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Research article

Association of quantitative traits and genetic diversity in Ethiopian sesame (*Sesamum indicum* L.) genotypes

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ABSTRACT

To enhance sesame yield, it is important to utilize diverse parents in breeding programs and implement an effective selection procedure, which exploits the association of quantitative traits. Therefore, the objective of this experiment was to explore the correlation among quantitative traits and assess genetic variability and diversity using both qualitative and quantitative traits. Correlation coefficients indicated a noteworthy ($P < 0.001$) positive phenotypic (r_p) and genotypic (r_g) correlation between seed yield and various traits: plant height ($r_p = 0.60$; $r_g = 0.58$), length of the capsule-bearing zone ($r_p = 0.77$; $r_g = 0.80$), number of capsules on the main stem ($r_p = 0.80$; $r_g = 0.85$), primary branches ($r_p = 0.66$; $r_g = 0.66$), and capsules per plant ($r_p = 0.90$; $r_g = 0.91$). In contrast, a negative correlation ($P < 0.001$) was observed between yield and bacterial blight disease severity, both phenotypically ($r_p = -0.60$) and genotypically ($r_g = -0.76$). The analysis of path coefficients indicated that the most substantial positive direct effect on yield (0.77) was attributed to capsules per plant, whereas other traits associated with yield exhibited a significant indirect influence on yield through capsules per plant. Qualitative traits exhibited diversity, except for plant growth type, plant growth habit, and stem branching. Shannon-Weaner (*H*) and Simpson (*1-D*) diversity indices were higher for interior corolla color ($H = 1.63$; *1-D* = 0.66), seed color ($H = 1.50$; *1-D* = 0.46), and capsule beak type ($H = 1.08$; *1-D* = 0.50). The analysis of variance indicated a notable variation among the examined genotypes regarding quantitative traits, excluding internode length. The plant materials were divided into five clusters through cluster analysis, where clusters I to V consisted of 21, 29, 4, 4, and 6 genotypes, respectively. The current study has shown that the yield of sesame can be enhanced through indirect selection for traits associated with yield, particularly the highest number of capsules per plant. Furthermore, examinations of genetic diversity confirmed the presence of variability within the assessed genotypes, providing valuable insights for upcoming sesame breeding programs.

1. Introduction

Sesame, scientifically known as *Sesamum indicum* ($2n = 26$) is grown as an oilseed crop valued for both its oil and nutritious seeds. It has been extensively produced in Africa and Asia [1]. The existence of diverse wild relatives on the continent [2,3], led Africa to be regarded as the primary center of origin for sesame. In Ethiopia, wild relatives (*Sesamum alatum* and *Sesamum latifolium)* have been discovered [4]. Sesame thrives in tropical and subtropical ecological zones worldwide, but is susceptible to water logging [5]. In

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Ethiopia, suitable agro-ecologies for sesame exist in the Amhara, Tigray, Oromia, and Benishangul Gumuz regions [6], which accounted for 99.46% of total production during the 2018/19 cropping season [7].

Sesame ranks as Ethiopia's second most significant agricultural export product, following coffee. It has a well-established market, and serves as a source of cash for smallholder farmers and investors. The global consumption of sesame is on a continuous rise due to the high nutritional value of sesame oil [8]. The crop is cultivated in 70 countries globally [9], with Sudan, India, Tanzania, Myanmar, and China being the top five sesame producers [10]. Ethiopia ranks ninth in terms of production for the 2021 cropping year. In Ethiopia, 201664.64 tons of sesame was produced on 294819.49 ha of land during the 2018/19 main cropping season with a national average productivity of 0.68 tons per hectare [7].

Despite the economic importance of sesame, the productivity of cultivars grown in Ethiopia remains low due to genetic and environmental factors. In Ethiopia, sesame breeders strive to create varieties with improved seed quality, resistance to prevalent diseases, and higher yield potential. Understanding the associations of quantitative traits and assessing the existence of adequate genetic variation are prerequisites for formulating crop improvement programs and developing improved varieties with desirable characteristics. Knowledge of trait associations and their effects on yield and quality helps in developing an ideal genotype. Studies on association play a pivotal role in comprehending the individual contributions of various traits, allowing for the selection of yield-maximizing components [9]. Trait-based indirect selection for higher yield could be more efficient with a thorough documentation of yield-related traits [11]. Furthermore, understanding the relationships of quantitative traits helps to assess their critical importance and whether they can be easily combined or if compromises need to be made [12]. Additionally, assessing genetic diversity provides information to propose effective breeding method and conservation strategies [13]. Genetic variation can be exploited through hybridization or backcrossing [9]. Therefore, this experiment was conducted to examine the association between quantitative traits and assess genetic variability and diversity using both qualitative and quantitative traits.

2. Materials and methods

2.1. Experimental site, plant materials and design

The experiment was carried out during the 2019 growing season at the main research station of the Pawe Agricultural Research Center, situated in the Metekel zone within the Benishangul Gumuz region of Ethiopia. Pawe Agricultural Research Center is situated approximately 562 km north-west of Addis Ababa, at a latitude of 11°18′ N and longitude 36°24′ E. The location experiences an average

Table 1
Genotypes tested and their collection region.

S.No	Entry	Collection region	S.No	Entry	Collection region
1	EBI17697	Oromia	33	ASARC-ACC-SA-017	Benishangul Gumuz
2	EBI17702	Oromia	34	ASARC-ACC-SA-019	Benishangul Gumuz
3	EBI17703	Oromia	35	ASARC-ACC-SA-020	Benishangul Gumuz
4	EBI17704	Oromia	36	ASARC-ACC-SA-022	Benishangul Gumuz
5	EBI17708	Oromia	37	ASARC-ACC-SG-005	Benishangul Gumuz
6	EBI23548	Benishangul Gumuz	38	ASARC-ACC-SG-013	Benishangul Gumuz
7	EBI23565	Benishangul Gumuz	39	ASARC-ACC-SG-018	Benishangul Gumuz
8	EBI28301	Amhara	40	GK-012 (1)	Benishangul Gumuz
9	EBI28302	Amhara	41	GK-012 (2)	Benishangul Gumuz
10	EBI28303	Amhara	42	GM-012 (1)	Benishangul Gumuz
11	EBI28304	Amhara	43	GM-012 (2)	Benishangul Gumuz
12	EBI28306	Amhara	44	Gondar-1	*
13	EBI28308	Amhara	45	HM-012 (1)	Amhara
14	EBI28309	Amhara	46	HM-012 (2)	Amhara
15	EBI28316	Amhara	47	Humera-1	
16	EBI28318	Amhara	48	KG-012 (1)	Oromia
17	EBI28320	Amhara	49	KG-012 (2)	Oromia
18	EBI202514	Benishangul Gumuz	50	MG-012 (1)	Benishangul Gumuz
19	EBI207957	Gambella	51	MG-012 (2)	Benishangul Gumuz
20	Abasena	*	52	MT-023 (1)	Benishangul Gumuz
21	ASARC-ACC-S-001	Benishangul Gumuz	53	MT-075 (1)	Amhara
22	ASARC-ACC-S-003	Benishangul Gumuz	54	Setit-1	*
23	ASARC-ACC-S-004	Benishangul Gumuz	55	Setit-2	*
24	ASARC-ACC-S-006	Benishangul Gumuz	56	TM-023 (2)	Benishangul Gumuz
25	ASARC-ACC-S-010	Benishangul Gumuz	57	TZ-013 (1)	Amhara
26	ASARC-ACC-S-022	Benishangul Gumuz	58	TZ-013 (2)	Amhara
27	ASARC-ACC-SA-002	Benishangul Gumuz	59	TZ-054 (1)	Amhara
28	ASARC-ACC-SA-007	Benishangul Gumuz	60	TZ-054 (2)	Amhara
29	ASARC-ACC-SA-008	Benishangul Gumuz	61	ZT-013 (1)	Amhara
30	ASARC-ACC-SA-009	Benishangul Gumuz	62	ZT-013 (2)	Amhara
31	ASARC-ACC-SA-011	Benishangul Gumuz	63	ZT-054 (1)	Amhara
32	ASARC-ACC-SA-016	Benishangul Gumuz	64	ZT-054 (2)	Amhara

Note: * = Improved variety.

yearly rainfall of 1586 mm, located at an elevation of 1120 m above sea level. The average annual minimum and maximum temperatures are recorded at 16.50 °C and 32.60 °C, respectively.

For the experiment, a total of 64 different types of sesame genotypes were used (Table 1). These included 59 accessions and five improved varieties, namely Abasena, Gondar-1, Setit-1, Setit-2, and Humera-1. The accessions were acquired from the Ethiopian Biodiversity Institute (EBI), Werer Agricultural Research Center (WARC), and Assosa Agricultural Research Center (AsARC). The Humera Agricultural Research Center (HuARC) provided three different varieties, namely Setit-1, Setit-2, and Humera-1. Additionally, WARC contributed the Abasena variety, while the Gondar Agricultural Research Center (GARC) provided the Gondar-1 variety. The plant materials were evaluated using an 8 × 8 lattice design, implemented with two replications. Each plant material was planted in a plot comprising 2 rows, each measuring 4 m in length. The spacing between rows was 40 cm, while the spacing between plants was 10 cm, which has been maintained by thinning.

2.2. Data collected

In this study, 11 qualitative and 16 quantitative traits were considered. The qualitative traits were assessed in accordance with the sesame descriptor [14], as illustrated in Table 2.

During the period of flowering, an evaluation was conducted to determine the severity of bacterial blight disease (BBDS) caused by *Xanthomonas campestris pv. sesami*. Five random plants were evaluated using a rating scale of 1–9 [15]. A rating of 1 indicated high resistance, 3 indicated resistance, 5 indicated moderate resistance, 7 indicated susceptibility, and 9 indicated high susceptibility. The data that was originally recorded on a scale of 1–9 was transformed into the percentage severity index (PSI) in accordance with [16] using the following conversion:

$$\text{PSI}\ (\%) = \frac{\text{Sum of all disease scores}}{\text{Number of ratings} \times \text{Maximum disease grade}} \times 100$$

Data regarding the number of days to 50% flowering (DF) and 90% maturity (DM) was recorded per plot. Five randomly selected plants were observed for their height (PH), the height at which the first branching occurred (PHFB), the length of the zone on the main stem (LCBZ), internode length (IL), the number of capsule-bearing primary branches (PBPP), the number of capsules on the main stem (NCMS), and the total number of capsules (CPP), hereinafter referred to as the number of capsules per plant. Five randomly selected capsules were used to measure their length (CL), width (CW), and the number of seeds (SPC) they contained. Seed yield, the weight of 1000 seeds, and oil content were the most important quantitative traits considered in the study. The seed yield per plant (SYPP) was determined by averaging the yields of five randomly selected plants. Data regarding the weight of 1000 seeds (TSW) and the oil content (OC) percentage were recorded from seed samples taken following the recording of seed yield data.

2.3. Statistical analyses

2.3.1. Correlation and path coefficients analysis

The standard procedures [17] were followed to estimate the phenotypic and genotypic correlation coefficients, using the *proc candisc* procedure of SAS 9.0 software [18]. To ascertain the direct and indirect effects of traits on seed yield, a path coefficient analysis [19] was conducted for traits that showed significant correlations with seed yield at the genotypic level. This analysis was performed using the *path.analysis* program in the *agricolae* package [20] within R software [21].

2.3.2. Descriptive statistics for qualitative and quantitative traits

The phenotypic frequency of genotypes representing a specific phenotype for 11 qualitative traits was calculated for 11 qualitative traits using Microsoft Excel as follows:

Table 2
Qualitative traits, coding, and description used to collect the data.

S. No.	Qualitative traits	Numeral codes and description
1	Growth type	"1″ corresponds to indeterminate and "2″ corresponds to determinate
2	Growth habit	"1″ denotes prostrate, "2″ denotes semi-erect, and "3″ denotes erect
3	Branching pattern	"0″ corresponds to non-branching, "1″ corresponds to basal-branching, and "2″ corresponds to top-branching
4	Stem branching	"1″ represents opposite, "2″ represents alternative, "3″ represents ternate, and "4″ represents mixed
5	Interior corolla color	"1″ denotes white, "2″ denotes white with pink shading, "3″ denotes white with deep pink shading, and "4″ denotes purple
6	Flowers per node	"1″ corresponds one flower and "2″ corresponds to more than one flower
7	Capsules per node	"1″ denotes mono-capsular nodes and "2″ denotes multi-capsular nodes
8	Carpels per capsule	"1″ corresponds bi-carpellate capsules and "2″ corresponds tetra-carpellate capsules
9	Locules per capsule	"1″ represents four-loculed capsules, "2″ represents six-loculed capsules, and "3″ represents mixed-loculed capsules
10	Capsule beak type	"1″ corresponds to short, "2″ corresponds to long, and "3″ corresponds to curved
11	Seed color	"1″ denotes white, "2″ denotes cream, "3″ denotes light brown, "4″ denotes medium brown, "5″ denotes dark brown, "6″ denotes red, and "7″ denotes tan

Table 3
Correlation analysis of 16 quantitative traits in evaluated sesame genotypes, depicted phenotypic (above diagonal) and genotypic (below diagonal) correlation.

	DF	BBDS	DM	PH	PHFB	LCBZ	IL	CL	CW	PBPP	NCMS	CPP	SPC	TSW	OC	SYPP
DF	**1.00**	0.10	0.33***	0.14	0.10	−0.04	−0.03	0.00	−0.10	0.10	0.00	0.03	0.15	−0.07	0.00	0.05
BBDS	0.13	**1.00**	−0.19	−0.47***	−0.08	−0.66***	0.00	−0.13	−0.07	−0.54***	−0.63***	−0.65***	−0.34***	−0.12	−0.22*	−0.60***
DM	0.39**	−0.22*	**1.00**	0.29***	0.22*	0.11	−0.05	0.04	−0.16	0.25**	0.20*	0.22*	0.28**	−0.04	0.32***	0.17
PH	0.13	−0.47***	0.42***	**1.00**	0.51***	0.68***	−0.05	0.15	0.08	0.60***	0.64***	0.66***	0.25**	0.25**	0.17	0.60***
PHFB	0.14	−0.09	0.34**	0.68***	**1.00**	0.01	−0.10	0.09	0.10	0.12	0.06	0.04	0.20*	0.11	0.02	−0.01
LCBZ	−0.09	−0.76***	0.14	0.62***	0.07	**1.00**	−0.06	0.24**	0.01	0.54***	0.84***	0.79***	0.29***	0.21*	0.28**	0.77***
IL	−0.06	0.11	−0.12	−0.08	−0.18	−0.03	**1.00**	−0.09	0.12	0.04	0.01	0.01	−0.16	−0.03	−0.23**	−0.08
CL	−0.01	−0.10	0.03	0.13	0.14	0.21	−0.12	**1.00**	−0.08	0.00	0.13	0.13	0.52***	0.08	−0.10	0.21*
CW	−0.17	0.03	−0.20	0.00	0.07	−0.05	0.07	−0.11	**1.00**	0.03	0.08	0.05	−0.20*	0.12	−0.13	0.02
PBPP	0.05	−0.56***	0.29*	0.57***	0.21	0.50***	0.08	−0.06	0.07	**1.00**	0.54***	0.78***	0.20*	0.13	0.23**	0.66***
NCMS	−0.03	−0.73***	0.28*	0.62***	0.12	0.87***	0.02	0.11	0.09	0.53***	**1.00**	0.87***	0.22*	0.16	0.22*	0.80***
CPP	−0.02	−0.75***	0.28*	0.65***	0.17	0.80***	0.02	0.12	0.08	0.78***	0.89***	**1.00**	0.20*	0.14	0.27**	0.90***
SPC	0.16	−0.33**	0.33**	0.26*	0.24	0.29*	−0.22	0.52***	−0.30*	0.21	0.23	0.22	**1.00**	0.03	0.12	0.28**
TSW	−0.19	−0.01	−0.09	0.16	0.23	0.10	−0.03	0.05	0.31*	0.01	0.11	0.03	−0.01	**1.00**	0.14	0.23**
OC	0.01	−0.31*	0.35**	0.20	0.03	0.34**	−0.32*	−0.11	−0.16	0.29*	0.24	0.31*	0.14	0.18	**1.00**	0.24**
SYPP	−0.03	−0.76***	0.24	0.58***	0.10	0.80***	−0.08	0.21	0.10	0.66***	0.85***	0.91***	0.33**	0.14	0.30*	**1.00**

Note: DF (days to 50% flowering), BBDS (bacterial blight disease severity), DM (days to 90% Maturity), PH (plant height), PHFB (plant height to the first branch), LCBZ (length of capsule-bearing zone), IL (internode length), CL (capsule length), CW (capsule width), PBPP (primary branches plant^{-1}), NCMS (capsules on the main stem plant^{-1}), CPP (capsules plant^{-1}), SPC (seeds capsule^{-1}), TSW (1000 seed weight), OC (oil content), SYPP (seed yield plant^{-1}). Statistical significance is denoted as *** ($P < 0.001$), ** ($P < 0.01$), * ($P < 0.05$).

$$Frequency\ (\%) = \frac{Number\ of\ individuals\ with\ distinct\ phenotype}{Total\ number\ of\ tested\ genotypes} * 100$$

Descriptive statistics were conducted for the 16 quantitative traits using the *desc_stat* program in the *metan* package [22] in R software [21]. This allowed us to estimate the minimum, maximum, mean, coefficient of variation, and standard error.

2.3.3. Analysis of variance

An analysis of variance was conducted for the 16 quantitative traits using the *PBIB.test* program in the agricolae package [20] and R software [21]. The ANOVA utilized the following model:

$$y_{ijk} = \mu + rep_i + block_j\ (rep_i) + gen_k + e_{ijk}$$

Where y_{ijk} denotes an observed effect, μ denotes the mean, rep_i denotes the ith replicate, and $block_j$ (rep_i) denotes the jth incomplete block within the ith replicate, gen_k is the kth genotypic effect, and e_{ijk} is the experimental error.

2.3.4. Shannon-Weaver and Simpson's diversity indices based qualitative traits

The Shannon-Weaver [23] and Simpson's [24] diversity indices were calculated for qualitative traits. These indices were computed using the *index.bio* program in the *agricolae* package [20] within the R software [21].

2.3.5. Cluster analysis

Data recorded from ordinal-scaled qualitative traits and 16 quantitative traits were taken into account during the cluster analysis. The cluster analysis was carried out by R software [21]. Before proceeding with the cluster analysis, the data was subjected to standardization using the *scale* function to avoid bias caused by different scales of measurement [25]. Genotypes were hierarchically clustered by employing the squared Euclidean distance produced by the *dist* function. The genotypes were clustered into genetically distinct groups using the complete linkage method, and this was done using the *hclust* and *plot* functions. To identify the ideal number of clusters, the scree plot's elbow point was assessed on the curve generated by the *fviz_nbclust* function within the *factoextra* package [26]. The *cutree* function was used to compute the inter and intra cluster distances.

3. Results

3.1. Correlation and path coefficient analyses

Table 3 presents phenotypic (r_p) and genotypic (r_g) correlation coefficients among the 16 quantitative traits. In this study, seed yield per plant exhibited a significant ($P < 0.001$) positive phenotypic and genotypic correlation with various traits: plant height ($r_p = 0.60$; $r_g = 0.58$), length of the capsule-bearing zone ($r_p = 0.77$; $r_g = 0.80$); and number of primary branches ($r_p = 0.66$; $r_g = 0.66$), capsules on the main stem ($r_p = 0.80$; $r_g = 0.85$), and capsules per plant ($r_p = 0.90$; $r_g = 0.91$) per plant. Additionally, these seed yield-related morphological traits exhibited a significant positive interrelationship, both phenotypically and genotypically. Moreover, the correlation coefficients between seed yield and its related traits were higher in magnitude at the genotypic level compared to the phenotypic level, except for plant height and number of primary branches. Phenological characteristics like the duration to 50% flowering and 90% maturity, were found to have a significant positive correlation at the genotypic and phenotypic level ($r_p = 0.33$; $r_g = 0.39$). However, there was no statistically significant correlation between these traits and seed yield. The correlation between yield and seed count per capsule ($r_p = 0.24$; $r_g = 0.33$) was found to be significant ($P < 0.01$). The length of the capsule and seed count per capsule revealed a significant ($P < 0.001$) positive correlation ($r_p = 0.52$; $r_g = 0.52$), while the capsule width exhibited a significant ($P < 0.05$) negative correlation ($r_p = -0.20$; $r_g = -0.30$) with seeds per capsule. The results of the current study indicate that there is a positive correlation between oil content and seed yield, both phenotypically ($P < 0.01$; $r_p = 0.24$) and the genotypically ($P < 0.05$; $r_g = 0.30$). Additionally, there is a significant positive correlation between oil content and days to 90% maturity, both phenotypically ($P < 0.001$;

Table 4
Direct (highlighted in bold along the diagonal) and indirect effects of various traits on seed yield in the assessed sesame genotypes.

	BBDS	PH	LCBZ	PBPP	NCMS	CPP	SPC	OC	rg_{xy}
BBDS	**−0.07**	0.04	−0.08	0.03	−0.07	−0.58	−0.04	0.00	−0.76***
PH	0.03	**−0.10**	0.06	−0.03	0.06	0.50	0.03	0.00	0.58***
LCBZ	0.05	−0.06	**0.10**	−0.02	0.08	0.61	0.04	0.00	0.80***
PBPP	0.04	−0.05	0.05	**−0.05**	0.05	0.60	0.03	0.00	0.66***
NCMS	0.05	−0.06	0.09	−0.02	**0.09**	0.68	0.03	0.00	0.85***
CPP	0.05	−0.06	0.08	−0.04	0.08	**0.77**	0.03	0.00	0.91***
SPC	0.02	−0.02	0.03	−0.01	0.02	0.17	**0.12**	0.00	0.33**
OC	0.02	−0.02	0.03	−0.01	0.02	0.24	0.02	**−0.01**	0.30*
Residual									0.13

Note: *BBDS (bacterial blight disease severity), PH (plant height), LCBZ (length of capsule-bearing zone), PBPP (primary branches plant^{-1}), NCMS (capsules on the main stem plant^{-1}), CPP (capsules plant^{-1}), SPC (seeds capsule^{-1}), OC (oil content), rg = genotypic correlation, x = independent variable, y = seed yield). Statistical significance is denoted as *** (P < 0.001), ** (P < 0.01), * (P < 0.05).*

$r_p = 0.32$) and genotypically ($P < 0.01$; $_{rg} = 0.35$). Thousand seeds weight exhibited a significant ($P < 0.01$) positive phenotypic correlation ($r_p = 0.23$), but a non-significant ($P > 0.05$) genotypic correlation ($r_g = 0.14$) with seed yield. According to the present study, both the phenotypic and genotypic correlations between 1000 seeds weight and oil content were non-significant. Furthermore, capsule width exhibited a significant ($P < 0.05$) positive genotypic correlation ($r_g = 0.31$) with 1000 seeds weight. There was a strong negative correlation ($P < 0.001$) found between bacterial blight disease severity and the seed yield, evident at both the phenotypic and genotypic levels ($r_p = -0.60$; $r_g = -0.76$). Additionally, bacterial blight disease severity exhibited a significant ($P < 0.001$) negative correlation with various traits, including plant height, length of the capsule-bearing zone, number of primary branches, number capsules on the main stem, number of capsules, number of seeds, and oil content, observed both phenotypically and genotypically.

Table 4 shows the analysis of path coefficients, which considered traits that showed significant genotypic correlation with seed yield as independent variables and seed yield as the dependent variable. The most substantial positive direct effect on seed yield (0.77) was attributed to the number of capsules per plant, while other traits associated with seed yield had a more significant indirect influence on seed yield through capsule count per plant. Bacterial blight disease severity (−0.07), plant height (−0.10), number of primary branches (−0.05), and oil content (−0.01) exhibited adverse direct effects on seed yield. Conversely, the length of the capsule-bearing zone (0.10), the number of capsules on the main stem (0.09), and seeds per capsule (0.12) exerted positive direct effects on seed yield. Bacterial blight disease severity (−0.58) exhibited an adverse indirect impact on seed yield through capsule count per plant. In this study, plant height (0.50), the length of the capsule-bearing zone (0.61), primary branches per plant (0.60), oil content (0.24), and seeds per capsule (0.17) demonstrated a positive indirect effect on seed yield through the total capsule count per plant.

3.2. Analyses of genetic diversity

Genetic variability in qualitative traits was revealed among genotypes, except for plant growth type, plant growth habit, and stem branching, which remained consistent across genotypes. The genotypes were entirely indeterminate, erect, and had opposite branching for their growth type, growth habit, and stem branching, respectively (Table 5). Among the studied genotypes, the highest proportion exhibited white with pink shading for interior corolla color, basal branching for branching pattern, and one flower for the number of flowers per node. Additionally, genotypes that have monocapsular-node (Fig. 1A), bicarpellate-capsule (Fig. 1B), four-locule capsule (Fig. 1C), and white seed coat color (Fig. 1D) were more frequent. Out of the 64 genotypes evaluated, ASARC-ACC-S-003, ASARC-ACC-S-006, ASARC-ACC-S-022, ASARC-ACC-SA-009, ASARC-ACC-SA-020, and ASARC-ACC-SG-018 had a multi-capsular node (Fig. 2A). Regarding capsule characteristics, four genotypes were found to have a tetracarpellate-capsule (Fig. 2B). Out

Table 5
Proportion of morphotypes for 11 qualitative traits and descriptive statistics for 16 quantitative traits of sesame genotypes tested.

Qualitative traits					
Growth type	Indeterminate (100%)				
Growth habit	Erect (100%)				
Branching pattern	Basal-branching (90.63%) and top-branching (9.37%)				
Stem branching	Opposite (100%)				
Interior corolla color	White with pink shading (40.62%), white (35.94%), white with deep pink shading (21.88%), and purple (1.56%)				
Flowers per node	One flower (90.63%) and more than one flowers (9.37%)				
Capsules per node	Monocapsular (90.63%) and multicapsular (9.37%)				
Carpels per capsule	Bicarpellate (93.75%) and tetracarpellate (6.25%)				
Locules per capsule	Four-loculed (93.75%), mixed-loculed (4.69%), and six-loculed (1.56%)				
Capsule beak type	Curved (57.81%), short (40.63%), and long (1.56%)				
Seed color	White (71.87%), red (9.37%), medium brown (7.81%), cream (4.68%), light brown (3.12%), tan (1.56%), and dark brown (1.56%)				
Quantitative traits	Minimum	Maximum	Mean	SEM	CV (%)
Days to 50% flowering	45.00	62.00	56.59	0.24	4.87
Bacterial blight severity index (%)	33.33	91.11	56.98	1.18	23.41
Days to 90% maturity	92.00	123.00	110.80	0.54	5.51
Plant height (cm)	49.50	131.00	98.70	1.31	15.04
Plant height to first branching (cm)	17.20	62.00	34.65	0.68	22.12
Length of capsule-bearing zone on main stem (cm)	18.25	68.40	44.71	0.88	22.36
Internode length (mm)	24.00	68.00	41.17	0.77	21.04
Capsule length (mm)	16.60	37.20	24.70	0.35	15.97
Capsule width (mm)	5.75	9.40	7.63	0.07	11.04
Primary branches per plant	0.60	5.40	2.98	0.09	35.08
Capsules on the main stem per plant	7.00	41.60	20.56	0.64	35.26
Capsules per plant	10.00	98.20	43.23	1.77	46.44
Seeds per capsule	53.20	100.60	70.04	0.78	12.58
1000 seed weight (g)	2.00	3.00	2.30	0.02	11.94
Oil content (%)	44.00	60.26	52.77	0.27	5.74
Seed yield per plant (g)	3.17	12.30	6.20	0.18	32.76

Note: SEM =Standard Error of the Mean and CV (%) = Coefficient of Variation.

of the four tetracarpellate-capsuled genotypes, the three genotypes EBI202514, ASARC-ACC-S-010, and ASARC-ACC-SA-016 had a mixed-loculed capsule, while a solitary genotype ASARC-ACC-SG-005 was found to have a six-locule capsule.

Estimates for the minimum, maximum, and mean values, as well as the standard error of the means and coefficient of variation, are presented for 16 quantitative traits (Table 5). The sesame genotypes considered in the study exhibited a considerable range of variation for these traits. For instance, the days to 50% flowering ranged from 45 to 62 days, the days to 90% maturity from 92 to 123 days, and the bacterial blight disease severity ranged from 33.33% to 91.11%. Additionally, a wide range of variation was observed for the number of capsules (10.00–98.20), number of seeds (53.20–100.60), 1000 seed weight (2.00 g–3.00 g), oil content (44.00%–60.26%), and seed yield (3.17 g–12.30 g).

Table 6 shows the mean squares of 16 quantitative traits resulting from the analysis of variance. The genotype mean square values revealed significant differences ($P < 0.01$) among the plant materials for characteristics such as days to 50% flowering, days to 90% maturity, plant height, plant height to first branching, length of capsule-bearing zone, capsule length, number of primary branches, number of capsules on the main stem, number of capsules, number of seeds, and oil content. Moreover, the examined genotypes exhibited significant differences ($P < 0.05$) in terms of bacterial blight disease severity, capsule width, 1000 seeds weight, and seed yield. Nevertheless, among the 16 quantitative traits under consideration, no statistically significant differences were observed in internode length among the tested genotypes.

The analysis of the Shannon-Weaver diversity index (*H*) was carried out to measure phenotypic diversity within the tested genotypes for each qualitative trait. The tested genotypes showed polymorphism for eight out of the 11 qualitative traits considered. Therefore, diversity indices were computed for only these eight traits, as illustrated in Table 7. The Shannon-Weaver diversity indices ranged from 1.63 for interior corolla color to 0.34 for the number of carpels per capsule. High Shannon-Weaver diversity indices were observed for interior corolla color, capsule beak type, and seed color. These indices were consistent with Simpson's diversity indices. Simpson's diversity indices were higher for interior corolla color, capsule beak type, and seed color, while lower indices were observed for branching pattern, number of flowers per node, capsules per node, carpels per capsule, and locules per capsule. The Simpson diversity index was computed to estimate diversity indices and phenotypic evenness with in the population for the qualitative traits considered. Consequently, high phenotypic dominance was observed for branching pattern, number of flowers per node, capsules per node, carpels per capsule, and locules per capsule. On the other hand, low dominance was seen for capsule beak type and seed color.

The plot of the total within sum of squares against the number of clusters showed that five clusters were found to be optimal for distinguishing the 64 sesame genotypes (Fig. 3). The members of each cluster are presented in the dendrogram (Fig. 4). Cluster II and cluster I consisted of the highest number of genotypes, with 29 and 21 genotypes, respectively. Cluster III and cluster IV each consisted of four genotypes, while cluster V was represented by six genotypes.

Table 8 shows the mean values for the traits considered in the cluster analysis. The characteristics that most prominently differentiated the studied genotypes into distinct clusters included the number of flowers per node, capsules per node, days to 50% flowering and 90% maturity, bacterial blight disease severity, plant height, number of capsules, number of seeds, and seed yield. Genotypes

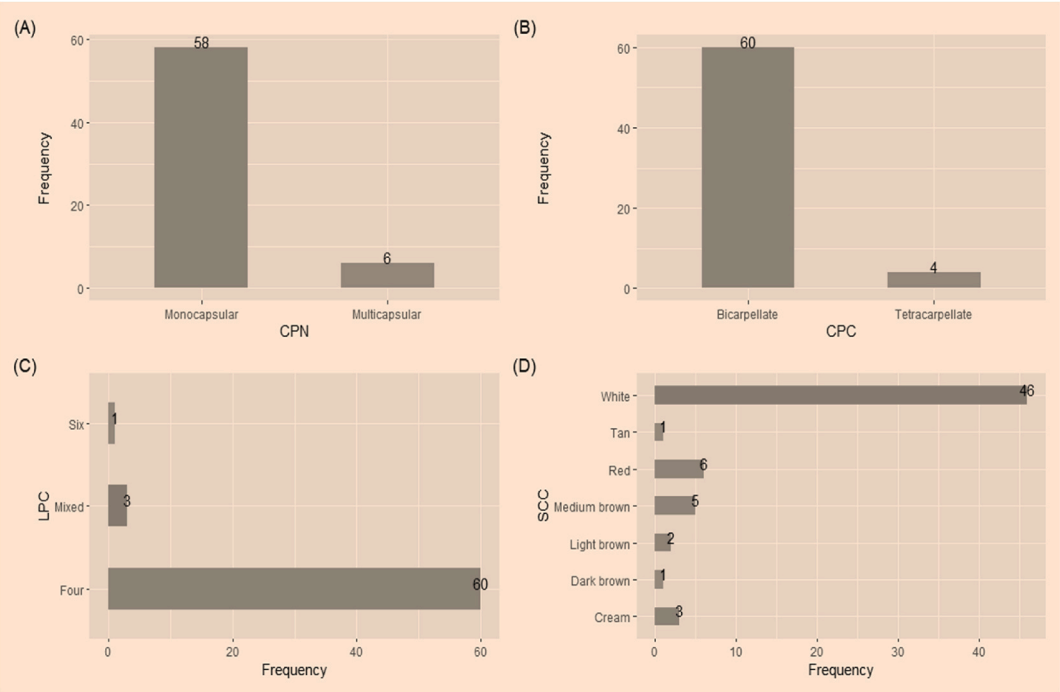

Fig. 1. Capsule per node (A), carpel per capsule (B), locule per capsule (C), and seed coat color (D). (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

Fig. 2. Multicapsular-node (A) and tetracarpellate-capsule (B).

Table 6
Mean squares of 16 quantitative traits of sesame genotypes that were evaluated.

	Mean Squares			
	Replication (df = 1)	Block (Replication) (df = 14)	Genotype (df = 63)	Error (df = 49)
Days of 50% flowering	9.57	2.70	11.84**	2.06
Bacterial-blight susceptibility index (%)	7.56	239.13	201.64*	121.44
Days of 90% physiological-maturity	34.03	11.63	61.99**	6.80
Plant height (cm)	309.76	344.08	257.30**	131.63
Plant height to the first branch (cm)	339.50	46.02	74.09**	29.07
The length of capsule-bearing zone (cm)	523.95	89.15	123.85**	57.38
Internode length in mm	204.02	86.90	78.38ns	61.56
Capsule length in mm	10.45	8.96	25.30**	4.76
Capsule width in mm	3.70	0.58	0.82*	0.52
Primary branches per plant	2.65	1.36	1.39**	0.51
Capsules on the main stem per plant	46.95	37.15	75.50**	19.28
Capsules per plant	885.05	381.46	553.35**	194.16
Seeds per capsule	6.60	43.55	122.87**	24.34
1000 seed weight (g)	0.78	0.04	0.09*	0.05
Oil content (%)	0.74	0.76	16.22**	0.52
Seed yield per plant (g)	13.02	5.02	4.85*	2.74

Note: df represents degrees of freedom, ** indicates highly significant ($P < 0.01$), * denotes significance ($P < 0.05$), and ns signifies non-significant ($P > 0.05$).

Table 7
Shannon-Weaver and Simpson's diversity indices for qualitative traits of sesame genotypes that were tested.

Traits	No. of phenotypes observed	Shannon-Weaver diversity index (Richness)			Simpson's Dominance (*D*)	Simpson's diversity index		
		H	Lower class limit at 95%	Upper class limit at 95%		*1-D*	Lower class limit at 95%	Upper class limit at 95%
ICC	4	1.63	0.64	1.99	0.34	0.66	0.19	0.75
FPN	2	0.45	0.45	1.00	0.83	0.17	0.17	0.50
BP	2	0.45	0.45	1.00	0.83	0.17	0.17	0.50
CBT	3	1.08	0.34	1.58	0.50	0.50	0.09	0.67
CPN	2	0.45	0.45	1.00	0.83	0.17	0.17	0.50
CPC	2	0.34	0.34	1.00	0.88	0.12	0.12	0.50
LPC	3	0.39	0.24	1.58	0.88	0.12	0.06	0.66
SCC	7	1.50	1.17	2.67	0.54	0.46	0.32	0.84

Note: H=Shannon-Weaver diversity index (richness), D = Simpson's dominance,1-D = Simpson's diversity index, ICC=Interior Corolla Color, FPN=Flowers Node^{-1}, BP=Branching Pattern, CBT=Capsule Beak Type, CPN=Capsules Node^{-1}, CPC=Carpels Capsule^{-1}, LPC = Locules capsule^{-1}, and SCC=Seed Coat Color.

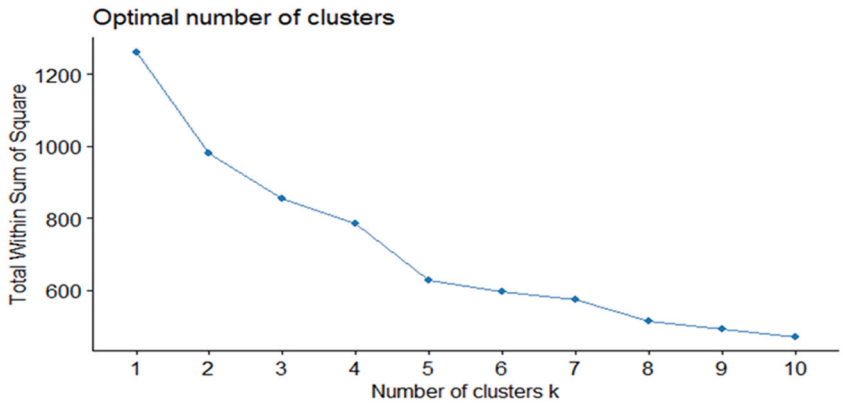

Fig. 3. Scree plot showing that retaining five clusters is optimal according to the elbow method.

grouped in cluster I had the lowest mean for bacterial blight disease severity, but the highest mean values for plant height, length of capsule-bearing zone, number of primary branches, number of capsules, oil content, and seed yield. In contrast, genotypes belonging to cluster II recorded the highest mean for bacterial blight disease severity, while these genotypes showed the lowest mean for length of capsule-bearing zone, number of capsules, and seed yield. Cluster III consisted of short genotypes with an early flowering and maturity period. On the other hand, cluster IV was represented by genotypes with a tetracarpellate capsules, which had the highest number of seeds per capsule. Furthermore, genotypes grouped in cluster IV had capsules characterized as tetracarpellate. Out of the 4 genotypes grouped in cluster IV, one genotype had six-loculed capsules, whereas the other three genotypes exhibited mixed-loculed capsules. Cluster V comprised groups of genotypes which had more than one flower per node and were characterized by their multicapsular nodes.

As shown in Table 9, the Euclidean squared distance (D^2) computed from the standardized data revealed that the maximum distance between clusters (10.68) was noted between cluster I and IV, whereas the minimum inter-cluster distance (8.88) was observed for cluster II and III. Sesame genotypes grouped in cluster II exhibited the maximum intra-cluster distance (7.73). In contrast, the minimum intra-cluster distance (5.38) was observed among the genotypes (Setit-1, Setit-2, Humera-1, and EBI28320) clustered under cluster III.

4. Discussion

4.1. Association of quantitative traits

The seed yield per plant showed a significant positive correlation, both at the phenotypic and genotypic levels, with various traits including plant height, length of the zone where capsules are produced, number of primary branches per plant, capsules on the main stem per plant, capsules per plant, and seeds per capsule Previous studies [27–29] have demonstrated a significant and positive relationship between the number of capsules per plant and seed yield in sesame. Similarly, there was a highly significant positive phenotypic correlation between seed yield and various traits, including the length of the capsule-bearing zone, the number of capsules per plant, and primary branches per plant [30]. In Bulgarian sesame breeding for mechanized harvesting and higher seed yield, the most crucial traits identified for enhanced seed yield were the number of capsules per plant and the number of capsules on the main

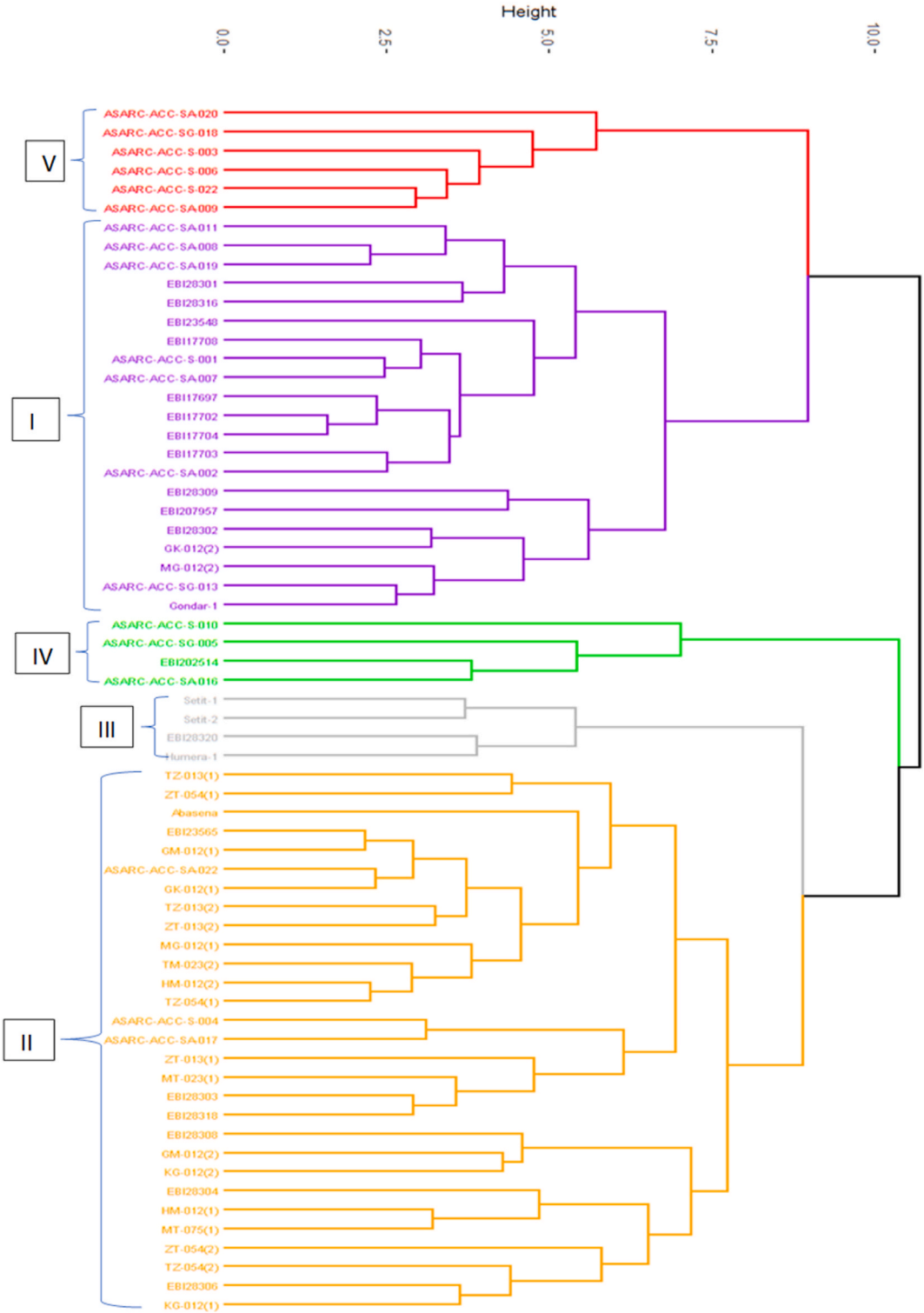

Fig. 4. Cluster dendrogram depicting genetic relationships among the 64 sesame genotypes.

stem per plant [31]. Based on this study, it is suggested that achieving maximum seed yield in sesame can be more effective by selecting genotypes based on various characters including plant height, length of the capsule-bearing zone, number of primary branches per plant, capsules on the main stem per plant, capsules per plant, and seeds per capsule. The relationship between seed yield and

Table 8
Cluster mean values for the 20 traits of sesame genotypes that were grouped by hierarchical clustering.

Traits	Cluster				
	I	II	III	IV	V
Flowers per node	1.00	1.00	1.00	1.00	2.00
Capsules per node	1.00	1.00	1.00	1.00	2.00
Carpels per capsule	1.00	1.00	1.00	2.00	1.00
Locules per capsule	1.00	1.00	1.00	2.75	1.00
Days to 50% flowering	56.56	56.97	52.72	58.23	56.31
Bacterial blight disease severity (%)	48.63	64.85	54.55	52.71	52.62
Days to 90% maturity	113.14	110.13	95.68	113.09	114.37
Plant height (cm)	108.12	93.37	85.96	98.08	100.36
Plant height to first branching (cm)	37.09	35.09	23.30	35.37	31.09
Length of capsule-bearing zone on main stem (cm)	51.58	38.28	48.49	47.68	47.25
Internode length (mm)	3.95	4.17	3.85	3.83	4.80
Capsule length (mm)	2.62	2.44	2.49	2.53	2.02
Capsule width (mm)	0.75	0.76	0.78	0.74	0.80
Primary branches per plant	3.70	2.53	2.11	2.82	3.34
Capsules on the main stem per plant	25.34	15.29	18.77	24.70	27.76
Capsules per plant	59.79	30.32	33.87	40.08	56.01
Seeds per capsule	75.00	67.99	61.81	81.64	60.35
1000 seed weight (g)	2.33	2.28	2.38	2.31	2.25
Oil content (%)	54.19	51.74	52.37	53.01	52.94
Seed yield per plant (g)	7.77	5.02	5.71	6.42	6.63

Table 9
Intra-cluster (highlighted diagonally and in bold) and inter-cluster Euclidean squared distances (D^2) among various groups of sesame genotypes.

Cluster	Cluster				
	I	II	III	IV	V
I	**6.78**	10.52	9.80	10.68	8.97
II		**7.73**	8.88	10.36	10.58
III			**5.38**	9.81	9.68
IV				**7.00**	10.31
V					**5.71**

morphological characteristics such as plant height, length of the zone where capsules are formed, and the number of primary branches per plant reveals that taller genotypes with more primary branches that bear capsules and a longer zone where capsules are formed result in higher seed yield in sesame. The height of the plants, the length of the zone containing capsules, the number of branches per plant, capsules on the main stem per plant, and capsules per plant all showed a strong and positive relationship. This confirms that conducting selection based on multiple traits is feasible for enhancing seed yield. A notable and robust genotypic correlation between seed yield and traits associated with yield, coupled with higher genotypic correlation coefficients relative to phenotypic coefficients between seed yield and some of its related traits, indicates the existence of inherent associations between seed yield and these traits. This indicates that achieving reliable results in seed yield can be accomplished through indirect selection. Whenever there is a correlation among traits primarily attributed to the genetic components, heritability increases, and a reliable response can be anticipated through selection [32]. The non-significant correlation between seed yield per plant and phenological traits indicates that the timing of flowering and maturity does not affect the productivity of the tested genotypes. In this study, oil content showed a positive correlation with seed yield per plant at both the phenotypic and genotypic levels, suggesting that these two key traits can be simultaneously improved through selection. Nevertheless, a conflicting finding was documented by Refs. [28,29], asserting a negative correlation between seed yield and oil content. Capsule length and seeds per capsule exhibited a notable positive correlation, both phenotypically and genotypically. Similarly, capsule length and seeds per capsule had a noteworthy positive genotypic correlation [33]. Therefore, these findings indicate that genotypes with longer capsules will produce a higher number of seeds per capsule. Conversely, capsule width exhibited a significant negative correlation, both phenotypically and genotypically, with the number of seeds per capsule, implying that wider capsules result in a lower seed count per capsule. There was a notable positive genotypic correlation between capsule length and 1000 seed weight, indicating that genotypes with elongated capsules tend to have larger seeds. In this study, there is no significant correlation between the weight of 1000 seeds and the oil content, implying that selecting for one of these traits will not affect the other. Bacterial blight disease severity showed a robust inverse relationship with seed yield, confirming previous reports that the disease can result up to 100% yield reduction depending on the cultivar and weather conditions [6]. The severity of bacterial blight disease is negatively correlated with yield components, both phenotypically and genotypically, indicating that the disease is a significant genetic factor that limits sesame production in the study area. Thus, the findings propose that sesame breeders should consider bacterial blight disease in their sesame seed yield improvement programs.

Correlation measures only the mutual association of two characteristics. Therefore, indirect selection for polygenic traits like seed yield using correlation coefficients can be misleading [32]. To avoid this, path coefficient analysis proves to be a potent statistical

approach that precisely assesses the relative significance of various yield components [27,28]. In the present study, path coefficient analysis at the genotypic level performed that the number of capsules per plant exerted the most substantial direct positive effect on seed yield. Earlier investigation [28] similarly indicated that the number of capsules held a noteworthy direct effect on sesame seed yield. These findings corroborate that opting for a greater number of capsules per plant can indeed enhance sesame seed yield effectively. Additionally, there were larger indirect positive effects of plant height, the length of the capsule-bearing zone, the number of primary branches, and number of capsules on the main stem. These characteristics exhibited minimal to negligible direct effects on seed yield, yet their considerable indirect positive influence through the number of capsules suggests that they should be regarded as secondary traits in the selection process to enhance seed yield. However, the little direct effects of these traits suggest that selecting of sesame genotypes based solely on their performance for these traits will not be effective unless the genotypes are also evaluated for the number of capsules. The analysis of path coefficients revealed that the severity of bacterial blight disease had a significantly larger indirect negative effect on the seed yield. This indirect effect occurs through the number of capsules. This indicates that the disease reduces sesame seed yield through inhibiting capsule production. The residual effect (0.13) from the path coefficient analysis indicates that the traits under examination elucidated 87% of the variability in seed yield. The remaining 13% of the variance may be due to excluded seed yield-related traits.

4.2. Genetic diversity based on qualitative and quantitative traits

The study found that there was a variation among the evaluated genotypes for eight out of the eleven qualitative traits that were considered. Similar findings have been documented in previous studies for traits such as the number of capsules per node [3,34], branching pattern [3], and seed color, which spans from white to black [3,35]. The phenotypic proportions showed that morphotypes representing monocapsular nodes, bicarpellate capsules, four-loculed capsules, and white seed color. The higher proportion of white-seeded genotypes indicates that Ethiopian farmers prefer to grow white seeded cultivars, which are also in demand in the global market. White-seeded varieties have gained attention in most sesame-producing nations [35,36]. On the other hand, morphotypes representing multicapsular nodes, tetracarpellate capsules, and six to mixed loculed capsules were rarely found. Similarly, sesame genotypes with multicapsular nodes and tetracarpellate capsules were reported in low proportions [37]. Multicapsular genotypes produce a higher number capsules per unit length on the main stem compared to genotypes with monocapsular nodes. This can potentially increase seed yield, particularly in moisture-stressed areas where sesame plants do not branch. In such areas, the contribution of capsules to seed yield is solely determined by the number of capsules produced on the main stem. Sesame genotypes with multicapsular nodes play a pivotal role in plant breeding programs aiming to increase the density of capsules per unit length. This is particularly significant, as the number of capsules stands out as the most crucial trait contributing to seed yield in sesame [37]. The results of Shannon-Weaver and Simpson's diversity indices for qualitative traits were consistent with the phenotypic frequency of morphotypes. High Shannon-Weaver and Simpson's diversity indices signify the existence of substantial diversity among the genotypes regarding qualitative traits. Concurrently, this study recommends prompt implementation of conservation measures for rarely found morphotypes of qualitative traits, ensuring their availability for future breeding programs.

Summary statistics for data collected on quantitative traits revealed a wide range of variation across all traits, underscoring the presence of diversity among the genotypes. The observed variability in seed yield and associated traits substantiates the potential for enhancing sesame seed yield through selective breeding. Furthermore, considerable variation has been noted for both oil content and 1000 seed weight, which is consistent with the previous report [38], that assures the existence of genetic variations in Ethiopian sesame genotypes to improve seed size and oil content. An analysis of variance conducted for data collected on 16 quantitative traits revealed the existence of genetic variability among the examined genotypes for nearly all considered traits, except for internode length. Similar results were reported for the number of capsules per plant, number of seeds per capsule, 1000 seed weight, and seed yield [27, 39]. Previous reports have highlighted significant variations among sesame genotypes in traits such as days to flowering, days to maturity, plant height, and the number of primary branches [30]. Furthermore, the observed genetic variability in sesame genotypes for oil content aligns with findings from a prior study [3]. The existence of variability within the population is a prerequisite for initiating crop improvement programs. Therefore, the current study confirms the existence of genetic potential that can be utilized to improve seed yield, seed size, and oil content by selecting promising genotypes.

Cluster analysis demonstrated genetic diversity among the evaluated genotypes, aligning with prior findings that reported genetic diversity in sesame [28]. To identify elite genotypes for potential release as new varieties or for use as breeding lines, it is crucial to examine the characteristics of individuals within each cluster. The traits that mostly distinguished the genotypes included the days to 50% flowering and 90% maturity; the number of carpels, seeds and locules per capsule; the number of flowers and capsules per node; as well as seed yield per plant. Similar traits, such as days to maturity and seed yield, have been used to characterize distinct groups of sesame genotypes [28]. Elite genotypes from cluster I can be selected for inclusion in variety trials to improve seed yield. Additionally, potential parents with desirable traits can be chosen from different clusters for desirable traits. For instance, genotypes in cluster IV, which have the highest number of seeds per capsule, can be selected while individuals in cluster V, which have multicapsular nodes, can be considered for enhancing capsule density per plant. The largest distance between clusters was observed between cluster I and IV, followed by cluster I and V. This suggests that combining individuals from these distant clusters through hybridization could result superior segregating populations. Potential parental lines can be selected from distant clusters [38]. Therefore, this study confirms the availability of genetic potential that can be utilized in sesame breeding programs.

5. Conclusions

Correlation analysis confirmed that improving seed yield in sesame can be achieved through indirect selection for resistance to bacterial blight disease, increased plant height, an elongated capsule-bearing zone, higher number of primary branches per plant, higher number of capsules per plant both on the main stem and the whole plant, and an increased number of seeds per capsule. Additionally, the analysis of path coefficients suggested that effective enhancement of sesame seed yield can be attained through indirect selection for a high number of capsules per plant. Furthermore, the present study has discovered that there is genetic variation within the examined genotypes in terms of both qualitative and quantitative traits. This finding is of great importance for future sesame breeding programs. For instance, we could recommend incorporating elite sesame genotypes into variety trials with the potential for variety release. Moreover, the current study has identified distant genotypes, that could be utilized to develop superior segregating populations.

Data availability statement

The data from our study has been publicly deposited on the Harvard Dataverse Repository.DOI: https://doi.org/10.7910/DVN/7GKPIU.

CRediT authorship contribution statement

Sintayehu Gedifew: Writing – review & editing, Writing – original draft, Formal analysis, Data curation, Conceptualization. **Habtamu Demelash:** Visualization, Formal analysis. **Alemu Abate:** Writing – review & editing, Supervision. **Tiegist Dejene Abebe:** Writing – review & editing, Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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