J Genet Resour 2025; 11(1): 76-87 *Homepage: http://sc.journals.umz.ac.ir/*

RESEARCH ARTICLE *DOI: 10.22080/jgr.2025.28309.1415*

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Characterization of Okra (*Abelmoschus esculents* [L.] Moench) Accessions for Agronomic Traits in Assosa District, North Western Ethiopia

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ARTICLE INFO

Article history:
Received 08 October 2024
Accepted 10 January 2025
Available online 30 January 2025

Keywords:
Accessions
Agronomic traits
Ethiopia
Genetic diversity
Okra

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p-ISSN 2423-4257
e-ISSN 2588-2589

ABSTRACT

Okra (*Abelmoschus esculents* [L.] Moench) is an important vegetable crop grown primarily in tropical and subtropical regions worldwide. It is a nutritionally rich and economically significant vegetable crop, providing vitamins, fats, carbohydrates, fiber, iron, iodine, and amino acids. In Ethiopia, the crop is cultivated in lowland areas, including Tigray, Gambella, Benishangul Gumuz, and various parts of the Amhara region, relies on landraces, with limited exchange of genetic material between farmers, especially in the southwestern and western regions. However, there is limited information on the genetic variability and yield performance of Okra, with few studies focusing on the diversity among different genotypes available in Ethiopia. To address this gap, a field experiment was conducted during the 2020/21 cropping season at Assosa district, which is located in north-western Ethiopia. The aim of the experiment was to assess the genetic variability of Okra accessions in terms of both qualitative and quantitative traits. The study involved nineteen Okra accessions from the Ethiopian Biodiversity Institute, arranged in a randomized complete block design with three replications. The agronomic data recorded using an Okra descriptor list documented by the International Board for Plant Genetic Resource Institute and subjected to statistical analysis using GenStat statistical software with its 15th edition version. The genotypes AB 29410, AB 29417, AB 29411, AB 240584, and AB 29413 demonstrated relatively high fresh fruit yields (>15,000 kg/ha), with genotype AB 29410 producing the highest yield. Evaluation of agronomic and morphological traits provided a more accurate measure of genetic diversity, essential for plant breeding programs focusing on crossing. The study contributed to identifying key traits for the improvement of Okra genotypes in future breeding efforts to improve the crop.

Please cite this paper as: Paulos, M., Loha, G., & Gebrie, G. (2025). Characterization of Okra (*Abelmoschus esculents* [L.] Moench) accessions for agronomic traits in Assosa district, North Western Ethiopia. *Journal of Genetic Resources*, 11(1), 76-87. doi: 10.22080/jgr.2025.28309.1415

Introduction

Okra (*Abelmoschus esculents* [L.] Moench) is an important vegetable crop grown primarily in tropical and subtropical regions worldwide (Swamy, 2023). It belongs to the *Malvaceae* family, likely originated in Ethiopia, and is widely distributed across tropical, subtropical, and warm temperate regions worldwide (Benchasri, 2012; Swamy, 2023). It is also called as "ladyfinger" and is grown in both gardens and commercial farms. It thrives in hot weather, especially in areas with warm nights (Khaskheli *et al*., 2024; Temam *et al*., 2021; Yaseen and Mukhtar, 2024).

Okra is a versatile crop, with its leaves, buds, flowers, pods, stems, and seeds all having various uses. The fruit is rich in vitamins A, B, and C, as well as carbohydrates, fat, fiber, iron, and iodine, making it a key protein source in many developing countries (Awas, 2007; Basnet *et al*., 2023; Fekadu Gemede *et al*., 2015; Schippers, 2000). It also contains glycosides, calcium, magnesium, and potassium, and is used in medical preparations such as plasma substitutes and blood level expanders (Grubben and Denton, 2004). In parts of West and East Africa, all parts of the plant are consumed for food (Ahiakpa *et al*., 2014; Oppong-Sekyere *et al*., 2012). Various national institutions across several countries, including Ethiopia, Ghana, Pakistan, and Nigeria, maintain a collection of Okra genetic resources (Mkhabela *et al*., 2022).

In Ethiopia, Okra is cultivated mainly by small-scale farmers in lowland areas, including Tigray, Gambella, Benishangul Gumuz, and and various parts of the Amhara region (Mohammed *et al*., 2022b; Temam *et al*., 2020). The plant is valued not only as food but also for its medicinal properties. Its seeds are diuretic, and the leaves serve as nutritious cattle feed with therapeutic benefits (Elkhalifa *et al*., 2021; Gemede *et al*., 2015). Despite its importance, research on Okra cultivation and genetic diversity in Ethiopia has been limited, with little data on its production areas and productivity (Mohammed *et al*., 2022b).

Most Okra cultivation in Ethiopia relies on landraces, with limited exchange of genetic material between farmers, especially in the southwestern and western regions (Temam *et al*., 2020). This lack of research and conservation has led to a call for urgent action to conserve Okra germplasm. Limited studies have also failed to assess the genetic variability of Okra genotypes, particularly in the major growing regions.

Geographic distances and environmental differences are the two major causes of genetic diversity among plant populations (Alemu *et al*., 2015). Traditionally, a combination of morphological and agronomic traits has been used to measure genetic diversity (Kyriakopoulou *et al*., 2014), which is the basis for germplasm conservation and for the exploitation of useful traits in plant breeding (Mohammed *et al*., 2022b). Thus, understanding the genetic diversity of Okra is crucial for improving breeding programs and conserving the crop's genetic resources in its cultivation area.

This study aims to assess the variability of Okra accessions in terms of key qualitative and quantitative traits to inform breeding strategies and germplasm conservation efforts, particularly in the Benishangul Gumuz Regional state of Ethiopia, where diverse genotypes are available but understudied.

Materials and Methods

Study area

A field experiment was carried out during the 2020/21 cropping season in the Assosa district (

Fig. **1**), located in the Asossa zone of northwestern Ethiopia.

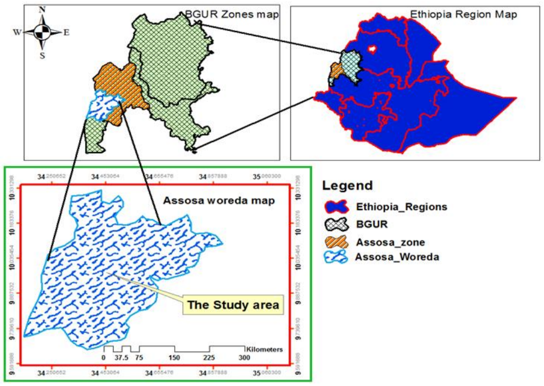

Fig. 1. The study area map of the experiment from BGUR stands for Benishangul Gumuze Regional State.

The site's approximate geographical coordinates are 10° 01' 25" N latitude and 34° 33' 50" E longitude, at an elevation of 1553 meters above sea level. The region experiences a uni-modal rainfall pattern, beginning at the end of April and lasting until mid-November, with peak rainfall occurring from June to October. The area receives an average annual rainfall of 1275 mm, and the temperatures range from a minimum of 14.33°C to a maximum of 28.43°C. The soil in the experimental area is classified as Nitosols, with a slightly acidic pH of 5.5.

Experimental materials and design

The treatments consisted of 19 Okra (*A. esculents* [L.] Moench) accessions obtained from the Ethiopian Biodiversity Institute (Table 1).

Table 1. Okra (*A. esculents* [L.] Moench) accessions and their area of collection and elevation.

Accessions	Regional state	Districts	Altitude (m.a.s.l)
AB 29411	Gambella	Akobo	700
AB 29615	Benshagul	Dangur	1200
AB 40416	Gambella	Akobo	680
AB 29415	Benshagul	Guba	700
AB 240613	Gambella	Abobo	645
AB 294009	Benshagul	Mandura	1500
AB 29052	Benshagul	Mandura	1450
AB 29417	Benshagul	Guba	750
AB 29407	Benshagul	Guba	600
AB 29410	Benshagul	Guba	600
AB 29413	Gambella	Abobo	810
AB 240584	Gambella	Akobo	750
AB 29616	Benshagul	Guba	668
AB 29414	Benshagul	Mandura	598
AB 29412	Benshagul	Mandura	1489
AB 29408	Benshagul	Menge	1000
AB 29051	Benshagul	Mandura	1400
AB 24612	Benshagul	Pawe	1200
AB 240589	Benshagul	Asosa	1400

The treatments were laid out in a randomized complete block design (RCBD) with three replicates. The plot size was 3.5 m wide and 1.5 m long, with a total gross area of 5.25 m^2. Before planting, the experimental area was plowed, pulverized, and leveled to obtain a fine seedbed for planting. Seeds were hand-planted by placing two seeds per hill at inter- and intra-row spacing of 70 cm and 30 cm, respectively. Thinning was performed after emergence to maintain plant density per plot. Crop management activities, such as fertilization, hoeing, and weeding, occur during the crop-growing season.

Data collections

Agronomic traits were recorded using an Okra descriptor list documented by the International Board for Plant Genetic Resource Institute (IPGRI, 1991). Qualitative traits were scored based on arbitrary scales found in the Okra descriptor list as observation references. All quantitative data were measured by taking the mean value of five plants that were tagged randomly before data collection. Data on crop phenology and growth traits, including days to 50% flowering, days to 90% maturity, plant height, leaf length, number of leaves per plant, number of nodes per plant, and number of branches per plant, were recorded. Yield and yield components, such as the number of fruits per plant, fruit length, fruit diameter, number of ridges per fruit, hundred seed weight (HSW), number of seeds per pod, and fruit weight per plant, were measured from five randomly selected plants per plot within representative areas of the net plot at harvest. The fruit yield was harvested from the net area of the plot, excluding border rows; and the morphological traits; plant growth habit, stem color, leaf blade size, flower size, ridges on fruit, matured fruit color, depth of lobbing, dentation of margins, leaf pubescence, fruit pubescence, color between veins, and immature fruit color.

Statistical analysis

The data were analyzed using analysis of variance (ANOVA) in an RCBD, following the General Linear Model (GLM) in GenStat 15th edition (International, 2020). Interpretations were based on the procedure outlined by Gomez and Gomez (1984). Mean comparisons for significant treatment effects were performed using the least significant difference (LSD) test at a 5% probability level.

Genetic parameters were estimated to assess genetic variability among accessions and to evaluate the extent of environmental influence on various traits. Variance components for the phenotype (σ^2p), genotype (σ^2g), and environment (σ^2e) were calculated using formulas proposed by Burton and Devane (1953), to evaluate genetic variability among the accessions and to quantify the extent of environmental influence on various traits. Variance components for the phenotype (σ^2p), genotype (σ^2g), and environment (σ^2e) were determined using formulas proposed by Burton and De Vane (1953), which are also briefly discussed by Gebrie *et al.* (2022) as indicated below:

$$\text{Genotypic variance } (\sigma 2g) = \frac{MSg - MSe}{r}$$

$$\text{Phenotypic variance } (\sigma 2p) = \sigma 2g + \sigma 2e$$

$$\text{Environmental variance } (\sigma 2e) = \text{Error mean square}$$

Where: MSg= mean squares due to genotypes; MSe= mean squares due to error; r= number of replications.

The phenotypic and genotypic coefficients of variance are also estimated as expressed by Singh *et al*. (2007) and indicated by Gedifew *et al.* (2022) as:

$$PCV = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Population mean for trait}} \text{ or } \quad PCV = \frac{\sigma 2P}{X} x\ 100$$

$$GCV = \frac{\sqrt{\text{Genotypic variance}}}{\text{Population mean for trait}} \text{ or } \quad GCV = \frac{\sigma 2g}{x} x\ 100$$

Where: PCV= phenotypic coefficient of variation; GCV= Genotypic coefficient of variation; X= the grand mean of a character.

Heritability in a broad sense was also calculated for each quantitative trait using the formula indicated by Allard (1999) as:

$$H^2\ (\%) = \frac{\sigma 2g}{\sigma 2p}\ x100$$

Where: H= heritability in a broad sense; σ^2g= genotypic variance; σ^2_p= Phenotypic variance.

Genetic advance (GA) under selection, assuming a selection intensity of 5%, was calculated based on the description by Johnson *et al*. (1955) as:

$$GA = K.\sqrt{\sigma 2p}.\frac{\sigma 2g}{\sigma 2p} = K.H*\sqrt{\sigma 2p}$$

Where: GA= expected genetic advance; K= the selection differential (K= 2.06 at 5% selection intensity).

Genetic advancement as a percentage of the mean was calculated to compare the extent of predicted advances of different traits under selection using the formula proposed by Falconer (1996), as indicated below.

$$GAM = \frac{GA}{x}\ X\ 100$$

Where: GAM= Genetic advance as a percent of the mean; GA= Genetic advance under selection; X= Mean value.

Results

Growth habit and degree of branching

Table 2 discusses the study's results on the qualitative traits of nineteen Okra landrace collections. Approximately 85% of the accessions exhibited an erect growth habit, while 10% displayed medium growth, and 5% demonstrated a procumbent growth habit. These findings indicate variability in vigor and branching patterns among the accessions.

Stem color, flower size, and surface between veins

Regarding stem color, green was predominant, observed in 95% of the accessions, while 3% displayed green with red, and 2% were entirely red (Table 2). For leaf blade size, approximately 57% of the genotypes had large leaves, 36% had medium-sized leaves, and 7% had small leaves. Observations on flower size indicated that 58% of the accessions had small flowers, 30% had large flowers, and 12% had medium-sized flowers. In terms of the surface between veins, about 51.4% of the genotypes exhibited a convex shape, 39.6% had a flat surface, and 9% showed a concave shape.

Depth of leaf lobbing, dentation, and pubescence on leaf and fruit

The findings on leaf lobbing depth revealed that 37.2% of the genotypes exhibited deep lobbing, 36% had shallow lobbing, and 26.8% displayed medium lobbing (Table 2). Similarly, strong dentation of leaf margins was predominant, observed in 64.8% of the genotypes, followed by medium dentation in 25.2%, while the remaining 10% showed weak dentation. Variations in leaf pubescence were noted across the Okra germplasms, with 63% of accessions exhibiting conspicuous pubescence, 33% being glabrous, and 4% showing slight pubescence. Regarding fruit pubescence, prickly fruit pubescence was most common, observed in 64.5% of the accessions, followed by slight pubescence in 25.5%. The remaining 10% were characterized by downy fruit pubescence.

Quantitative traits of the landraces

The analysis of variance for quantitative traits among the nineteen Okra accessions revealed significant variation in plant height, branches per plant, fruits per plant, fruit length, fruit diameter, number of ridges per fruit, hundred seed weight, and fruit yield (Table 3). These findings indicate a substantial variation among accessions, likely due to their inherent genetic differences. The study demonstrated considerable genetic variation within the population for yield and yield-related traits, which could be leveraged in Okra improvement programs. Conversely, traits such as days to 50% flowering, days to 90% maturity, leaf length, leaf number per plant, nodes per plant, seeds per pod, and fruit weight per plant did not vary significantly among the accessions.

Table 2. Frequencies of qualitative characters studied in 19 Okra accessions grown at Abrhamo during 2020/21 cropping season

Characters	Variables	Frequencies (%)	Characters	Variables	Frequencies (%)
Plant growth habit	Erect	85	Depth of lobbing	Deep	37.2
	medium	10		Shallow	36
	Procumbent	5		Medium	26.8
Stem color	Green	95	Dentation of margins	Strong	64.8
	Green with red	3		Medium	25.2
	Red	2		Week	10
Leaf blade size	Large	57	Leaf pubescence	Conspicuous	63
	Medium	36		Glabours	33
	Small	7		Slight	4
Flower size	Small	58	Fruit pubescence	Prickly	64.5
	Large	30		Slightly rough	25.5
	Medium	12		Downy	10
Ridges on fruit	Convex	51.4	Color between veins	Green	70
	Flat	39.6		Green with red	16
	Concave	9		Red	14
Matured fruit color	Dark with red	47.1	Immature fruit color	Green with red	43.3
	Yellowish green	34.9		Yellowish green	34.7
	Dark red	15.5		Dark red	18.5
	Green	2.5		Dark green	3.5

Table 3. Mean squares from analysis of variance for quantitative traits studied in 19 Okra accessions grown at Abrhamo district during the 2020/21 cropping season

Trait	Block (DF = 2)	Accessions (DF= 18)	Error (DF= 36)	CV	Grand mean
Days to flowering	52.44	122.12^{NS}	46.58	21.6	51.07
Days to maturity	86.43	37.98^{NS}	25.56	6.3	97.88
Plant height	917.09	2603.60*	1689.84	33.4	123.13
Leaf length	11.02	8.72^{NS}	3.72	18.9	15.65
Leaf number per plant	17.54	14.71^{NS}	6.71	24.9	15.4
Nodes per plant	19.11	48.51^{NS}	31.31	31.2	22.32
Branches per plant	4.91	1.46*	1.41	33.4	3.55
Fruits per plant	11.11	10.35*	9.99*	14.1	4.3
Fruit length	113.47	81.92*	62.83	5.63	17.19
Fruit diameter	40.71	33.37*	16.63	36.4	15.87
Ridges per fruit	3.01	2.09*	1.5	30	4.82
Hundred seeds weight	179.53	118.55*	109.22	20.7	50.55
Seeds per pod	1.33	326.61^{NS}	169.57	30.7	58.86
Fresh fruit weight/plant	7.39	200.61^{NS}	109.31	39.9	35.51
Fruit yield	286	1710000*	1480000	28.9	14280

*= significant at 5% probability level; NS=not significant; DF= degree of freedom.

Crop phenology and growth traits days to flowering and maturity

The analysis of variance revealed no significant differences among genotypes in terms of days to flowering and maturity (Table 4). This indicates that the accessions exhibited relative homogeneity in these traits. Such uniformity suggests that the genotypes are similar in their flowering and maturity timelines, which could facilitate synchronized harvesting and support the practicality of mechanized operations in commercial production. These findings imply that the genotypes interacted similarly with their growing environment concerning phenological traits. However, contrasting results were reported by Mohammed *et al*. (2022a), who observed variation among Okra genotypes in days to flowering and maturity.

Table 4. Mean phenological and growth traits performance of 19 Okra accessions grown at Abrhamo during 2020/21 cropping season

Accessions	Days to flowering	Days to maturity	Plant height (cm)	Leaf length (cm)	Leaves per plant	Nodes per branch	Branches per plant
AB 29411	51	101.33	154.67^{ab}	16	15.33	27	4.67^{a}
AB 29615	49	95.67	162.50^{a}	17.33	14.67	21.33	3.83^{a-c}
AB 40416	54	96.67	144.00^{a-b}	16	15.5	19	4.00^{a-c}
AB 29415	51.67	95	96.00^{a-d}	15.67	14	26	3.67^{a-c}
AB 240613	51.33	97.67	97.67^{a-d}	15	17.33	21.33	3.67^{a-c}
AB 294009	46.33	95.67	96.00^{a-d}	15.33	15	19.33	3.33^{a-c}
AB 29052	44.67	95	90.67^{b-d}	15	12.67	17	2.67^{bc}
AB 29417	58	99.67	124.00^{a-d}	16.33	18	26.67	4.68^{a}
AB 29407	48.33	97.67	163.33^{a}	16	15.33	21	3.33^{a-c}
AB 29410	53	103.33	154.00^{ab}	17.67	15	23	3.67^{a-c}
AB 29413	52	101.67	151.67^{ab}	16.33	18.33	21.33	4.33^{ab}
AB 240584	56.67	100	116.33^{a-d}	15.33	16.33	25.33	4.00^{a-c}
AB 29616	50.33	95.33	72.33^{d}	16	14	18	2.67^{bc}
AB 29414	48.67	97	125.00^{a-d}	14.67	16.33	26	2.33^{c}
AB 29412	57.67	97	77.33^{cd}	16.33	16	23	2.67^{bc}
AB 29408	48.33	94.67	98.33^{a-d}	15	13.33	22.67	3.00^{a-c}
AB 29051	44.33	94	137.33^{a-d}	14.33	14.67	17	3.67^{a-c}
AB 24612	51	99.33	135.67^{a-d}	14.33	14.33	24	3.00^{a-c}
AB 240589	54	103	142.67^{a-c}	16.67	16.33	25	4.33^{ab}
LSD	NS	NS	68.07	NS	NS	NS	1.96
CV (%)	21.64	6.3	33.39	18.87	24.91	31.21	33.4

Note: Means followed by the same letter within a column are not significantly different at 5% probability level. NS, not significant

Plant height, leaf length, and leaf number per plant

Analysis of variance indicated that Okra accessions (genotypes) differed significantly in plant height (Table 4). In general, plant height for accessions ranged from the shortest of 72.33 cm for accession AB 29616 to the tallest of 163.33 cm for AB 29407. However, leaf length and number per plant were not significantly different between Okra accessions (Table 4).

Branches per plant and nodes per branch

The analysis of variance showed significant differences among Okra accessions in the number of branches per plant, a key growth trait. The number of branches per plant ranged from 2.33 to 4.68, with the highest value (4.68) recorded for accession AB 29417 and the lowest (2.33) for AB 29414 (Table 4). This wide variation among genotypes highlights the diversity within Okra, an annual plant characterized by robust stems and erect growth reaching up to 4 meters in height. In contrast, the number of nodes per branch did not differ significantly among the genotypes (Table 4).

Yield components and fruit yield

The Okra accessions showed significant variation in the number of fruits per plant, fruit length, and fruit diameter (Table 5). The number of fruits per plant ranged from 11.83 to 22.67, with the highest value (22.67) observed in accession AB 29407 and the lowest (11.83) in accession AB 29052. Similarly, fruit length varied from 10.96 to 30.00 cm, and fruit diameter ranged from 1.64 to 2.13 cm.

Accession AB 2240584 recorded the longest fruit length, while accession AB 294410 had the thickest fruit diameter (Table 5). The Okra accessions displayed significant variation in the number of ridges per fruit and hundred seed weight (HSW), as shown in Table 5. The number of ridges per fruit ranged from 3.33 to 6.00, while HSW varied from 34.82 to 67.67 g. The highest mean number of ridges per fruit (6.00) was observed in accession AM 29615, whereas the lowest (3.33) was recorded for AB 240589. Similarly, the highest HSW (67.67 g) was noted in genotype AB 240584, and the lowest (34.82 g) was recorded in genotype AB 29616. The variance analysis revealed notable differences in fresh fruit yield among the Okra accessions (Table 6). Yields ranged from 9,100 to 18,150 kg/ha, with genotype AB 29410 producing the highest yield (18,150 kg/ha), closely followed by genotype AB 28417 with an average yield of 18,000 kg/ha. In contrast, genotype AB 24612 had the lowest yield at 9,100 kg/ha. However, there was no significant variation in fruit yield per plant across the Okra accessions (Table 6).

Table 5. Mean yield components performance of 19 Okra accessions grown at Abrhamo during 2020/21 cropping season

Accessions	Fruits per plant	Fruit length (cm)	Fruit diameter (kg)	Ridges per fruit	HSW (g)	Seeds per pod
AB 29411	16.33^{ab}	16.00^{ab}	2.10^{a}	5.33^{ab}	51.67^{a-c}	59.33
AB 29615	16.33^{ab}	24.50^{ab}	1.90^{ab}	6.00^{a}	50.00^{bc}	61.33
AB 40416	15.67^{ab}	15.61^{ab}	2.02^{ab}	5.00^{ab}	51.00^{a-c}	57.33
AB 29415	15.00^{ab}	14.83^{b}	1.89^{ab}	5.33^{ab}	48.39bc	50.00
AB 240613	14.33^{ab}	16.71^{ab}	1.72^{ab}	4.67^{ab}	51.33^{a-c}	65.67
AB 294009	14.50^{ab}	12.57^{b}	1.87^{ab}	4.00^{ab}	48.17^{bc}	54.33
AB 29052	11.83^{b}	14.46^{b}	1.87^{ab}	4.00^{ab}	43.17^{bc}	46.00
AB 29417	19.00^{ab}	17.85^{ab}	2.04^{ab}	5.67^{ab}	56.33^{ab}	72.33
AB 29407	22.67^{a}	13.83^{b}	1.78^{ab}	4.33^{ab}	48.17^{bc}	49.67
AB 29410	16.33^{ab}	18.17^{ab}	2.13^{a}	5.33^{ab}	53.67^{ab}	62.67
AB 29413	15.00^{ab}	16.77^{ab}	1.85^{ab}	4.67^{ab}	51.58^{a-c}	58.67
AB 240584	18.30^{ab}	30.00^{a}	1.80^{ab}	5.33^{ab}	67.67^{a}	73.33
AB 29616	13.83^{ab}	13.50^{b}	1.93^{ab}	4.33^{ab}	34.82^{c}	53.33
AB 29414	15.00^{ab}	24.50^{ab}	1.82^{ab}	4.67^{ab}	52.17^{ab}	61.67
AB 29412	16.00^{ab}	17.15^{ab}	1.64^{b}	5.67^{ab}	50.00^{bc}	61.67
AB 29408	14.00^{ab}	16.80^{ab}	1.92^{ab}	4.67^{ab}	46.67^{bc}	52.67
AB 29051	13.67^{ab}	10.96^{b}	1.81^{ab}	4.00^{ab}	47.67^{bc}	50.67
AB 24612	16.67^{ab}	15.83^{ab}	1.79^{ab}	5.33^{ab}	52.67^{ab}	62.00
AB 240589	17.00^{ab}	16.67^{ab}	1.95^{ab}	3.33^{b}	55.33^{ab}	65.67
LSD	9.56	14.98	0.42	2.39	17.30	NS
CV (%)	14.10	5.63	36.41	29.98	20.67	30.69

Note: Means followed by the same letter within a column are not significantly different at 5% probability level. NS, not significant

Table 6. Mean yield components performance of 19 Okra accessions grown at Abrhamo during 2020/21 cropping season

Accessions	Fruit weight per plant	Fresh fruit yield	Accession	Fruit weight per plant	Fresh fruit yield
AB 29411	39	16789^{ab}	AB 240584	39.67	16600^{ab}
AB 29615	33.67	13800^{a-c}	AB 29616	34	13753^{a-c}
AB 40416	34.33	14662^{a-c}	AB 29414	32.67	14695^{a-c}
AB 29415	32.33	12529^{a-c}	AB 29412	42.67	14751^{a-c}
AB 240613	40	14183^{a-c}	AB 29408	31.33	13467^{a-c}
AB 294009	33.67	14863^{a-c}	AB 29051	26.33	13510^{a-c}
AB 29052	27.67	13033^{a-c}	AB 24612	38.33	9100^{c}
AB 29417	46	18000^{a}	AB 240589	41.67	10900^{bc}
AB 29407	30.33	13123^{a-c}	LSD	NS	6836
AB 29410	45	18150^{a}	CV (%)	30.69	28.91
AB 29413	26	15417^{a-c}			

Means followed by the same letter within a column are not significantly different at 5% probability level. NS, not significant; Fruit weight per plant= kg; Fresh fruit yield= kg/ha.

Phenotypic and genotypic variations

Phenotypic and genotypic coefficients of variation are commonly used to assess variability within a population (Burton and De Vane, 1953; Zeven *et al*., 1999). In this study, the phenotypic variance among Okra genotypes ranged from 1.70 for the number of ridges per fruit to 14,876.67 for fresh fruit yield. High phenotypic variance (≥ 100) was observed for traits such as plant height, fruit weight per plant, 100-seed weight (HSW), number of seeds per fruit, and fresh fruit yield (Table 7). Moderate phenotypic variance (50-100) was noted for days to flowering and fruit length, while low phenotypic variance (< 50) was recorded for traits including days to maturity, leaf length, number of nodes per branch, branches per plant, fruits per plant, fruit diameter, and ridges per fruit.

Genotypic variance, on the other hand, ranged from 0.02 to 766.67. High genotypic variance was found for plant height and fresh fruit yield, while moderate genotypic variance ($\sigma^2 g$) was observed for the number of seeds per fruit. In contrast, low genotypic variance ($\sigma^2 g$) was recorded for traits such as days to flowering, days to maturity, leaf number per plant, leaf length, nodes per branch, branches per plant, fruits per plant, fruit length, fruit diameter, fruit weight per plant, ridges per fruit, and HSW (Table 7).

Broad sense heritability and genetic advance

Overall, broad-sense heritability (H^2) varied between 1.19% for the number of fruits per plant, the lowest value, and 51.53% for fresh fruit yield, the highest. Heritability was categorized as low when below 30%, moderate between 30% and 60%, and high when exceeding 60% (Johnson *et al*., 1955). According to this classification, none of the traits exhibited high heritability (H^2). Moderate heritability (30–60%) was observed for traits such as days to flowering, leaf number, leaf length, and fresh fruit yield, likely due to environmental influences on their polygenic nature. Low heritability was recorded for traits including days to maturity, plant height, nodes per branch, branches per plant, fruits per plant, fruit length, fruit diameter, fruit weight per plant, ridges per fruit, 100-seed weight (HSW), and seeds per fruit. The low heritability of these traits limits their utility for selecting desirable genotypes in breeding programs. Genetic advancement was categorized as low (< 10%), moderate (10-20%), or high (> 20%). Among the traits analyzed, only fresh fruit yield demonstrated a high genetic advance. Moderate genetic advances were observed for days to flowering, days to maturity, plant height, leaf number, fruit diameter, and fruit weight per plant (Table 7).

Table 7. Phenotypic and genotypic coefficient of variability, heritability, and genetic advance for 19 Okra accessions grown at Abrhamo during the 2020/21 cropping season

Traits	$\sigma 2\mathrm{p}$	$\sigma 2\mathrm{g}$	$\sigma 2\mathrm{e}$	**PCV (%)**	**GCV (%)**	**H^2 (%)**	**GA (%)**
Days to flowering	71.76	25.18	46.58	16.59	9.83	35.09	11.96
Days to maturity	29.70	4.14	25.56	5.57	2.08	13.94	14.24
Plant height	1994.43	304.59	1689.84	36.27	14.17	15.27	11.41
Leaf number per plant	10.38	3.67	6.71	20.92	12.44	35.36	15.24
Leaf length	5.39	1.67	3.72	14.83	10.67	30.98	9.47
Nodes per plant	37.04	5.73	31.31	27.27	10.72	15.47	8.69
Number of branches	1.43	0.02	1.41	33.69	3.98	1.40	0.97
Fruits per plant	10.11	0.12	9.99	73.95	8.06	1.19	1.81
Fruit length	69.19	6.36	62.83	48.39	14.67	9.19	9.16
Fruit diameter	22.21	5.58	16.63	29.70	14.88	25.12	15.37
Fruit weight per plant	139.74	30.43	109.31	33.29	5.22	21.78	14.94
Ridges	1.70	0.20	1.50	27.05	9.27	11.76	6.55
100 seed weight	112.33	3.11	109.22	20.97	3.48	2.77	1.20
Seeds per fruit	221.81	52.24	169.57	25.30	12.28	23.55	12.28
Fresh fruit yield	14876.67	766.67	1480.00	85.38	19.39	51.53	28.56

Discussion

The nineteen Okra accessions tested in this study exhibited both qualitative and quantitative variability. In terms of qualitative traits, the accessions displayed distinct characteristics, allowing for their classification into different categories. Dominant traits included an erect growth habit, green stem color, large leaf blades, convex fruit ridges, dark-red mature fruit color, strongly dentate leaf margins, conspicuous leaf pubescence, prickly fruit pubescence, and green areas between leaf veins. Phonologically, the accessions showed uniformity in days to flowering and maturity, simplifying harvest processes and enabling mechanization for commercial production. Significant differences in plant height were observed among the accessions, with tall and thin-stemmed plants prone to lodging near harvest, potentially reducing fruit yield. Thus, selecting short-statured accessions is crucial for breeding programs. Nonetheless, taller genotypes with high dry biomass could serve as livestock feed during dry seasons in addition to their fruit and seed yield. The number of ridges per fruit, 100-seed weight (HSW), and fruit yield also varied significantly across the accessions, reflecting inherent genotypic differences and environmental influences.

This variability aligns with the findings of Paulos *et al*. (2022), who highlighted the importance of traits like plant height and HSW for crop improvement. Prior studies also reported significant variability in fruit yield among Okra genotypes, emphasizing the wide genetic diversity available for selection (Alam *et al*., 2020; Mohammed *et al*., 2022a). Estimates of variability parameters showed that high phenotypic variance (≥ 100) occurred for plant height, fruit weight per plant, HSW, seeds per fruit, and fresh fruit yield, with notable environmental influence on these traits (Burton and De Vane, 1953). Moderate phenotypic variance (50–100) was found in days to flowering and fruit length, while low phenotypic variance (< 50) was recorded for traits such as days to maturity, leaf length, nodes per branch, branches per plant, fruits per plant, fruit diameter, and ridges per fruit. Genotypic variance ranged from 0.02 to 766.67, with high values observed for plant height and fresh fruit yield, indicating potential for early selection. Moderate genotypic variance was recorded for the number of seeds per fruit, while other traits exhibited low genotypic variance.

The phenotypic coefficient of variation (PCV) was classified as high (> 20%), moderate (10–20%), or low (< 10%), as documented by Sivasubramaniam and Madhava Menon (1973). High PCV was observed for plant height, leaf number per plant, nodes per branch, branches per plant, fruits per plant, fruit length, fruit diameter, fruit weight, ridges per fruit, HSW, seeds per fruit, and fresh fruit yield.

According to Johnson *et al*. (1955), heritability (H^2) can be categorized as low (< 30%), moderate (30-60%), or high (> 60%). No traits exhibited high heritability. Moderate heritability was observed for days to flowering, leaf number, leaf length, and fresh fruit yield, likely due to environmental effects on polygenic traits. Low heritability was recorded for days to maturity, plant height, nodes per branch, branches per plant, fruits per plant, fruit length, fruit diameter, fruit weight per plant, ridges per fruit, HSW, and seeds per fruit. This low heritability indicates limited potential for improving these traits through direct selection in breeding programs.

Genetic advance as a percentage of the mean ranged from 0.97% for branches per plant to 28.56% for fresh fruit yield. Selecting the top 5% of genotypes could achieve improvements within this range. According to Thirupathi Reddy *et al.* (2012), genetic advance is classified as low (< 10%), moderate (10-20%), or high (> 20%). Only fresh fruit yield showed high genetic advance, while traits such as days to flowering, days to maturity, plant height, leaf number, fruit diameter, and fruit weight per plant exhibited moderate genetic advance.

Conclusion

The Okra genotypes displayed variability in both qualitative and quantitative traits, reflecting their genetic diversity. Genotypes AB29410, AB29417, AB29411, AB240584, and AB29413 produced relatively higher fresh fruit yields (greater than 15,000 kg/ha), with AB29410 achieving the highest yield. These genotypes demonstrated better adaptation to the testing location. Agronomic and morphological evaluations provided a more precise assessment of genetic diversity, offering valuable resources for plant breeding. Overall, this study facilitated the identification and selection of key traits for improving Okra genotypes in future breeding programs.

Acknowledgments

The authors express their gratitude to the staff of the Department of Plant Sciences at Wolaita Sodo University and Assosa Biodiversity Center for offering technical support to carry out this study. Finally, the Biodiversity Institute of Ethiopia is acknowledged for providing the planting materials.

Funding

This work was funded by the Assosa Biodiversity Center for the characterizing of some important horticulture species for crop improvement programs.

Data availability

The data used to support the findings of this study are available at the request of the responsible author.

Author contribution statement

MP Conceptualization, data curation, formal analysis, investigation, methodology, writing original draft; **GL** as a main advisor involved in conceptualization, reviewing, and editing; **GG** as a corresponding author involved in reviewing, editing, and shaping the article with facilitating the publication process.

Conflict of interest

The authors declare no conflict of interest.

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