke, diabetes and cancer (Gemedet et al. 2015). The crop is one of the most important vegetable crops grown in various tropical, subtropical and Mediterranean regions of the world. Okra is cultivated for its immature fruits, leaves and seeds. It contains mucilage in various parts of the plant (Mkhabela et al. 2020). Okra contains proteins, carbohydrates and vitamins and plays a vital role in human diet. It can be consumed in different forms, where fruits can be boiled or fried. Okra seeds contain about 20% protein and 20% oil. Okra leaves can be also used as animal feed and okra mucilage is suitable for industrial and medicinal applications. Knowledge on genetic diversity and genetic control of yield and other secondary components in okra is vital for improving adaptation of okra to South African agroecological conditions (Habtamu et al. 2018).

Characterisation and evaluation of the collected accessions are very important for both conservation and breeding for the selection of superior traits for further improvement (Aminu et al. 2016). There are limited preliminary reports focusing on the agronomic, nutritional and drought screening of okra aimed at the development of new improved cultivars that are well adapted to the diverse

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agroecological conditions in South Africa (Mkhabela et al. 2022). The knowledge of phenotypic plasticity is basic and the initial step for hybridisation, as it determines the choices of parents to undergo general and specific combining ability (Aminu et al. 2016) in breeding activities. The information on phenotypic variation is used to translate considerable phenotypic diversity and genetically superior individuals (Mohammed, Mohammed & Shiferaw 2022). The background genetic information would be useful for selecting efficient okra breeding approaches for developing new cultivars of this vegetable crop. In addition, the parental lines that are well adapted to the local production conditions will benefit growers and end-users. Hence, the objective of the study was to assess the phenotypic plasticity of okra accessions using agronomic traits for tracking parental lines for breeding.

## Material and methods

### Study site, experimental design and data collection

The experiment was conducted at the Loskop Research Station in Limpopo province, South Africa (25.1773°S latitude; 29.3936°E longitude; 920 m above sea level), during the 2020 and 2021 cropping seasons. Loskop is characterised by average annual rainfall of 140 mm and average temperature of 24.2 °C. The soil type at the research station is loam, with pH ranging between 5.8 and 7.5. The field experiment was carried out using a randomised complete block design with three replications. Each plot consisted of 4 m rows, with inter- and intra-row spacing of 1 m and 30 cm, respectively. Two seeds were sown and later thinned to one seedling per stand. The trial was planted under rain-fed conditions, and irrigation was supplied when needed to avoid growth and development stress. Agronomic management practices were carried out as recommended for the crop. Data were recorded using the descriptor list for okra species (IPGRI 1991), and parameters that were measured on a plot basis were plant height (PH), fruit length (FL), fruit width (FW), number of fruits per plant (NFP), number of seeds per fruit (NSF), hundred-seed weight (HSWt), grain yield per plant (YPP) and grain yield (GY).

### Plant materials

The 24 okra accessions used in this study were obtained from the National Plant Genetic Resources of South Africa in Pretoria (Table 1).

### Data analysis

#### Analysis of variance

The analysis of variance (ANOVA) was conducted on the quantitative data collected using the SAS statistical software (SAS Institute 2004). Least significant differences test was used to compare the mean performance of significant genotypes based on their mean squares. Correlation analysis conducted between pairs of variables was determined using Pearson's correlation coefficient, and two-way test correlation against the correlation matrix was conducted at 5% confidence

**TABLE 1:** The Okra accessions used in the study.

Entry	Accessions code	Accessions name
1	Acc No. 1778.3.1.2	Okra 1
2	Acc No. 1827.2.3.1	Okra 2
3	Acc No. 1197.3.2.1	Okra 3
4	Acc No. 1233.2.3.1	Okra 4
5	Acc No. 1900.2.3.1	Okra 5
6	Acc No. 1622.2.3.1	Okra 6
7	Acc No. 1181.2.1.1	Okra 7
8	Acc No. 1470.2.2.1	Okra 8
9	Acc No. 1741.3.1.1	Okra 9
10	Acc No. 1161.2.1.1	Okra 10
11	Acc No. 1733.3.1.2	Okra 11
12	Acc No. 1806.2.3.1	Okra 12
13	Acc No. 1214.3.1.2	Okra 13
14	Acc No. 4225.1.1.1	Okra 14
15	Acc No. 2224.1.1.1	Okra 15
16	Acc No. 1169.3.1.2	Okra 16
17	Acc No. 1856.2.3.1	Okra 17
18	Acc No. 1181.3.1.2	Okra 18
19	Acc No. 1161.3.1.3	Okra 19
20	Acc No. 1760.2.3.1	Okra 20
21	Acc No. 1206.2.3.1	Okra 21
22	Acc No. 1250.2.3.1	Okra 22
23	Acc No. 1912.2.3.1	Okra 23
24	Acc No. 1859.2.3.1	Okra 24

for all the quantitative traits measured using AGROBASE Generation II SQL version 38 (2019). Principal component analysis and biplot analysis were performed using GenStat version 23 (2023).

### Genetic parameters

The mean square of ANOVA model was used to compute genetic coefficient of variation for genotypic, phenotypic and error variance (Burton & Devane 1953). Genotypic variance across environments was determined by the formula:

$$\sigma^2g = \frac{MSg - Mge}{re} \quad [\text{Eqn 1}]$$

The phenotypic variance across environments was determined by the formula:

$$\sigma^2p = \sigma^2g + \sigma^2ge/e + \sigma^2\mathcal{E}/ge \quad [\text{Eqn 2}]$$

where  $\sigma^2g$  = genotypic variance;  $\sigma^2p$  = phenotypic variance;  $\sigma^2ge$  = genotype by environment variance; environmental error ( $\sigma^2\mathcal{E}$ ) = error mean squares;  $MSg$  = mean squares for genotype;  $MSge$  = mean squares for genotype by environment;  $r$  = number of replication and  $e$  = number of environments. Genotypic coefficient of variation (GCV) was determined by the formula:

$$\text{GCV} = \frac{\sqrt{\sigma^2g}}{\mu} \times 100 \quad [\text{Eqn 3}]$$

Phenotypic coefficient of variation (PCV) was determined by the formula:

$$\text{PCV} = \frac{\sqrt{\sigma^2p}}{\mu} \times 100 \quad [\text{Eqn 4}]$$

where  $\sigma^2g$  = genotypic variance;  $\sigma^2p$  = phenotypic variance and  $\mu$  = grand mean (Raval et al. 2018).

## Results and discussions

### Mean performance of accessions across environments

The analysis of variance for combined environments exhibited a significant ( $p < 0.05$ ) genotype by environment interaction for PH, FW, NFP, NSF, HSWt, GYPP and GY (Table 2 and Table 3). The measured traits revealed significant variation across the two cropping seasons. The average plant height was 163.65 cm, with Acc No. 1859.2.3.1 exhibiting the tallest height (232.64 cm) among the test accessions, while Acc No. 1778.3.1.2 was the shortest (87.68 cm) across the two cropping seasons. Similarly, Muluken, Wassu and Endale (2016) reported significant variation in the mean performances for growth traits. According to Mohammed et al. (2022), selecting the tallest genotypes can be advantageous for

farmers, not only for their fruit and grain yield but also for providing feed for livestock.

The number of fruits per plant varied significantly among okra accessions. Fruits ranged from 9 to 21, with Acc No. 1733.3.1.2, Acc No. 1169.3.1.2 and Acc No. 1760.2.3.1 having the most fruits per plant and Acc No. 1741.3.1.1, Acc No. 1827.2.3.1 and Acc No. 1233.2.3.1 having the fewest fruits per plant (Table 3). Fruit length varied among accessions where the longest fruit was recorded in Acc No. 1859.2.3.1 (with a mean value of 17.20 cm) and Acc No. 1622.2.3.1 (with a mean value of 16.29 cm). The accessions that recorded a higher number of seeds per fruit were Acc No. 1900.2.3.1 and Acc No. 1250.2.3.1, whereas the accessions that recorded a lower number of seeds per fruit were Acc No. 1778.3.1.2 and Acc No. 4225.1.1.1.

The highest hundred-seed weight recorded was in Acc No. 1859.2.3.1 (24.63 g) and Acc No. 2224.1.1.1 (22.86 g). The

**TABLE 2:** Analysis of variance showing the mean square values across environments.

Sources	DF	PH	FL	FW	NFP	NSF	HSWt	GYPP	GY
Env	1	5556.21**	2.33	36.63**	588.22**	2410.41**	49.80*	434.86**	20.87*
Env(Rep)	4	8.28	2.58	33.60**	67.72	26.33	3.69	56.98*	0.52
Entry	23	4026.44**	58.38*	915.31**	1061.00**	5425.08**	161.30**	981.29**	133.60**
EntryxEnv	23	11.95	3.65	7.78	13.44	506.25*	14.33	1.62	5.83

Env, environments; PH, plant height (cm); FL, fruit length (cm); FW, fruit width (mm); NFP, number of fruits per plant; NSF, number of seeds per fruit; HSWt, hundred-seed weight (g); GYPP, grain yield per plant (g); GY, grain yield (kg/ha); Rep, replication.

\*, Significant at 5%; \*\*, Significant at 1%.

**TABLE 3:** Combined analysis of variance and mean performance-based quantitative phenotypic traits.

Genotypes	PH	FL	FW	NFP	NSF	HSWt	GYPP	GY
Okra 1	87.70	16.00	22.60	14.00	15.00	8.80	15.90	80.00
Okra 2	161.40	15.90	20.50	11.00	33.00	21.70	36.50	70.00
Okra 3	166.90	15.90	22.50	14.00	28.00	20.20	34.40	90.00
Okra 4	154.00	14.90	18.70	11.00	23.00	13.50	48.00	80.00
Okra 5	195.70	15.50	21.70	15.00	41.00	12.60	14.80	290.00
Okra 6	135.50	16.30	16.30	14.00	33.00	17.00	121.70	110.00
Okra 7	158.80	15.70	19.30	16.00	35.00	12.20	129.70	100.00
Okra 8	154.00	15.60	19.70	12.00	32.00	17.20	144.90	140.00
Okra 9	182.30	14.70	23.30	9.00	21.00	15.10	132.50	80.00
Okra 10	158.30	14.70	19.80	16.00	26.00	17.80	191.00	150.00
Okra 11	177.30	15.20	20.10	21.00	27.00	9.20	137.00	80.00
Okra 12	136.40	14.90	21.20	15.00	22.00	20.60	109.80	180.00
Okra 13	168.20	14.60	19.40	17.00	21.00	16.60	116.00	60.00
Okra 14	171.70	14.90	25.10	18.00	19.00	4.90	25.70	150.00
Okra 15	184.90	16.00	23.40	15.00	28.00	22.90	55.20	110.00
Okra 16	177.30	15.80	16.80	19.00	25.00	18.60	179.20	60.00
Okra 17	175.60	16.00	23.30	11.00	26.00	17.50	217.40	110.00
Okra 18	147.10	14.60	22.40	16.00	31.00	19.60	133.80	110.00
Okra 19	158.90	15.40	23.10	12.00	22.00	17.00	36.40	110.00
Okra 20	167.50	16.20	15.20	18.00	25.00	17.50	156.10	110.00
Okra 21	163.10	15.80	20.10	15.00	24.00	20.30	196.50	80.00
Okra 22	144.90	15.20	23.20	16.00	37.00	5.60	73.80	130.00
Okra 23	167.50	14.90	21.70	13.00	33.00	11.70	47.40	130.00
Okra 24	232.60	17.20	22.40	14.00	32.00	24.60	299.40	400.00
Overall mean	163.70	15.50	20.90	15.00	27.00	15.90	110.60	120.00
Mean squares	2101.10**	43.30*	88.60**	60.60**	104.80**	99.80**	2996.90**	3.95**
LSD	16.50	2.60	3.20	3.68	3.90	3.80	10.67	0.08
CV (%)	6.20	10.30	9.30	15.70	9.00	14.60	0.90	8.67

PH, plant height (cm); FL, fruit length (cm); FW, fruit width (mm); NFP, number of fruits per plant; NSF, number of seeds per fruit; HSWt, hundred-seed weight (g); GYPP, grain yield per plant (g); GY, grain yield (kg/ha).

\*, Significant at 5%; \*\*, Significant at 1%.

accessions that recorded the lowest hundred-seed weight were Acc No. 4225.1.1.1 (4.93 g), Acc No. 1250.2.3.1 (5.55 g), Acc No. 1778.3.1.2 (8.78 g) and Acc No. 1733.3.1.2 (9.23 g). The okra accessions displayed a significant difference in grain yield, ranging between 60 kg/ha (Acc No. 1859.2.3.1) and 400 kg/ha (Acc No. 1214.3.1.2). The overall mean for grain yield of the genotypes was 120 kg/ha. The highest yields were observed in Acc No. 1859.2.3.1 (grain yield = 400 kg/ha) and Acc No. 1900.2.3.1 (grain yield = 290 kg/ha). The lowest grain yields were observed in Acc No. 1214.3.1.2 and Acc No. 1169.3.1.2, both registering a grain yield of 60 kg/ha.

The results are in agreement with studies conducted by Temam, Mohamed and Aklilu (2020) who also found significant variations for plant height, fruit length, fruit width and fruit yield. Tesfa and Yosef (2016) reported significant differences among genotypes for phenology and growth traits. Similarly, Mohammed et al. (2022) also reported significant differences among 36 okra genotypes for growth traits and phenology. When cultivating okra, fruit length and weight play important roles, as many consumers favour tender, medium-sized fruits weighing between 28 g and 30 g and measuring 18 cm to 20 cm in length (Paththinige, Ranaweera Banda & Fonseka 2008). Hence, the current study has demonstrated that the 24 studied accessions had acceptable fruit length. The significant variation in plant height and fruit length will serve as valuable criteria for selecting potential parent plants in okra improvement breeding programmes.

### Estimation of variance components and heritability of quantitative agronomic traits

Genotypic coefficient of variance was highest for grain yield (58.08%) and lowest for plant height (24.50%). Phenotypic coefficient of variance varied between 11.15% and 25.56% (Table 4). Genotypic coefficient of variance was higher than PCV for all the measured parameters. The parameters PH, PL and NSF reported low PCV, which is in agreement with findings by Adeoluwa and Kehinde (2011) and Mohammed et al. (2022). All the parameters revealed a GCV of more than 20%, in agreement with Aminu et al. (2016) who reported fresh pod length, fresh pod yield per plant and fresh seed per fruit. The results indicated that the environmental interactions played a minimal role in influencing the expression of traits of interest and hence the high GCV, which implies the possibilities for accessions improvement through selection.

Johnson, Robinson and Comstock (1955) and Sravanthi (2017) classified heritability as low (< 30%), medium (30% – 60%) and high ( $\geq$  60%). The heritability estimates for the current study revealed medium for PH, FL, FW, NFP, NSF, HSWt and GYPP (30% – 60%) and high ( $\geq$  60%) for grain yield (Table 4), indicating that the expression of traits was mainly due to the additive effect. High heritability values also mean that the parameters might enhance the response to breeding gains and selection when backcrossing is used in future (Temam et al. 2020).

### Correlations among quantitative traits

Correlation analysis is used for providing information on the association between traits that could be effectively exploited in selection strategies for breeding (Patel et al. 2019). Correlation coefficients on agronomic quantitative traits for the current study are summarised in Table 5. The results revealed a positive significant correlation between grain yield (kg/ha) and grain yield per plant ( $r = 0.39$ ). Moreover, grain yield correlated significantly with number of seeds per fruit ( $r = 0.33$ ) and fruit length ( $r = 0.31$ ). The results further revealed that grain yield per plant showed a positive significant correlation with plant height ( $r = 0.32$ ). The results are in agreement with Patel et al. (2019) who showed a positive and highly significant correlation between fruit yield per plant and fruits per plants, plant height at final harvest, fruit weight and number of branches per plants. Similar results were also reported by Kumar and Reddy (2016) and Raval et al. (2019). Simon, Gashua and Musa (2013) reported positive and highly significant correlation for hundred-seed weight with fruit weight as well as with number of branches per plants. These results indicate that the grain yield can be improved through strategic recombination of the identified genotypes. A negative correlation was observed between number of seeds per fruit and fruit width ( $r = -0.10$ ) and between grain yield per plant and fruit width ( $r = -0.07$ ; Table 5; Figure 1). Similar results were observed in a previous study by Yadav et al. (2017).

### Principal component and biplot analyses

Principal components analysis revealed PCs that contributed the most in variations (Table 6). Specifically, PC1, PC2 and PC3 accounted for 25.08%, 18.69% and 14.72% of the total variation, respectively, with a total variation of 68.85%. The

**TABLE 4:** Estimates of mean, variance, genotypic, phenotypic coefficients of variation and broad-sense heritability for quantitative phenotypic traits of okra.

Traits	PH	FL	FW	NFP	NSF	HSWt	GYPP	GY
Mean	163.65	15.50	20.89	14.50	26.96	15.92	110.55	3.12
MSge	2101.95	43.33	88.60	60.57	104.80	99.80	2996.98	3.95
MSE	103.87	1.53	3.81	5.15	5.89	5.40	7.32	0.13
$\sigma^2_e$	103.87	1.53	3.81	5.15	5.89	5.40	7.32	0.13
$\sigma^2_g$	1607.52	24.04	55.47	29.59	76.66	51.97	1724.66	3.29
$\sigma^2_{ge}$	333.01	6.97	14.13	9.24	16.49	15.73	498.28	0.64
GCV%	24.50	31.64	35.65	37.52	32.48	45.27	37.56	58.08
PCV%	11.15	17.03	17.99	20.96	15.06	24.91	20.19	25.56
H <sup>2</sup> %	57.33	41.17	47.95	35.51	55.57	38.13	42.16	60.46

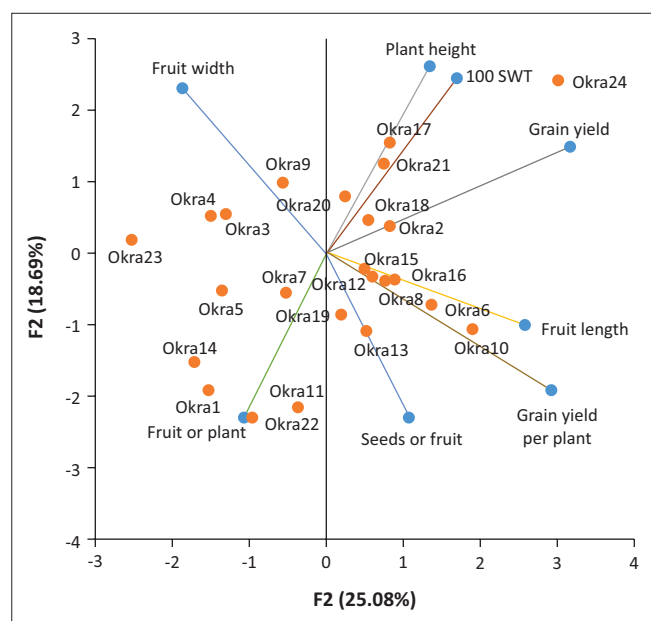
PH, plant height (cm); FL, fruit length (cm); FW, fruit width (mm); NFP, number of fruit per plant; NSF, number of seeds per fruit; HSWt, hundred-seed weight (g); GYPP, grain yield per plant (g); GY, grain yield (kg/ha); GCV, genotypic coefficient of variation; PCV, phenotypic coefficient of variation; MSE, mean square error; MSg, mean square of genotypes;  $\sigma^2_g$ , genotypic variance;  $\sigma^2_p$ , phenotypic variance.

**TABLE 5:** Correlation coefficients showing associations of agronomic traits of okra accessions across two environments.

Variables	PH	FL	FW	NFP	NSF	HSWt	GYPP	GY
PH	1	-	-	-	-	-	-	-
FL	0.09	1	-	-	-	-	-	-
FW	0.02	0.22	1	-	-	-	-	-
NFP	-0.13	-0.03	-0.10	1	-	-	-	-
NSF	0.20	-0.16	-0.11	-0.08	1	-	-	-
HSWt	0.09	0.10	-0.16	-0.24	-0.14	1	-	-
GYPP	0.33*	0.27	-0.07	-0.15	-0.16	0.31	1	-
GY	0.03	0.31*	0.23	0.01	0.33*	0.00	0.39*	1

PH, plant height (cm); FL, fruit length (cm); FW, fruit width (mm); NFP, number of fruits per plant; NSF, number of seeds per fruit; HSWt, hundred-seed weight (g); GYPP, grain yield per plant (g); GY, grain yield (kg/ha).

\*, Significant at 5%.



100 SWT, hundred-seed weight.

**FIGURE 1:** Biplots displaying percentage in variation accounted for PC1 vs. PC2 of principal components.

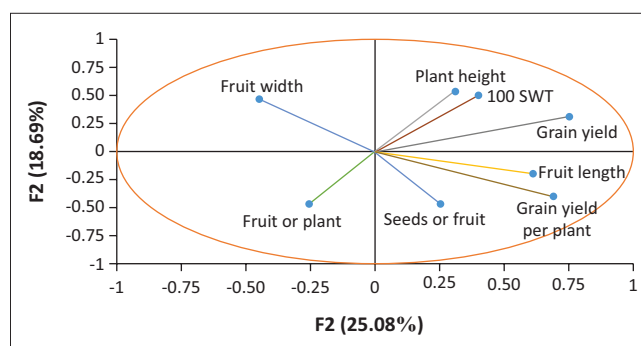
variables that contributed to the most variation at PC1 were grain yield, grain yield per plant and fruit length. In addition, the parameters that contributed the most for variation in PC2 were plant height and hundred-seed weight; while for PC3, the number of fruits per plant and hundred-seed weight were the predominant factors influencing the variation. Grain yield associated positively with Acc No. 1859.2.3.1 and Acc No. 1900.2.3.1, whereas the number of fruits per plant associated positively with Acc No. 1733.3.1.2 and Acc No. 4225.1.1.1 (Figure 1). Grain yield demonstrated a positive association with most of the measured traits. Notably, grain yield per plant, fruit length and number of fruits per plant exhibited a significant correlation (Figure 2). The results are in accordance with Bhardwaj et al. (2019) who indicated that grain yield contributed most to PC1, and similarly, Ahiakpa et al. (2017), Amoatey et al. (2015) and Nwangburuka et al. (2011) reported high contribution by fruit length, hundred-seed weight, number of seeds per fruit and yield per plant, respectively. A biplot between PC1 and PC2 (Figure 1) showed the contribution of various traits, which are responsible for variation in okra accessions. Figure 2 shows the association among the agronomic traits.

**TABLE 6:** Principal component analysis showing eigenvectors, percent and cumulative variation of agronomic traits among 24 okra accessions.

Variables	Principal components		
	PC1	PC2	PC3
PH	0.31	<b>0.54</b>	0.47
FL	<b>0.61</b>	-0.20	0.20
FW	0.25	-0.46	<b>0.62</b>
NFP	-0.25	-0.47	-0.24
NSP	-0.45	0.47	<b>0.51</b>
HSWt	0.40	<b>0.51</b>	-0.46
GYPP	<b>0.75</b>	0.31	-0.12
GY	<b>0.69</b>	-0.39	0.02
Eigenvectors	2.01	1.49	1.18
Percentage variation (%)	25.08	18.69	14.72
Cumulative variation (%)	25.08	43.77	58.48

Note: The bold values are significant at 1%.

PH, plant height (cm); FL, fruit length (cm); FW, fruit width (mm); NFP, number of fruits per plant; NSF, number of seeds per fruit; HSWt, hundred-seed weight (g); GYPP, grain yield per plant (g); GY, grain yield (kg/ha).



100 SWT, hundred-seed weight.

**FIGURE 2:** Biplot showing associations of agronomic traits.

## Conclusions

The research identified three accessions which exhibited better performance and had a positive association with yield and other secondary traits. The presence of variability among the tested accessions indicates the possibility to develop improved varieties through crossing and selection. The traits that exhibited high heritability might enhance the response to breeding gains and selection when backcrossing is used in future.

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## Competing interests

The authors declare that they have no financial or personal relationship(s) that may have inappropriately influenced them in writing this article.

## Authors' contributions

A.S.G. contributed towards the conceptualisation, data curation, investigation, visualisation, methodology, validation, resources, supervision, funding acquisition, writing – review and editing, project administration. B.M.M. contributed towards the conceptualisation, methodology, formal analysis, writing – original draft, visualisation, writing – review and editing. L.K. contributed towards the conceptualisation, methodology, investigation, visualisation, writing – review and editing. A.M. contributed towards the visualisation, methodology, investigation, writing – review and editing. M.B. contributed towards the conceptualisation, visualisation, resources, funding acquisition, writing – review and editing, project administration. L.A.M. contributed towards the investigation, visualisation, methodology, funding acquisition, writing – review and editing. P.S. contributed towards the investigation, visualisation, methodology, funding acquisition, writing – review and editing. M.T. contributed towards the visualisation, resources, funding acquisition, writing – review and editing. S.V. contributed towards the visualisation, project administration, resources, funding acquisition, writing – review and editing.

## Ethical considerations

This article followed all ethical standards for research without direct contact with human or animal subjects.

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## Data availability

Data sharing is not applicable to this article as no new data were created or analysed in this study.

## Disclaimer

The views and opinions expressed in this article are those of the authors and are the product of professional research.

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