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Estimates of genetic variability and correlation coefficient for yield and its traits in black cumin (*Nigella sativa* L.) genotypes in South Wollo Ethiopia

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Abstract: Black cumin (*Nigella sativa* L.) is a valuable annual spice used in food, cosmetics, and industrial products. However, productivity is limited by the lack of improved varieties, mainly due to insufficient knowledge of the genetic diversity within Ethiopian black cumin populations. A study was conducted to assess genetic variability and interrelationships among traits related to seed yield in various black cumin genotypes. Twenty-five genotypes were tested using a 5x5 simple lattice design in Hara, Tehuledere district, Ethiopia during the 2022/2023 growing season. Analysis of variance revealed significant differences for most parameters, except stand count at harvest and thousand seed weight. Broad-sense heritability (H^2) and genetic advance as a percentage of the mean (GAM) ranged from 8.24% for days to 90% maturity to 89.56% for the number of tertiary branches per plant, and 4.51% for days to 90% maturity to 84.85% for the number of tertiary branches per plant, respectively. High to moderate estimates of genetic and phenotypic coefficients of variation (GCV and PCV), heritability, and GAM were observed for the number of tertiary branches per plant, number of flowers, number of capsules, biological yield, seed yield, and harvest index. The results also showed significant positive correlations between seed yield and various traits, including plant height, number of primary and tertiary branches, flowers, capsules, and seeds per capsule, biological yield, and harvest index, at both the genotypic and phenotypic levels. The study concluded that significant genetic variability exists, offering potential for targeted selection to enhance specific traits.

1. Introduction

Black cumin (*Nigella sativa* L.) belongs to the Ranunculaceae family within the Ranales order, which includes more than 70 genera and approximately 3,000 species, all having a diploid chromosome number of

(2n = 2x = 12). It is one of the 14 annual herb species in the Nigella genus (Weiss, 2004). The name «Nigella» is derived from the Latin words «nigellus» or «niger,» meaning «black». Commonly known as black cumin, across the globe, this plant goes by many different names. In Ethiopia, it is called "tikurazmud" in Amharic and "awosetta" in Tigrinya (Jansen, 1981).

According to Nergiz and Otles (1993), black cumin features a slightly hairy stem, shiny green trifoliate leaves, and attractive flowers that bloom at the end of the stem. The flowers are typically milky white with a subtle blue or green tint at the tips. The seeds are housed in black, slightly curved seedpods with three edges. This annual crop grows to a height ranging from 15.04 to 30.08 cm (Nadaf *et al.,* 2015). black cumin is native to the Mediterranean region and has been cultivated for over 3,000 years (Khan, 2009). However, it is widely cultivated in Sub-Saharan Africa (Iqbal *et al.,* 2019).

Black cumin seeds are rich in nutrients, comprising 26.7% protein, 28.5% fat, 24.9% carbohydrates, 8.4% crude fiber, and 4.8% total ash. They also provide a significant quantity of various vitamins and minerals, including copper (Cu), phosphorus (P), zinc (Zn), and iron (Fe). The content and composition of the essential oil in black cumin can vary due to genetic factors, environmental conditions, and the plant's origin (Abera and Hirko, 2020). High acid and peroxide values are also characteristic of black cumin oils (Dabrowski *et al.,* 2024).

Black cumin is effective for curing a variety of health issues, including neurological and mental disorder cardiovascular diseases, cancer, diabetes, inflammatory conditions, infertility, and numerous infectious diseases caused by bacteria, fungi, parasites, and viruses (Yimer *et al.,* 2019). Additionally, some evidence suggests that components of black cumin seeds, such as thymoquinone, may offer significant therapeutic potential against COVID 19 (Badary *et al*., 2021). In Ethiopia, black cumin is utilized for flavoring bread and sauces and is a key ingredient in hot pepper spice mixtures, providing farmers with a better income and serving traditional medicinal purposes (Herms, 2015; Shimelis, 2021).

Studies indicated that black cumin contributes approximately 39.88% to farming income in certain regions of Ethiopia (Teshome and Anshiso, 2019). In terms of export capacity, it ranks third overall, and in value, it stands second to ginger (Yimer, 2010). In the 2013-2014 period, black cumin accounted for 9% of total spice exports, valued at approximately USD 2.4 million (Herms, 2015). The Ethiopian Ministry of Agriculture and Natural Resources reported that 21,550 hectares were dedicated to black cumin, yielding around 17,072 tons annually.

In the South Wollo region, smallholder farmers cultivate twelve spice species, with black cumin being the predominant one, followed by coriander, mustard, basil, and rue. To optimize crop performance and enhance systematic productivity, black cumin can be intercropped with pepper and other crops in Ethiopia (Gelaye, 2025).The production and productivity of black cumin in South Wollo are estimated at about 365 quintals per hectare and 4.93 quintals per hectare, respectively (Tiru *et al.,* 2017). Despite its potential, black cumin faces low productivity and production challenges, primarily due to a lack of improved varieties. This issue is intensified by limited information on the genetic variability of local populations of black cumin in Ethiopia, leading farmers to cultivate mainly landraces or traditional varieties. The restricted large-scale production and development of enhanced varieties result from minimal information concerning inter and intra-specific variability and genetic relationships among black cumin genotypes.

According to the Ministry of Agriculture and Natural Resources (MANR, 2016), only eight varieties of black cumin have been released from national and regional research centers in Ethiopia. This limited progress may result from insufficient knowledge about the genetic diversity of cultivated black cumin genotypes.

Moreover, few studies have explored the extent of genetic variation, phenotypic traits, trait relationships, and their effects on seed yield among Ethiopian black cumin genotypes. Therefore, this research aims to address the information gaps related to the genetic characteristics of black cumin and serve as a guide for selecting improved varieties. This is important for evaluating genetic variability and the association of traits among genotypes is essentiall for developing effective selection strategies. The objective of the study was to investigate the genetic variability of black cumin genotypes and estimate their genetic parameters concerning seed yield and its components.

2. Materials and Methods

Description of the study area

The experiment was conducted at the farmer field of Hara,Tehuledere Woreda, South Wollo, Amhara National Regional State, during the 2022 rainy season (Fig. 1).

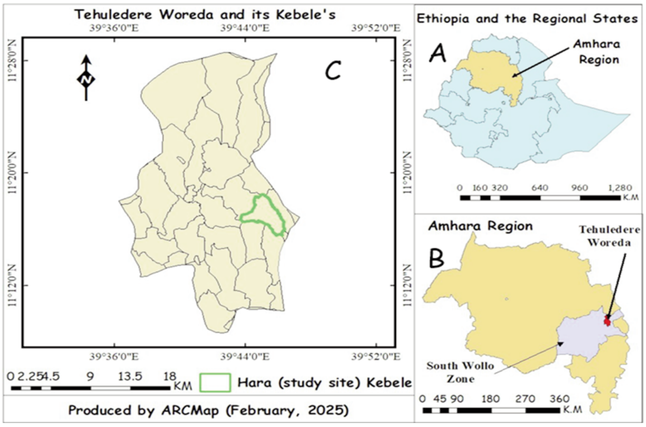

Fig. 1 - Map of the study area: where, A= Map of Ethiopia, B= Map of Amhara region, C= Map of the specific study area; ARCMap= A desktop geographic information system (GIS) application primarily used for mapping.

The site is situated in major cereal growing belts which are 448 km North East of Addis Ababa with a geographic co-ordinate of 11° 20′0» N and 39°44′0» E at an elevation of 2136 meter above sea level. The site has the minimum and maximum annual mean temperature of is 10°C and 25°C, respectively. The average annual rainfall for the site ranges from 900 to 1100 millimeter with a bimodal distribution. The soil of this area belongs to the group of well-drained vertisol soils.

Experimental materials

In total, 25 black cumin genotypes were used for this study, of which 24 were collected from various altitudes across the Amhara regional state.

The planting materials, along with supporting information like passport data were obtained from the Ethiopia Biodiversity Institute (EBI). Additionally, 'Dershaye' as a standard genotype that was supplied by Sirinka Agricultural Research Center (Table 1).

Experimental design and field management

The experiment was designed using a 5 x 5 simple

Table 1 - List of black cumin (*Nigella sativa* L.) genotypes collected from different locations of Amhara region and obtained from the database of the Ethiopian Biodiversity Institute

Genotype	Region	Zone	Latitude (North)	Longitude (East)	Altitude (m asl)
223072	Amhara	MirabGojam	11-07-02	37-11-32	2737
9069	Amhara	MirabGojam	10-38-48	37-05-09	2002
9071	Amhara	MirabGojam	10-38-21	37-05-13	1970
9068	Amhara	MirabGojam	11-45-40	37-05-4	1854
9067	Amhara	MirabGojam	11-41-08	37-01-12	1840
215319	Amhara	MisrakGojam	10-32-19	37-47-28	2754
223069	Amhara	MisrakGojam	11-00-08	37-00-11	2475
90505	Amhara	MisrakGojam	20-20-00	38-00-00	2024
90506	Amhara	MisrakGojam	20-20-00	38-00-00	2011
31114	Amhara	Semen Gonder	37-11-14	12-21-27	1834
31109	Amhara	Semen Gonder	37-22-51	12-25-31	1810
205167	Amhara	Semen Gonder	12-42-34	37-00-15	1289
31110	Amhara	Semen Gonder	37-23-55	12-23-41	1811
90507	Amhara	Semen Gonder	12-16-00	37-05-00	1760
207539	Amhara	Semen Gonder	12-20-00	37-14-00	1800
31112	Amhara	Semen Gonder	37-16-50	12-22-57	1868
19921	Amhara	Semen Gonder	12-33-20	37-06-40	1944
31111	Amhara	Semen Gonder	37-17-56	12-25-31	1821
207540	Amhara	Debub Gonder	12-10-59	39-32-20	1222
31108	Amhara	Debub Gonder	37-20-20	12-21-08	1800
212520	Amhara	Semen Shewa	10-27-00	39-15-00	2680
19590	Amhara	Semen Shewa	11-27-00	39-14-00	1993
242220	Amhara	Oromo spp zone	10-50-28	39-48-60	1480
242224	Amhara	Debub wollo	11-16-00	39-44-61	2170
Dershaye	Amhara	Semen Wollo	11-50-40	39-12-25	1800-2500

lattice layout. Each plot measured 1.5 m x 2 m (3 m^2) and maintained distances of 0.5 m between plots and 1 m between blocks. Each plot consisted of eight rows, with a spacing of 25 cm between rows and 15 cm between plants. Ten holes were prepared in each lined row, and three hundred twenty seeds were dibbled in each plot, with four seeds placed in each hole. Treatments were randomly assigned within each block. Planting took place during the last week of June 2022 at a depth of 3 cm. After sowing, the seeds were immediately covered with loose soil and gently pressed down by hand. A fertilizer application rate of 60 kg ha^{-1} of nitrogen (N) and 40 kg ha^{-1} of phosphorus pentoxide (P_2O_5) was utilized, following the guidelines provided by Yimama *et al.* (2015). Additional agronomic practices were carried out in accordance with the recommendations for black cumin (Hammo, 2008). Thinning was done to regulate the number of seedlings in each row. This process was conductedby hand to achieve the desired density of 10 plants per row and a total of 80 plants per plot. All agronomic practices were consistently applied across all plots.

Data collection and analysis

Data collected included days to 50% flowering, days to 90% maturity, biomass yield (kg ha^{-1}), seed yield per hectare (kg ha^{-1}), and harvest index (%) on a plot basis. Additionally, plant-based measurements were taken for plant height (cm), number of flowers per plant, number of secondary branches per plant, number of tertiary branches per plant, number of capsules per plant, number of seeds per capsule, and 1000-seed weight (g).

Before the detailed analysis, the normality distribution of the data was cheeked using Shapiro test in R statistical software. Then, data for each quantitative trait was analyzed using one-way ANOVA with the general linear model. The analysis of variance for each characteristic was performed according to the standard statistical methods outlined by Gomez and Gomez (1984) and was conducted using R statistical software. Following the ANOVA, the least significant difference was calculated at a 5% probability level.

Estimates of genetic parameter

Variance components. Variance components, including phenotypic, genotypic, and environmental variations, were estimated using the method proposed by Burton and Vane (1953). The calculations for the genotypic, phenotypic, and environmental variance were conducted accordingly.

Genotypic variances: $$\sigma^2 \ g = \frac{\mathrm{Msg} - \mathrm{Mse}}{\mathrm{r}} \qquad (1)$$

Where, Msg = mean square due to genotypes, Mse = error mean square, and r = number of replications.

Environmental variance: $$\sigma^2 g = Mse \qquad (2)$$

Where, Mse = error mean square.

Phenotypic variance: $$\sigma^2 p = \sigma^2 g + \sigma^2 e \qquad (3)$$

Where, $\sigma^2 p$= phenotypic variance, $\sigma^2 g$= genotypic variance and e= error mean square.

Estimates of coefficients of variations

The estimates of coefficient of variations was calculated using the following formulas.

Phenotypic CV: $$\mathrm{PVC} = \frac{\sqrt{\sigma^2 \mathrm{p}}}{\mathrm{x}} \cdot 100 \qquad (4)$$

Where, phenotypic variance; x= grand mean of the character

Genotypic CV: $$\mathrm{GCV} = \frac{\sqrt{\sigma^2 \mathrm{g}}}{\mathrm{x}} \cdot 100 \qquad (5)$$

Where, σ^2g = genotypic variance and x = grand mean of the character.

The values of Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were classified into low, moderate, and high categories according to the criteria established by Sivasubramaniah and Menon (1973).

Low = 0-10%, Moderate = 10-20% and High = >20%.

Heritability (in the broad sense)

Heritability in percent was computed based on the formula given by Allard (1960).

$$\mathrm{H}^2 = \frac{\sigma^2 \mathrm{g}}{\sigma^2 \ \mathrm{p}} \cdot 100 \qquad (6)$$

In this context, H^2 represents heritability, σ^2g stands for the total genotypic variance, and σ^2p denotes the total phenotypic variance. According to Johnson *et al.* (1955), heritability percentages are classified as low (0-30%), moderate (30-60%), and high (greater than 60%). When the heritability of a trait is very high (60% or above), it is easier to select that trait because there is a strong correlation between genotype and phenotype, with the environmental influence on the phenotype being relatively minimal. Conversely, selection may prove challenging for traits with low heritability (less than 30%) due to the masking effects of environmental factors.

Expected genetic advance under selection

The genetic advance in absolute units (GA) and as a percentage of the mean (GAM), based on selecting the top 5% of genotypes, was calculated using the methods described by Johnson *et al.* (1955).

The genetic advance was estimated as follows:

$$\mathrm{GA} = k\sqrt{\sigma^2 \mathrm{p}} \cdot \mathrm{H}^2 \quad (7)$$

where GA = Genetic advance, K= selection intensity at 5% (K= 2.063), $\sqrt{\sigma^2 p}$ = Phenotypic variance on a mean basis, H^2 =Heritability in the broad sense

Genetic advance as a percent of the mean: it was estimated as follows:

$$\mathrm{GAM} = \frac{\mathrm{GA}}{\mathrm{x}} \cdot 100 \quad (8)$$

Where, GAM= Genetic advance as percent of mean, GA=Genetic advance, and x= Population mean

Estimation of genotypic and phenotypic correlation coefficients

The genotypic and phenotypic correlation coefficients between yield and yield-attributing traits were computed as described by Singh *et al*. (2001) and using R statistical software.

I. Genotypic correlation:

$$\mathrm{Cov\ (g)\ (XY)} = \frac{\mathrm{cov(g)\ x\ y}}{\sqrt{\sigma^2\ \mathrm{(g)x} \cdot \sigma^2\ \mathrm{(g)y}}} \quad (9)$$

Where, Cov (g) (xy) = genotypic covariance between the variables x and y; σ^2 (g) x = genotypic variance of the variable x; σ^2 (g) y = genotypic variance of the variable y.

Genotypic correlation coefficients were tested for significance using the formula described by Robertson (1959)

$$t = \frac{\mathrm{rgxy}}{\mathrm{SErgxy}} \quad (10)$$

The calculated «t» value was compared with the tabulated «t» value at (n-2) degrees of freedom at a 5% level of significance.

Where, n = number of genotypes;

$$\mathrm{SEr}_{\mathrm{gxy}} = \sqrt{\frac{1-r^2 gxy}{\mathrm{2Hx \cdot Hy}}} \quad (11)$$

Where, H^2_x = Heritability of trait x; H^2_y = Heritability of trait y.

II. Phenotypic correlation:

$$\mathrm{Cov\ (ph)\ (xy)} = \frac{\mathrm{cov(ph)\ x\ y}}{\sqrt{\sigma^2\ \mathrm{(ph)x} \cdot \sigma^2\ \mathrm{(ph)y}}} \quad (12)$$

Where, Cov (p) (xy)=phenotypic covariance between the variables x and y. σ^2 (p) x=phenotypic variance of the variable x. σ^2 (p) y=phenotypic variance of the variable y.

The calculated phenotypic correlation value was tested for its significance using a t-test:

$$t = \frac{\mathrm{rp}}{\mathrm{SE\ (rp)}} \quad (13)$$

Where, r_p= phenotypic correlation; SE (r_p) = standard error of phenotypic correlation was obtained using the following procedure (Sharma, 1998).

The calculated absolute t-value was tested against the tabulated "t" value at n-2 degree of freedom at a 5% level of significance.

$$\mathrm{SE} = \sqrt{\frac{1-r^2 \mathrm{p}}{\mathrm{n}-2}} \quad (14)$$

Where, SE = standard error, n = the number of genotypes tested and r_p = the phenotypic correlation coefficient.

3. Results

Analysis of variance for seed yield-related traits

As shown in ANOVA Table 2, there were highly significant differences among genotypes ($p<0.01$) for several traits, including days to 50% flowering, days to 90% maturity, plant height, the number of primary, secondary, and tertiary branches, biological yield, seed yield, and harvest index. Additionally, significant variations were found among genotypes ($p<0.05$) for days to 50% emergence and the number of seeds per capsule. However, no significant variations were observed for stand count at harvest and thousand seed weight.

Genotypic and phenotypic coefficients of variation

Burton and Vane (1953) categorized PCV and GCV values greater than 20% as high, values below 10% as low, and those ranging from 10% to 20% as medium. Following this framework, high values were found for the number of tertiary branches (GCV at 45.34%, PCV

Table 2 - Mean squares for different traits evaluated in 25 black cumin genotypes evaluated at Hara, Tehuledere Woreda in 2022 GC

Traits	Treatment (Unadj) (Df= 24)	Rep (Df=1)	Block within rep (Df=8)	Intra block error (Df=16)	RCBD error	Efficiency of SL relative to RCBD	CV
DF	21.88 **	33.6	7.07	6.70	6.83	98.09	3
DM	31.50**	0.32	2.42	2.20	2.278	96.57	0.9
PH	36.78 **	26.06	5.08	4.21	4.51	93.34	3.6
NPB	2.80 **	2.51	0.86	0.49	0.61	80.32	8.9
NSB	8.51 **	0.0008	1.86	1.59	1.68	94.64	9.7
NTB	8.75 **	6.09	0.93	0.79	0.84	94.04	20.3
NF	120.44 **	0.01	4.03	8.08	6.74	119.88	5.4
NEC	126.17 **	5.9	3.20	10.29	7.93	129.76	6.3
NSC	84.84 *	1.62	21.60	28.84	26.43	109.11	6.5
TSW	0.61 NS	0.19	0.19	0.34	0.29	116.39	18.7
BY	472586**	6341	30770	23661	26030	90.89	6.1
SY	60649 **	4592	5832	3388	4203	80.60	8.9
HI	6.68 **	12.52	6.61	3.74	4.70	79.57	7.5

*, **, NS = significant at 5% probability level and highly significant at 1% probability level, non significant, respectively.
Df = Degree of freedom; Rep= Replication; RCBD = Randomized Complete Block Design; SL= Simple lattice design; CV= Coefficient of Variation.
DF= Days to 50% flowering, DM= Days to 90% maturity; PH= Plant height; NPB= Number of primary branches; NSB= Number of secondary branches; NTB= Number of tertiary branch; NF= Number of flowers; NEC= Number of effective capsules; NSC= Number of seed per capsule; TSW= Thousand seed weight; BY= Biological yield; SY= Seed yield; HI= Harvest index.

Fig. 2 - Pictures of black cumin genotypes during a field trial. A= Planting, B= Seedling stage, C= Vegetative stage, D= At Flowering, E= At maturity, F= Harvested Black cumin seeds.

at 49.92%) and seed yield (GCV at 25.67%, PCV at 27.25%). This high GCV shows that there is a substantial amount of genetic diversity present in the population.

Table 3 presents estimates of mean, range, and variance, genotypic and phenotypic coefficients of variability, broad-sense heritability, and genetic advance as a percentage of the mean for the studied traits. Medium GCV and PCV values were noted for the primary branch (13.30%, 16.63%), secondary branch (14.26%, 17.43%), number of flowers (14.42%, 15.25%), number of effective capsules (15.12%, 16.1%), biological yield (18.70%, 19.76%), and harvest index (12.37%, 14.97%). Result suggests that these traits are less influenced by environmental factors, making phenotypic selection a viable breeding strategy for their improvement. Supporting this, Seid *et al.* (2013) found medium GCV and PCV values for the number of secondary branches (15.1% and 14.16%, respectively).

On the other hand, low GCV and PCV values were observed for days to 50% flowering (3.15%, 4.35%), days to 90% maturity (2.35%, 2.53%), plant height (7.02%, 7.94%), and number of seeds per capsule (6.53%, 9.02%) (Table 3). These low GCV and PCV values reflect limited potential for selection and improvement, indicating a low level of genetic variation among the genotypes for these traits. This indicates that these traits exhibit low variability and are relatively stable, with limited potential for improvement through selection. The small difference between GCV and PCV suggests minimal environmental influence, implying that the observed variability is largely genetic in origin. Similar findings were reported by Hika *et al.* (2015) and Tewodros *et al.* (2018), showing low GCV and PCV values for days to 50% flowering and days to 90% maturity, suggesting minimal environmental influence on the expression of these traits, which facilitates selection based on phenotypic characteristics.

Heritability in broad sense (H2)

According to Johnson *et al.* (1955), heritability is categorized as high when it is greater than or equal to 60%, medium when it falls between 30% and 60%, and low when it is below 30%. A heritability of 100% indicates that genotypic variance equals phenotypic variance, suggesting that phenotypic performance is a perfect indicator of genotypic value. Based on this classification, as shown in Table 3, high heritability estimates were found for several traits, including plant height (78.17%), number of primary branches (63.98%), number of secondary branches (66.78%), harvest index (68.35%), biological yield (89.56%), seed yield (87.04%), days to 90% maturity (86.51%), number of tertiary branches (82.5%), number of flowers (89.41%), and number of effective capsules (88.18%). In this study, moderate heritability estimates were observed for days to 50% flowering (52.44%), number of seeds per capsule (52.49%), and thousand seed weight (35.66%) (Table 3). The estimate of GA values ranged from 0.49 for thousand

Table 3 - Estimates of mean, range and variance, genotypic, phenotypic coefficients of variability, broad sense heritability and genetic advance as percent of the mean for the studied characters

Traits	Units	Mean	Range		σ^2 g	σ^2 p	GCV	PCV	H2	GA	GAM
			Min	Max			%	%	%		
DF	Days	86.94	76.93	92.93	7.53	14.35	3.15	4.35	52.44	4.09	4.70
DM	Days	162.24	151.87	166.3		16.89	2.35	2.53	86.51	7.32	4.51
PH	CM	57.21	49.60	62.87	7.02	20.64	7.02	7.94	78.17	7.31	12.78
NPB	Number	7.86	5.16	9.96	1.09	1.71	13.30	16.63	63.98	1.72	21.92
NSB	Number	12.95	9.42	17.37	3.41	5.09	14.26	17.43	66.98	3.11	24.05
NTB	Number	4.38	1.8	8	3.95	4.79	45.34	49.92	82.5	3.72	84.85
NF	Number	52.27	39.50	73.4	56.85	63.59	14.42	15.25	89.41	14.68	28.09
NC	Number	50.84	35.5	71.4	59.12	67.04	15.12	16.10	88.18	14.87	29.25
NSC	Number	82.69	67	104	29.20	55.63	6.53	9.02	52.49	8.06	9.75
TSW	Kg	3.11	2	4	0.16	0.45	12.89	21.59	35.66	0.49	15.86
BY	Kg	2526.3	1835.5	3520	223277.6	249308	18.70	19.76	89.56	921.17	36.46
SY	Kg	654.38	428.89	1026.6	28222.8	32425.8	25.67	27.5	87.04	322.86	49.33
HI	%	25.74	19.46	33.91	10.15	14.85	12.37	14.97	68.35	5.42	21.08

σ^2 g= Genotypic variation; σ^2p= Phenotypic variation; GCV= Genotypic coefficient of variation; PCV= Phenotypic coefficient of variation; H2= Broad sense heritability; GA= Genetic advance; GAM= Genetic advance as percent of mean;

DF= Days of 50% flowering; DM= Days to 90% maturity; PH= Plant height; NPB= Number of the primary branch; NSB= Number of the secondary branch; NTB= Number of the tertiary branch; NF= Number of flower; NC= Number of capsule; NSC= Number of seed per capsule; TSW= Thousand seed weight; BY= Biological yield; SY= Seed yield; HI= Harvest index.

seed weight to 921.17 for biological yield.

Genetic advance (GA)

Genetic advances show the degree of gain that can be made in a particular character (Ogunniyan and Olakojo, 2014). As indicated in Table 3, the highest value of genetic advance was shown on biological yield (921.17), followed by seed yield (322.86), but the lowest value was observed on thousand seed weight (0.49). The traits exhibited a moderate estimate of genetic advance, which was observed on a number of flowers (14.68%) and effective capsules (14.87%). Low genetic advance was obtained from days of 90% maturity, number of seed per capsule, plant height, harvest index, days of 50% flowering, number of secondary branches per plant, number of tertiary branches per plant, number of primary branches per plant and thousand seed weight (Table 3).

Genetic advance as percent of mean (GAM)

The expected genetic advance from selecting the best genotypes, expressed as a percentage of the mean, ranged from 4.51% for days to 90% maturity to 84.85% for tertiary branches (Table 3). According to Johnson *et al.* (1995), a genetic advance as a percentage of the mean (GAM) of less than 10% is considered low, between 10% and 20% is moderate, and above 20% is classified as high. Based on these categories, traits such as seed yield (49.3%), biological yield (36.4%), number of effective capsules (28.09%), number of flowers (28.09%), number of primary branches (21.92%), number of secondary branches (24.05%), and harvest index (21.08%) exhibited high GAM.

Intermediate genetic gain values were observed for thousand seed weight (15.86) and plant height (12.78); In contrast, low values were reported for the number of seeds per capsule, days to maturity, and days to flowering (Table 3). Generally, traits such as seed yield, biological yield, number of primary, secondary, and tertiary branches per plant, number of flowers, number of capsules, and harvest index demonstrated high heritability along with a high genetic advance as a percentage of the mean.

Additionally, medium heritability coupled with a high genetic advance as a percentage of the mean was observed for the harvest index (5.42 and 21.08), respectively, suggesting that selecting for these characteristics would enhance the performance of the genotypes. Conversely, traits such as days to 50% flowering, days to 90% maturity, and number of seeds per capsule exhibited medium to high heritability but low genetic advance and genetic advance as a percentage of the mean.

4. Discussion and Conclusions

Analysis of variance for seed yield-related traits

The analysis of variance revealed a highly significant difference among genotypes. This signifies that the differences observed in the studied trait(s) are statistically significant and not just a result of random variation or environmental interference. Such findings imply that specific genotypes exhibit markedly better or worse performance compared to others, thereby offering a robust foundation for selection in plant breeding initiatives. The existence of significant differences further emphasizes the opportunity for genetic enhancement by identifying and applying superior genotypes in forthcoming breeding activities. This finding is in line with the results of Zigyalew *et al.* (2020), who reported significant differences among black cumin genotypes for days to maturity, plant height, secondary branches per plant, and seed yield. Similarly, Seid *et al.* (2013) noted significant differences among Ethiopian caraway genotypes for days to 90% maturity, plant height, and secondary branches per plant, and seed yield. Another finding also revealed significant variation among accessions for various traits (Tilahun *et al.,* 2024).

Furthermore, Tewodros *et al.* (2018) also found significant differences among black cumin genotypes for phonological parameters such as days to 50% flowering and days to 90% maturity, growth traits like plant height and primary and secondary branches per plant, as well as yield components including the number of capsules per plant, seeds per capsule, and seed yield. Consistent with these findings, Iqbal *et al.* (2019) reported significant differences among genotypes for all evaluated traits. Adam and Getinet (2006), who assessed 28 black cumin genotypes in Adet and Woreta, noted highly significant variation among genotypes for days to flowering, days to maturity, plant height, and the number of primary and secondary branches per plant, making a similar observation. Breeders can take advantage of this variability for selection purposes and may apply it in hybridization and gene transfer to other genotypes.

The substantial variability observed could be attributed to genetic diversity or variations in genetic makeup, as well as environmental factors influencing the phenotypic expressions (Sable *et al.,* 2020). In addition, Fikre (2023) reported that the differences in seed yield among genotypes were highly significant. This shows there is a potential genetic difference among the studied genotypes, which is very important to variety development of black cumin.

Genotypic and phenotypic coefficients of variation

To determine the variability present in the available materials, evaluating the genotypic and phenotypic coefficient of variation play a great role by showing the degree of variation among genotypes rather than calculating genetic variance alone (Kumar *et al.,* 2019). In this study, the individuals in the population differ significantly in their genetic makeup, leading to differences in how they express the trait (like seed yield). This may be due to crossbreeding, hybridisation, or natural genetic variation, which tends to exhibit higher genetic variability, leading to higher GCV. This occurs when diverse genetic backgrounds are included in the breeding population, increasing the potential for genetic differences (Begna and Teressa, 2024). High PCV indicates considerable variation in the observed phenotypes within the population. This data indicates that the trait is strongly influenced by environmental factors such as temperature, soil quality, water availability, and pest presence, which can strongly affect its expression. When environmental conditions vary significantly across populations or over time, they increase phenotypic variation (Dawa *et al.,* 2018).

Several studies have also reported high GCV and PCV for seed yield (Meena *et al.,* 2014; Hika *et al.,* 2015; Bitew, 2016; Preeti *et al.,* 2019). High GCV and PCV indicate sufficient variability within the gene pool, allowing for significant potential for genetic enhancement through selection in future breeding initiatives. This suggests that effective selection can be made on these traits, with their phenotypic expression serving as a reliable indicator of genetic potential (Hadru *et al.,* 2014). The high GCV values for these traits imply that they are relatively unaffected by environmental conditions. This means that the observed variation in that trait is largely due to genetic differences rather than environmental factors, suggesting greater potential for genetic improvement through selection. Conversely, while the thousand seed weight exhibited a high PCV (21.59%), its GCV was medium (12.89%), as shown in Table 3. This suggests that although there is substantial observable diversity in this characteristic, a considerable amount of it is affected by environmental influences. The significant difference between PCV and GCV demonstrates that environmental factors play a crucial role, while the genetic impact on the variability of the trait is moderate. Consequently, the selection for thousand seed weight might prove to be less effective unless the environmental factors are regulated.

Heritability in broad sense (H^2)

In this research high heritability estimates for characteristics such as plant height, the count of primary, secondary, and tertiary branches, harvest index, biological yield, seed yield, days to 90% maturity, number of flowers, and number of effective capsules suggest that the variation observed in these traits is predominantly attributable to genetic factors rather than environmental influences. This implies that these traits are consistently passed down from one generation to the next and can be effectively enhanced through selection in breeding programs. Consequently, breeders can anticipate considerable genetic improvements by concentrating on these traits, as their high heritability indicates robust genetic control and relatively minimal environmental variability. Previous research has reported high heritability in black cumin. Studies by Bairwa *et al.* (2015) and Iqbal *et al.* (2019) noted high heritability for seed yield and days to 90% maturity. Other researchers also identified high heritability for biological yield (87.92%), seed yield (99.81%), days to 90% maturity (95.32%), and the number of effective capsules (92.49%) (Mengesha and Getinet, 2011; Hika *et al.,* 2015). Similarly, Faravani *et al.* (2006) found maximum heritability for biological yield, harvest index, and stem branches in black cumin landraces, while high heritability was also reported for secondary branches of caraway (Seid *et al.,* 2013). Comparable findings were noted regarding the moderate heritability of the number of primary and secondary branches (Preeti *et al.,* 2019). High heritability trait indicate the expected response to selection in a segregating population. This suggests a reduced impact of environmental factors on the expression of these heritable traits, along with the predominance of additive gene action in their inheritance (Kassa *et al.,* 2019). Therefore, these traits are suitable for straightforward selection processes. Gebremedin *et al.* (2024) also reported high broad sense heritability values, along with high to moderate genetic advance as a percentage of mean values, for the number of capsules per plant and plant height. This indicates possibilities for improving these traits through selection.

Genetic advance (GA)

High GA was recorded on biological yield and seed yield whereas low GA was showed on the rest of the studied trait. A high genetic advance (GA) for biological yield and seed yield indicates that these characteristics have significant potential for enhancement through selection, as they are likely governed by additive gene effects and show a favorable response to breeding initiatives. Conversely, the low genetic advance noted for the other examined traits implies that these traits might be more influenced by non-additive gene effects or environmental influences, making genetic enhancement through selection less efficient or slower for those traits. Consequently, prioritizing biological yield and seed yield in breeding programs is expected to yield quicker and more significant improvements. Gebremedin *et al.* (2024), reported similar results on the thousand seed weight and number of seeds per plant of black cumin genotypes. Another research in line with this finding reported high genetic advance for traits such as biological yield and seed yield of black caraway, which implies that these traits are primarily governed by additive gene action and can be effectively improved through selection. This suggests strong breeding potential for enhancing yield-related characteristics in black caraway (Faravani *et al.,* 2015).

Genetic advance as percent of mean (GAM)

The results from the studied genotypes indicated that the additive genetic effect had a more significant influence on most of the traits tested, while the non-additive effect played only a minor role. Given the higher estimated GAM for the genotype, the findings suggest that selecting for these traits can be an effective breeding strategy for improvement (Gebregergs and Mekbib, 2020). Intermediate genetic gain values were observed for thousand seed weight and plant height, while lower values were recorded for the number of seeds per capsule, days to maturity, and days to flowering (Table 3). This finding is consistent with the study by Zigyalew *et al.* (2020), which reported high genetic advance as a percentage of the mean for biological yield and seed yield in black cumin genotypes. Similarly, Meena *et al.* (2014) also found a high genetic advance as a percentage of the mean for plant height, number of primary branches per plant, number of secondary branches per plant, and seed yield in caraway genotypes.

In general, high heritability coupled with a high genetic advance as a percentage of the mean was observed for traits such as seed yield, biological yield, primary branches per plant, number of secondary branches per plant, number of tertiary branches per plant, number of flowers, number of capsules, and harvest index. Meena *et al.* (2014) reported similar findings for traits like primary branches per plant, number of secondary branches per plant, and seed yield. Additionally, medium heritability with high genetic advance as a percentage of the mean was noted for harvest index, suggesting that selection based on these traits could lead to improve genotype performance. In contrast, traits such as days to 50% flowering, days to 90% maturity, and number of seeds per capsule showed medium to high heritability but low genetic advance and genetic advance as a percentage of the mean. This indicates that phenotypic selection for these traits may not effectively predict genotype performance due to environmental influence on their phenotypic expression. Therefore, genetic improvement through selection is challenging due to the environmental masking effect on genotypic traits.

In conclusion, the analysis of variance revealed significant differences among the tested genotypes for all the traits evaluated, highlighting the variability present in these genotypes. The phenotypic coefficient of variation was slightly higher for all traits, suggesting a limited impact of environmental factors on the phenotypic characteristics of the crop. However, this also indicates that environmental factors do influence the phenotypic expression of these traits to some extent. Notably, high phenotypic coefficients of variation was observed for biomass yield per plot, grain yield per plot, and the number of unfilled grains per panicle. The heritability estimates were moderately high for days to 85% maturity and thousand-grain weight, while they were lower for the remaining quantitative traits in this study. Low heritability suggests that environmental factors play a significant role in the expression of these traits.

Relatively high genetic advance was noted for biomass yield, unfilled grains per panicle, grain yield per plot, and fertile tillers per plant. Additionally, the estimates of genetic advance (as a percentage of the mean) for thousand-grain weight, days to 50% heading, plant height, and panicle length were also significantly high. In this study, thousand-grain weight exhibited moderately high heritability and a high genetic advance as a percentage of the mean, indicating a favorable opportunity for improving this trait using the evaluated genotypes.

Phenotypic correlation among other traits

A positive and highly significant correlation was found between days to 50% flowering and days to 90% maturity at the phenotypic level. Tewodros *et al*. (2018) also observed a similar association, suggesting early-flowering genotypes mature earlier. Plant height showed significant positive correlations with primary, secondary, and tertiary branches, flowers, capsules, and biological yield, and a positive correlation with seeds per capsule (Table 4). This trend leads to morphological differences as taller plants produce more branches, flowers, capsules, and achieve higher biological yield due to pleiotropic gene action and the stem’s role in producing nodes and internodes, which increase branches, flowers, seeds per capsule, and biological yield. Meena *et al.* (2014) reported similar findings in coriander genotypes, where plant height showed positive correlations with primary and secondary branches, flowering, capsules, and seeds per capsule, and maturity at the genotypic level.

Days to 50% flowering showed negative phenotypic correlations with most traits, except days to 90% maturity. Significant negative correlations were found with primary branches, secondary branches, seeds per capsule, and harvest index. This suggests that genotypes with more branches, seeds per capsule, and higher harvest index flower earlier. Negative, non-significant correlations were observed with plant height, flowers, effective capsules, tertiary branches, thousand seed weight, and biological yield. Days to 90% maturity showed negative significant correlations with primary branches, tertiary branches, flowers, and capsules. It showed negative, non-significant correlations with plant height, secondary branches, seeds per capsule, thousand-seed weight, biological yield, and harvest index. Additionally, it showed a positive, non-significant correlation with harvest index and a negative, non-significant correlation with thousand seed weight.

The number of primary branches showed a highly significant positive correlation with secondary and

Table 4 - Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients of quantitative traits among 25 genotypes of *N. sativa*

	DE	DF	DM	PH	NPB	NSB	NTB	NF	NC	NSC	TSW	BY	SY	HI
DF	0.004		0.86 **	-0.23	-0.42 *	-0.42 *	-0.35	-0.24	-0.29	-0.49 *	-0.08	-0.19	-0.43 *	-0.62 **
DM	0.009	0.60 **		-0.38	-0.46 *	-0.30	-0.48 *	-0.39 *	-0.44 *	-0.34	-0.07	-0.34	-0.32	-0.14
PH	0.25	-0.25	-0.35 *		0.9 **	0.87 **	0.83 **	0.84 **	0.85 **	0.44 *	-0.25	0.75 **	0.60 **	0.14
NPB	0.30 *	-0.31 *	-0.319 *	0.82 **		0.97 **	0.60 **	0.75 **	0.77 **	0.69 **	0.10	0.61 **	0.45 *	0.05
NSB	0.29 *	-0.27	-0.25	0.80 **	0.83 **		0.57 **	0.72 **	0.75 **	0.57 **	0.06	0.50**	0.36	0.06
NTB	0.05	-0.19	-0.39 **	0.64 **	0.41 **	0.33 *		0.89 **	0.85 **	0.47 *	-0.40 *	0.90 **	0.91 **	0.51 **
NF	0.19	-0.18	-0.33 *	0.77 **	0.66 **	0.66 **	0.77 **		0.99 **	0.56 **	-0.29	0.97 **	0.87 **	0.35
NC	0.18	-0.24	-0.35 *	0.76 **	0.67 **	0.66 **	0.74 **	0.98 **		0.51 **	-0.24	0.96 **	0.85**	0.31
NSC	0.19	-0.25	-0.21	0.34 *	0.27	0.37 **	0.23	0.41 **	0.41 **		0.28	0.48 *	0.60 **	0.53 **
TSW	-0.10	-0.06	-0.08	-0.095	0.004	-0.005	-0.17	-0.18	-0.15	-0.03		-0.29	-0.29	-0.19
BY	0.13	-0.17	-0.27 *	0.64 **	0.48 **	0.49 **	0.77 **	0.88**	0.87 **	0.34 *	-0.14		0.88 **	0.72 **
SY	0.05	-0.25	-0.29 *	0.48 **	0.48 **	0.31 *	0.31 *	0.75 **	0.73 **	0.48 **	-0.11	0.84 **		0.72 **
HI	-0.07	-0.27	-0.15	0.07	0.31 *	0.31 *	0.71 **	0.23	0.21	0.44 **	-0.01	0.21	0.69 **	

*, **, significant at P<0.05 and P<0.01, respectively. DE= Days to 50% emergence; DF days of 50% flowering; DM=days to 90% maturity; PH=Plant height; NPB= primary branches; NSB= number of secondary branches; NTB= number of tertiary branches; NF= number of flower; NC= number of capsule; NSC= number of seed per capsule; TSW= 1000 seed weight; BY= biological yield; SY= seed yield; HI = harvest index.

tertiary branches, flowers, capsules, seeds per capsule, and biological yield (Table 2), indicating that these factors improve simultaneously through selection. It had a positive, non-significant correlation with thousand seed weight and harvest index. Preti *et al.* (2019) and Zigyalew *et al.* (2020) reported similar positive associations with secondary branches, capsules, and biological yield.

Positive and highly significant associations were observed between the number of secondary branches per plant and the number of tertiary branches per plant, the number of flowers, the number of effective capsules, the number of seeds per capsule, and biological yield at the phenotypic level. This implies that improving secondary branches in black cumin genotypes will improve associated characters to some extent. This study was in agreement with Meena *et al.* (2014) and Preti *et al.* (2019), who reported that the number of secondary branches per plant had a positive and significant correlation with the number of effective capsules and biological yield at the phenotypic level. Tertiary branches showed highly significant positive correlations with flowers, capsules, biological yield, and harvest index. It showed a significant positive correlation with seeds per capsule and a significant negative correlation with thousand-seed weight.

Tertiary branches showed significant positive correlations with flowers, capsules, biological yield, and harvest index, as well as a negative correlation with thousand-seed weight. The number of seeds per capsule showed positive, significant correlations with biological yield and harvest index. Thousand-seed weight had a negative, non-significant correlation with both biological yield and harvest index, whereas biological yield was positively and significantly correlated with harvest index.

Genotypic correlation of seed yield with other yield component traits

The correlation of genotypes (Table 4) showed that seed yield per hectare had a highly significant ($p < 0.01$) and positive correlation with the number of flowers, number of effective capsules per plant, number of seeds per capsule, plant height, number of primary branches, harvest index, and biological yield. In addition, the significant correlations revealed that choices for such traits could be made to improve the development of high-yielding generic lines further. Therefore, by improving these traits, there is a possibility of enhancing the seed yield of black cumin, or selection of traits indirectly may be advisable. Haq *et al.* (2015) also reported a positive and significant genotypic correlation of seed yield of black cumin genotypes with thousand seed weight, number of capsules and number of seeds per capsule. Seid *et al.* (2013) in their study observed that seed yield was positively and significantly correlated with the number of primary branches per plant (0.48), the number of secondary branches per plant (0.5) and plant height (0.79).

Seed yield showed a negative, non-significant correlation with days to 90% maturity and seed weight, and a significant negative correlation with days to 50% flowering. As branches, plant height, flowers, capsules, seeds per capsule, biological yield, and harvest index increased, seed yield also increased, while days to maturity decreased. The delay in maturity is because flowers do not bloom and mature simultaneously. Early-flowering plants had more time for seed-bearing capsules to develop; however, longer germination times shortened the rainfall period for seed development, thereby reducing seed yield. This study is in agreement with the results of Sabaghnia (2025), who studied 27 different black cumin genotypes. The results showed that yield had a meaningfully positive association with most characters, except for leaf width, seed width, and thousand-seed weight. In addition, the analysis result coincides with Seid *et al.* (2013), who evaluated thirty-six local genotypes of Ethiopian caraway, and reported that seed yield was positive and highly significant with the number of primary branches per plant, number of secondary branches per plant, number of capsule per plant, number of seeds per capsule and plant height.

Haq *et al.* (2015) reported strong positive correlations between black cumin seed yield and various traits, including plant height, primary and secondary branches, seeds per capsule, capsules per plant, 1000-seed weight, and harvest index. Fufa (2016) found similar results in black cumin landraces, showing positive correlations between seed yield and plant height, capsules per plant, primary branches, and seeds per capsule, while seed yield was negatively correlated with days to flower and days to 90% maturity.

Genotypic correlation among other traits

Positive and significant correlations were observed between the days to 50% flowering and the days to 90% maturity at the genotypic level. This indicates that days to bloom are shorter, allowing for earlier maturation. Genotypes that flower earlier can mature on time without facing environmental challenges such as moisture stress, so these traits can be selected simultaneously. It had a negative and significant correlation with the number of primary branches per plant. Days to 50% flowering also had a negative and non-significant association with plant height, number of secondary branches per plant, number of flowers, number of capsules, number of tertiary branches per plant, number of seeds per capsule, thousand seed weight, biological yield, and harvest index at the genotypic level. The negative correlation between the number of days to 50% flower and the number of capsules per plant may be due to a higher number of flowers aborting in earlier plants than in late-flowering plants, resulting in a greater number of capsules bearing seeds. Likewise, Tewodros *et al.* (2018) reported a positive and significant association between days of 50% flowering with days of 90% maturity of black cumin genotypes. Fufa (2016) also reported a positive correlation between days to flowering and days to 90% maturity.

Days to 90% maturity showed negative, significant correlations with plant height, primary and tertiary branches, flowers, effective capsules, and biological yield, indicating maturity variation among branches.
Other traits, such as secondary branches, seeds per capsule, thousand-seed weight, and harvest index, had negative correlations at the genotypic level. Fufa (2016) also reported a negative correlation between primary branches and seeds per capsule with days to 90% maturity.

Plant height showed a positive and significant correlation with the number of primary, secondary and tertiary branches per plant, as well as the number of flowers, effective capsules, seeds per capsule, biological yield and seed yield at genotypic levels. This is because long height genotypes have a higher probability of producing more primary branches, which can bear capsules (flowers) and secondary and tertiary branches per plant, leading to an increment in biological yield and seed yield. So selecting this trait is important to improve the yield of black cumin genotypes. Positive and non-significant correlations were observed between plant height and harvest index. In contrast, negative and non-significant correlations were detected with seed weight.

In agreement with the present study, Zigyalew *et al.* (2020) noted that plant height was highly and significantly associated with the number of capsules per plant and seed yield ha^{-1}, but was negatively correlated with thousand seed weight. These findings are in agreement with (2014), who evaluated the character association of coriander genotypes and indicated that plant height showed positive and significant correlations with both the number of primary and secondary branches per plant.

Number of primary branches per plant had a positive and highly significant association with number of secondary branches per plant, number of tertiary branches per plant, number of flowers, number of capsules per plant and biological yield. This positive association of the number of primary branches per plant indicates that these traits improved simultaneously through selection. According to the results of studies by Preeti *et al.* (2019), there is a positive and significant association between the number of primary branches, the number of secondary branches, the number of capsules per plant, and the biological yield of black cumin genotypes. It had positive and non-significant associations with harvest index, thousand-seed weight, and number of seeds per capsule. Zigyalew *et al.* (2020) also reported that the number of primary branches per plant had a highly significant correlation with both the number of secondary branches per plant and the number of capsules per plant at the genotypic level. Fufa (2016) also reported that the number of primary branches per plant showed a highly significant and positive correlation with both the number of capsules per plant and the number of seeds per capsule, respectively. In addition, Yewubdinber (2020) reported that the number of primary branches per plant exhibited a positive and significant correlation with the number of capsule and plant height.

The number of secondary branches per plant showed a highly significant positive correlation with flowers, capsules, seeds per capsule, and biological yield. It was also positively correlated with tertiary branches and harvest index at the genotypic level. Thousand seed weight had a negative, non-significant correlation with secondary branches. This suggests that an increase in branches leads to a higher number of flowers, capsules, and a greater biological yield.

In addition, genotypes with more secondary branches tend to have more tertiary branches per plant, resulting in variation in immaturity among branches due to differences in maturity days between number of secondary and tertiary branches per plant. In line with this result, Zigyalew *et al*. (2020) pointed out that the number of secondary branches per plant had a highly significant correlation with the number of capsules per plant. These findings are consistent with those of Meena *et al.* (2014), who reported that the number of secondary branches was positively associated with the number of capsules per plant and the number of seeds per capsule. It showed a significant correlation with biological yield, a positive correlation with harvesting index, and a negative correlation with thousand-seed weight.

The number of tertiary branches per plant showed a highly significant positive correlation with flowers, effective capsules, seeds per capsule, biological yield, and harvest index at the genotypic level, indicating that more tertiary branches lead to higher seed yield and biological yield. Indirect selection for this trait is advisable. Thousand seed weight had a negative, non-significant correlation. Zigyalew *et al.* (2020) reported similar findings. The number of flowers was positively correlated with effective capsules, seeds per capsule, and biological yield, while harvest index had a positive, non-significant association and a negative, significant correlation with thousand seed weight.

The number of capsules had a positive and significant association with the number of seeds per capsule and biological yield at the genotypic level. Similar results were reported by Bardideh *et al*. (2013). This suggests that selecting for a greater number of capsules could enhance the biological yield of the plant, which may result in increased overall productivity. The harvest index had a positive and weak association with the number of capsules. As the quantity of capsules rises, there is a corresponding tendency for the harvest index also to increase. Nevertheless, characterizing this relationship as a weak association suggests that, although plants with a greater number of capsules generally exhibit a higher harvest index, the correlation is not particularly robust. This is in line with Zigyalew *et al.* (2020), who noted the harvest index exhibited a positive yet weak correlation with the number of capsules. However, seed weight showed a negative and non-significant correlation. This implies that larger seeds do not automatically result in increased overall yield or greater seed production efficiency.

Positive and highly significant correlations were detected for number of seeds per capsule with harvest index. It had a positive and significant association with biological yield at the genotypic level. Plants with more seeds per capsule are more efficient in converting biomass into seeds, which is beneficial for improving overall seed production. Selecting seeds per capsule could result in a higher harvest index, making the plant more efficient in seed yield production. Zigyalew *et al.* (2020) also reported similar results. Thousand seed weight showed negative and non-significant associations with the number of seeds per capsule, biological yield, and harvest index at the genotypic level. Our results suggest that heavier seeds may not necessarily lead to an increase in biomass or an improved harvest index, indicating that selecting heavier seeds does not ensure enhanced overall plant improvement in these traits. Biological yield showed a positive and non-significantly correlated relationship with harvest index. This non-noticeable association is due to inversely proportionality of biological yield and harvest index. In general, a positive and significant association between a pair of traits at both the genotypic and phenotypic levels justifies the possibility of correlated response to selection. However, negative correlation prohibits simultaneous improvement of those traits.

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