Genetic Variability, Heritability, and Genetic Advance ofGarlic (Allium sativum L.) GenotypesinBulb Yield Traitsat Kulumsa, Southeastern Ethiopia

Comment [ss1]: Italicize

Comment [ss2]: Among Bulb Yield and Related Traits

Abstract

One of the fundamental goals of plant breeding is to evaluate genetic diversity in crop species, which aids in the development of breeding approaches. Therefore, this field experiment was conducted to assess mean performance, the genetic variability in garlic genotypes on bulb yield and related traits. The field evaluation of thirteengarlic genotypes and one released variety Holetta local (HL) was conducted at Kulumsa Agricultural Research Centerusing a randomized complete block design with three replications during the main growing seasons of 2020 and2021. The analysis of variance indicated there were highly significant differences among the genotypes for all traits except clove diameter. Some of the genotypesG-043/19, G-005/19, G-045/19, G-009/19, G-134/19, G-010/19, and GOG-049/18 had mean performances higher than the standard check variety Holetta local (HL). Highest phenotypic (PCV) and genotypic (GCV) coefficients of variation recorded for total bulb yield tons per hectare and number of cloves per bulb, while the days to physiological maturity had the lowest heritability (h^2b) *in broad sense and genetic advance as a percent of mean (GAM) ranged between 37% (clove weight) to78% (plant height)and 1.84% (day to maturity) to 49.13% (total bulb yield per hectare) respectively. High phenotypic and genotypic coefficients of variation coupled with high heritability and genetic advance as percent of mean were observed for total bulb yield tons per hectare number of cloves per bulb and clove weight. Therefore, selection for these characters would be effective for selecting genotypes for future garlic breeding programs.*

Comment [ss3]: genotypes namely,

Key words: Bulb yield, Genetic variability, GCV, PCV, Mean performance

1. INTRODUCTION

Garlic (*Allium sativumL.*) is a bulbous perennial crop cultivated in different temperate and subtropical climates all over the world (Elsharkawy *et al.*, 2021). It belongs to the genus Allium, which includes almost 1008 species distributed in 15 subgenera and more than 70 sections (Friesen*etal.*, 2020,Parreno *etal.* 2023). After the onion it is the second most widely used cultivated bulb crops in the World (Benke *et al.*, 2021).It is widely grown in Ethiopia's central and highlands, both under irrigation and rain-fed conditions (Martha & Marie, 2019). But,the productivity is low primarily due to a lack of suitable plant material, cultivar with low yield potential, and their sensitivity to various environmental stresses (Dejen *et al.*, 2021; Tesfaye *et al.*, 2021). Garlic has a wide range of genetic diversity; depending on soil type, humidity, latitude, altitude, and cultural practices of its cultivation, even a single garlic accession would have a lot of phenotypic variabilities (Volk *et al.*, 2004; Tesfaye *et al.*, 2021). Natural variations in plant parts, for example, have economic significance and suggest the possibility of garlic

Comment [ss4]: italicize

Comment [ss5]: Check reference style of Journal and make changes throughout the manuscript (et al. or et al.,)

Comment [ss6]: Cite recent reference as Sharma et al. (2024):

Sharma A, Sharma S, Chaudhary DR, Rana SS, Sharma N, Ketan, Chauhan A, Choudhary A, Gola SK, Babanjeet, Sharma B, Sharma S, Ashish (2024)Herbicidal combinations for management of complex weed flora and economic analysis in garlic (*Allium sativum* L.). Theoretical Biology Forum 13(1): 30-39. DOI: 10.61739/TBF.2024.13.1.30

improvement (Hoogerheide*et al.*, 2017). In addition, a great number of cultivars have resulted through natural and human selection for adaptation in growing areas (Viana *et al*., 2015).

The degree of genetic variability in a population (Dejen *et al*.,2021), which is a universal feature of all species in nature (Hoogerheide*et al*., 2017), is a key factor in genetic improvement. When selecting genotypes/accessions for yield and related traits, the variability of the genotypes is the most essential component of breeding (Hoogerheide*et al*., 2017; Tesfaye, 2021). Due to garlic's mode of cultivation, which is usually by clonal propagation, which is an important breeding method and little work has been done on the association between different traits which are prerequisites for executive a selection programme (Singh *et al.* 2012). The basic pre-requisite for yield improvement is the presence of genetic variability in genetic stock and knowledge of inheritance and inter-relationship of the yield components, along with their relative influence on each other (Sharma and Saini, 2010). The degree of variability is a base for a successful breeding programme. Thus, the information on the native and magnitude of genetic variability present in the genetic stocks, heritability and genetic advance among various traits are of considerable use in selecting the suitable genotypes to include in future breeding programmes (khadi *et al.*2022) Information on the genetic variability, correlation and diversity between agronomic characters of different accessions with their yield are important for supporting breeding program of the plant (Hakim, 2008). In addition, knowledge of the nature of association of bulb yield with yield contributing characters is necessary for yield improvement through selection of better varieties (Haydar *et al*., 2007). An effective improvement programme in garlic, often based on clonal selection, depends on the availability of sufficient genetic variability in a collection (Gurpree*et al.*, 2013; Kumar *et al.*, 2017).

In Ethiopia, various diversity studies involving germplasm collection, characterization, and evaluation have resulted in the release of different improved varieties (EAA, 2021). However, the shortage of high yielding and stable varieties remains a major constraint for the low productivity and production of garlic in the country (Belay *et al.*, 2020). Production and productivity do not depend only on area and cultural practices but also on the genotypes of the crop and environmental conditions (Lawande*et al.*, 2009).Garlic yield is the integration of many variables that affect plant growth during the growing period. It is, therefore, necessary to study the genetic variability available in the Ethiopian accessions of garlic that new varieties with higher bulb yield and better bulb quality can be developed through selection from this rich

Comment [ss7]: Cite recent reference Sharma et al. (2024) as

Sharma S, Chaudhary DR, Sharma S, Harish B.M. (2024)Character Association and Path Analysis in Indian Garlic (*Allium sativum* L.) Accessions using Agro-Morphological Traits. Madras Agricultural Journal 111: 4-6. DOI: 10.29321/MAJ.10.00MA05

Comment [ss8]: In addition to Hakim, add recent reference of Sharma et al. (2023) as suggested:

Sharma S, Chaudhary DR, Sharma N (2023) Evaluating Indian Garlic Accessions using Multivariate Analysis Based on Agro-Morphological Traits. Frontiers in Crop Improvement 11(5): 2504-2509. Print ISSN: 2393-8234 On line ISSN: 2454-6011

Comment [ss9]: In addition to EAA, add recent reference: Sharma et al. (2024) as:

Sharma S, Chaudhary DR, Sharma N (2024) Characterization of Indian garlic accessions through IPGRI morphological descriptors. International Journal of Farm Sciences 14(1-2): 19-23.DOI: 10.5958/2250-0499.2024.00005.0

source.Therefore, this study was designed to evaluate the heritability, genetic advance and associations among characters of garlic genotypes and to estimate the contribution of each trait to yield improvement in garlic genotypes.

2. MATERIALS AND METHODS

Description of the Study Area

The field experiment was conducted at Kulumsa Agricultural Research Center, Southeastern Ethiopia during the rain growing season in 2019 and 2020. KARC is located between latitude and longitude of 8^{o}' to 8^{o} 2'N and 39^{o} 07' to 39^{o} 10' E coordinates.The altitude of KARC is 2200 meters above sea level and the annual minimum and maximum temperature of 10.5 and 22.8^{0}C respectively with annual rain fall 832 mm. The rainy season over the sites extends from May through October with soil type classified as clay loam soil with a pH of 6 (Abayneh *et al.*, 2003).

Experimental Materials and Design

A total of 14 garlic accessions/genotypes collected from different major garlic producing parts of the Region, Zone and District of Ethiopia, and maintained at Debre Zeit Agricultural Research Centre, including one released variety as standard check were used for the experiment (Table 1).Theexperiment was laid out as a Randomized Complete Block Design (RCBD) where each genotype was replicated three times. Healthy and normal cloves of each accessions were selected and planted on prepared plots of 2 m x 2.4m. Each plot consisted of four rows, with 20 plants per row, and a total of 80 plants per plot with pacing of 20 cm within a plant and 10 cm between plants. The recommended rate of 242 kg NPS ha^{-1} was applied at planting as source of phosphorous and 75 kg Nha^{-1}in the form of Urea in two splits, half rate after full emergence and half rate at the initiation of bulb. Field agronomic practices used were as recommended for the garlic crop (Getachew *et al.*, 2009)

Table 1: List of experimental materials included in the study

Accession code	Source	Accession code	Source
G-010/19	DzARC	GOG-015/18	DzARC
G-009/19	DzARC	GOG-025/18	DzARC
G-005/19	DzARC	GOG-049/18	DzARC

Comment [ss10]: Align left as per Journal's guidelines

Comment [ss11]: Go for the numbering of subheadings

Comment [ss12]: Use correct symbol for degree Celsius throughout the manuscript

Comment [ss13]: spacing

Comment [ss14]: spacing

Comment [ss15]: accession

Comment [ss16]: insert appropriate symbol (×) throughout the manuscript

Comment [ss17]: spacing

G-045/19	DzARC	GOG-056/18	DzARC
G-043/19	DzARC	GOG-060/18	DzARC
G-134/19	DzARC	GOG-070/18	DzARC
G-150/19	DzARC	HL	Released variety

*Sources******DzARC- DebreZeit Agricultural Research Center

Data Collection

Data collection included determination of days physiologicalto maturity, plant height, leaf length(cm), leaf width (cm), number of leaf per plant, number of clove per bulb, clove weight (g), clove height (cm), bulb polar diameter (cm), bulb diameter (equatorial)(cm), total bulb yield (tons per hectare). These were recorded from eight randomly sampled plants in the two central rows of each plot(Ipgri& Gr, 2001).

Comment [ss18]: bulb equatorial diameter

Comment [ss19]: Write it capital and properly

Comment [ss20]: Too lengthy, make it qualitative not quantitative

Statistical Analysis

Data collected for quantitative characters were subjected to analysis of variance (ANOVA) using Proc GLM procedures of SAS version 9.2 (SAS Institute Inc, 2008).The mean performance of genotypes at 5% and 1% level of significant mean squares was subjected to genetic analyses.

Phenotypic and Genotypic Variability

The variability present in the population was estimated by simple measures viz., range, mean, standard error, phenotypic and genotypic variances and coefficient of variations. The phenotypic and genotypic variances and coefficient of variations were estimated according to the following methods suggested by Burton and De vane (1953).

$$\delta_p^2 = \delta_g^2 + \delta_e^2 \quad \delta_g^2 = \delta_t^2 - \delta_e^2/r$$

Where δ_p^2 = Phenotypic variance, δ_g^2 = genotypic variance and δ_e^2 = environmental variance (error mean square); δ_t^2 = mean square of treatment and r = number of replications;

Genotypic coefficient of variation (GCV %) $= \frac{\sqrt{\sigma 2\ g}}{\bar{x}} *100$

Phenotypic coefficient of variation (PCV %) $= \frac{\sqrt{\sigma 2\ p}}{\bar{x}} *100$

Where, V_g = Genotypic variance, V_p = Phenotypic variance, $\bar{x}$ = Grand mean of the character. PCV and GCV were categorized as following: 0-10%: low, 10-20%: moderate, 20% and above high (Sivasubramanian and Menon, 1973).

Heritability in the Broad Sense:

Heritability on plot basis was calculated for each character based on the formula developed by Allard (1960) as:

$$H=\frac{\delta_g^2}{\delta_p^2} * 100$$

Estimated heritability values was classified according to (Singh, 2001) that heritability values greater than 80% were very high, values from 60–79% were moderately high, values from 40–59% were medium and values less than 40% were low.

Genetic advance:

The Genetic Advance (broad sense) expected under selection assuming the selection intensity of 5% was calculated by the formula suggested by Johnson *et al*. (1955) and Allard (1960):

Gs= (K) (δA) (H) Where, Gs = expected genetic advance, and K = the selection differential (K=2.06 at 5% selection intensity), δA= phenotypic standard deviation, H = heritability.

Genetic advance as percent of means (GAM):

Genetic advance as percent of mean was estimated (*IPGRIE*, 2001) as follows:

$GAM =\frac{GA}{\bar{x}} * 100$ Where, GA = Genetic advance, $\bar{x}$= Grand mean; Genetic advance as percent of mean was categorized as 0-10% = Low, 10-20% = Moderate, >20% = High

3. RESULTS AND DISCUSSION

3.1. Analysis of Variance

The combined analysis of variance (ANOVA) showed that there was a highly significant difference in garlic bulb yield in almost all traits. Thus, the mean squares from the analysis of variance for all traits of fourteen garlic accessions are presented in Table 2. There was a highly significant difference (P<0.01) among tested accessions for all traits: days to physiological maturity, plant height, number of leaves per plant, leaf width, leaf length, number of cloves per bulb, clove weight, clove height, bulb polar diameter, bulb diameter (equatorial), and total bulb

Comment [ss21]: genotypes, studied.

yield, except clove diameter, which had no significant effect. The highly significant differences indicate the existence of large genetic variability for the characters studied, which shows ample scope for the selection of promising genotypes from the present gene pool for increasing tuber yield. There were less coefficients of variation in most of the characters, indicating good precision in the experiment. These results indicate the presence of variability among the genotypes used for effective selection or vegetable improvement. In line with this study, Sandhu *et al.* (2015) reported that the analysis of variance showed a significant difference among all the genotypes for all the characters under study. In addition, Abebech*et al.* (2021) and (Dixit *et al.* 2021)found variability in garlic for tested characters, which supports the present result.

Table 2. Mean squares from analysis of variance for agronomic and yield traits of 14 potato genotypes tested fortwo years combined data at Kulumsa

Traits	**Mean square of**			**SME**	**CV (%)**
	Replication (DF=2)	**Genotypes (DF=13)**	**Error (DF=26)**		
Days to maturity	37.88	15.07**	4.37	1.21	4.74
Plant height (cm)	16.15	69.76**	6.12	1.43	5.61
Number of leaf	1.97	0.96**	0.23	0.27	1.08
Leaf width	0.04	0.18**	0.03	0.09	0.35
Leaf length (cm)	24.35	31.13**	5.71	1.38	5.42
Number of clove per bulb	5.21	47.66**	6.48	1.47	5.77
Clove weight (g)	0.51	0.73**	0.26	0.29	1.16
Clove height (cm)	0.08	0.11**	0.03	0.09	0.37
Clove diameter (cm)	0.04	0.08ns	0.12	0.20	0.79
Bulb Polar diameter (cm)	0.12	0.16**	0.04	0.11	0.45
Bulb equatorial diameter(cm)	0.53	0.25**	0.05	0.12	0.48

Comment [ss22]: No need to discuss non-significant results. So remove.

Comment [ss23]: Rewrite sentence

Comment [ss24]: In addition to Abebech, add most recent reference as Sharma et al. (2022)

Sharma S, Chaudhary DR, Himani (2022) Genetic variability studies in Indian garlic (*Allium sativum* L.) accessions using agro-morphological traits. Annals of Plant and Soil Research 24(2):267-271. DOI: https://doi.org/10.47815/apsr.2022.10159

Comment [ss25]: garlic?

Total bulb yield (t/ha)	9.06	15.39**	1.37	0.67	2.66

**, significant at $p<0.01$, ns= non-significant difference, CV (%) = coefficient of variation in percent, SME= Standard mean of error

3.2. Mean Performance of Genotypes

The pooled mean performance values for all traits showed a wide range of variation among the fourteen garlic genotypes. The analysis of variance revealed that there was a highly significant variation among the genotypes in terms of the number of days it took for physiological maturity; the values varied from 138 to 145 days (Table 3). Accession G-045/19 took the minimum mean (138) performances of days to maturity. The character's mean value was 137.67 days, but HL (standard check) achieved the highest mean (145) performances of days to maturity. Similar findings regarding variations in garlic maturity have been presented by Tsega *et al*. (2011), Yadav *et al*. (2012), Panse *et al.* (2013), and Bayisa (2021).The values for plant height varied significantly among the genotypes, ranging from 25.61 to 41.61 cm (Table 3). The genotype G-045/19 had the highest mean performance of plant height (80.80 cm), while GOG-056/18 had the lowest plant height (63.80 cm). For each genotype, the mean plant height was 35.41 cm. The inherent genetic differences between the various genotypes were the cause of the variation in plant height. Comparable outcomes were also attained by Abdlkafer-Halmy*et al*. (2011) and Islam *et al.*(2017).

Comment [ss26]: Somewhere you are using combined, somewhere pooled. Use a single term pooled because combine term can also be used for average.

Comment [ss27]: ranged. Follow throughout your manuscript

The genotype G-045/19 had the highest mean performance in terms of leaves per plant among all the others. The data analysis revealed that the average number of leaves per plant was 10.67, despite the fact that the minimum mean performance of the number of leaves per plant was recorded in GOG-070/18. Due to the different genetic components of each genotype, there was variation in the number of leaves per plant. The increased leaf count could be the result of physiological processes that have been triggered by stimulants that have an effect on the plant's growth and metabolism. The outcomes agree with the research conducted by Sandhu *et al.* (2015), Singh *et al.* (2015), and Bhat *et al.* (2017), which revealed there a significant variation in the mean performance of the number of leaves per plant was also reported in garlic.The genotypes varied significantly in terms of leaf width and length. It showed that the maximum (51.07 cm) and minimum (40.67 cm) mean performances of leaf length recorded in G-045/19

Comment [ss28]: add some recent references like Sharma et al. (2022-2024)

Comment [ss29]:

and GoG-056/18, respectively, varied from one another in terms of leaf length. There was an important difference in leaf width between the genotypes, ranging from 2.08 cm to 1.25 cm (Table 3). Ahmed *et al.*, (2018) and Abdlkafer-Halmy*et al.* (2011) also found similar results, demonstrating that there are notable differences in bulb and clove weight, number of cloves per bulb, and flower stack height within and between garlic families.

There were highly significant variations between the genotypes in terms of the number of cloves each bulb had. Per bulb, the range was 4.89 to 14.11 cloves (Table 3). It was found that the number of cloves per bulb had a maximum mean of 26.00 in G-150/19 and a minimum mean of 11.73 in GOG-049/18. The mean number of cloves per bulb was 17.69. The number of cloves per bulb varies significantly, according to reports of Tsega *et al.* (2011), Pervin *et al.* (2014), Singh *et al.* (2015), and Kumar *et al.* (2017).The results of the analysis of variance showed that there was a significant variation in clove weight and height among genotypes. The maximum clove height was found in G-010/19 (2.82 cm), while the minimum was found in HL (2.11 cm). The mean clove height varied from 3.13 (G-045/19) to 1.67 (GOG-056/18). Clove height had a mean value of 2.48 cm. These findings are closely in line with findings of Vatsyayan *et al.* (2013), Tadese (2015), Singh *et al.* (2015), and Kumar *et al.* (2017), who reported the mean clove length of 3.61, 2.80, and 2.45cm. The genotypes were not substantially different in clove diameter; the mean clove diameter was 1.13 cm (Table 3).

The polar and equatorial bulb diameters showed highly significant differences between the genotypes. Out of all the genotypes, genotype GOG-070/18 had the lowest mean bulb equatorial diameter (3.45cm), while genotype G-009/19 had the highest mean (4.25cm).The clove polar diameter varied from a minimum of 3.75 (GOG-056/18) to a maximum of 4.63 (G-009/19). The equatorial and polar bulb diameters had mean values of 3.86 cm and 4.26 cm, respectively. These results are consistent with the reported significant variation among the genotypes for this character in garlic by Tsega*et al.* (2011), Panse *et al.* (2013), Vatsyayan *et al.* (2013), and Ahmed *et al.* (2018). There was a high significant difference in bulb yield per hectare between the genotypes; G-043/19 had the highest bulb yield (11.36 t ha-1), while GOG-070 had the lowest (3.79 t ha^{-1}) with mean bulb yield of 7.97 t ha^{-1}. The character findings

Comment [ss30]: spacing

Comment [ss31]: spacing

Comment [ss32]: add recent references like Sharma et al. (2022-2024) published by Panse *et al*. (2013), Pervin *et al.* (2014), Khar *et al*. (2015) andBayisa (2021) are closely aligned with the results obtained.

Table 3. Combine mean performances of 14 garlic genotypes for bulb yield and other traits evaluatedat Kulumsa

Comment [ss33]: Pooled may be more appropriate?

Genotypes	DM	PH	NL	LW	LL	NCPB	CWT	CH	CD	BPD	BED	TY
G-010/19	141.67	67.40	10.67	2.08	48.00	18.40	2.60	2.82	1.03	4.05	4.51	9.89
G-009/19	140.33	72.40	11.27	2.06	48.53	17.93	2.40	2.64	1.09	4.25	4.63	10.09
G-005/19	141.33	70.07	11.27	1.92	47.73	23.47	2.13	2.52	1.00	3.86	4.58	10.75
G-045/19	138.00	80.80	11.33	1.91	51.07	13.93	3.13	2.71	1.08	4.03	4.35	10.45
G-043/19	139.00	78.60	10.67	1.78	49.73	17.27	2.20	2.63	1.13	4.18	4.53	11.36
G-134/19	142.00	76.00	10.53	1.49	46.60	17.40	1.73	2.53	0.98	3.99	4.48	8.03
G-150/19	142.67	66.87	10.93	1.58	45.07	26.00	1.73	2.38	1.02	3.78	4.14	6.96
GOG-015/18	144.00	69.80	9.87	1.55	42.00	17.93	1.80	2.36	1.07	3.77	4.19	7.71
GOG-025/18	142.67	69.07	10.80	1.48	45.67	13.87	2.73	2.38	0.92	3.51	3.84	5.99
GOG-049/18	142.67	70.60	10.47	1.67	44.47	11.73	3.07	2.63	1.19	3.90	4.45	8.23
GOG-056/18	145.00	63.80	10.47	1.25	40.67	16.33	1.67	2.42	1.4	3.71	3.75	4.87
GOG-060/18	140.67	67.67	10.20	1.50	43.00	17.47	2.13	2.32	0.86	3.68	4.11	5.16
GOG-070/18	138.33	66.20	9.47	1.49	41.63	13.67	1.93	2.32	0.85	3.45	3.87	3.79
HL	145.00	71.33	11.40	1.71	48.40	22.27	1.87	2.11	1.36	3.92	4.17	7.31
LSD(0.05)	3.758	4.146	0.995	0.257	4.067	4.307	0.839	0.287	0.577	0.351	0.447	2.341

DM is Days to maturity, PH is plant height (cm), NL is number of leaf plants, LW is leaf width(cm), LL is leaf length (cm), NCB is Number of clove per bulb, CWT is clove weight (g), CH is clove height (cm), CD clove diameter (cm),BPD is bulb polar diameter (cm), BED is bulb diameter (equatorial) (cm), TBY is total bulb yield (tons per hectare).

3.3. Genotypic Coefficient of Variation

The phenotypic and genotypic variances have been estimated to determine the extent to which genetic and environmental factors influenced the observed variations. There was a great deal of variation observed for every character that was being studied. Total variability, or phenotypic variability, is observable and is made up of environmental and genotype variation. The phenotypic and genotypic variances in the current study were high for bulb yield per hectare (30.85) and (27.13), and lowest for clove height (0.05) and (0.03) respectively (Table 4). The results revealed a wide range of variability among 14 garlic genotypes for quantitative traits. The phenotypic variance (δ^2p) of all traits was higher than the genotypic variance (δ^2g). The total bulb yields (t ha^{-1}) and the number of cloves per bulb had the highest genotypic and phenotypic coefficients of variation, respectively, whereas the days to physiological maturity had the lowest genotypic and phenotypic coefficients of variation (Table 4).

Comment [ss34]: No need to elaborate so remove the content.

For each traits, the phenotypic coefficient of variation was higher than the genotypic coefficient. The current study's findings showed that higher genotypic and phenotypic coefficients of variation were found for total bulb yield tons per hectare (27.13% and30.85%), the number of cloves per bulb (20.94% and 25.41%) respectively, and clove weight (29.06%) for PCV. High GCV and PCV estimates for garlic bulb weight and bulb yield were reported by Kassahun (2006). The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV), which is consistent with findings published by Awel*et al.* (2011). High estimates of genotypic and phenotypic coefficients of variation indicate that certain traits are highly likely to improve through selection, whereas other traits are difficult or nearly impossible to improve through selection.

Comment [ss35]: trait

Comment [ss36]: spacing

Comment [ss37]: add recent references like Sharma et al. 2022-24 which suits to your results

Leaf width had a moderate genotypic coefficient of variation (13.58%) and phenotypic coefficient of variation (16.39%), while the genotypic coefficient of variation for clove weight was 17.81%). This revealed the significant variability present, and genotype selection based on these traits would be useful for future advancements.On the other hand, days to physiological maturity (1.34% &1.98%), plant height (6.51%&7.39%), number of leaf (4.65% &6.46%), leaf length (6.34% &8.20%), clove height (6.64% &9.32%), bulb polar diameter (5.13% &5.19%), and bulb equatorial diameter (5.04% &7.98%)had the lowest GCV and PCV values respectively, (Table 4). Consequently, the larger proportion of phenotypic variance observed on these traits was contributed by the genotypic variance than the environmental variance, indicating that it can be used for breeding programs (Yebirzaf and Belete, 2017). The results of the phenotypic variance were, in general, higher than the genotypic variance for all characters studied, it implies that environmental factors, in addition to genetic variation, have a significant impact on how these traits appear.

Comment [ss38]: spacing b/w figures and &

3.4. Estimates of heritability and genetic advance

The proportion of genetic and environmental variation in the population can be determined using a broad-sense heritability estimate. The amount of genetic advance that can be expected as a result of phenotypic selection may be precisely estimated using genetic advance and a heritability estimate. Among the characters studied, high heritability estimates were found for bulb equatorial diameter (61%), number of cloves per bulb (68%), leaf length (60%), number width (69%), and plant height (78%). High heritability for the above characters clarified that they were least affected by environmental fluctuations, and selection based on phenotypic performance would be reliable for these traits. The results align with the observations made by Singh*et al*. (2012) and Tsega *et al.* (2010). The number of leaves (52%), the height (51%), the weight (37%), the number of days to physiological maturity (45%), and the bulb polar diameter (51%), showed moderate heritability. In general, heritability in the broadest sense suggests that, depending on the phenotypic expression, selection might be successful.

Comment [ss39]: No need to elaborate, just focus on results. So remove the same.

Comment [ss40]: Add recent references like Sharma et al. 2022-24 which suits the most for your results

The genetic advance varied from 1.84 to 49.13 as a percentage of the mean. The total bulb yield (49.13%), average clove weight (22.49%), number of cloves per bulb (35.55%), and leaf weight (23.18%) showed the highest genetic advance as a percentage of the mean, while plant height (11.81%) and leaf length (10.10%) showed the moderate. In comparison, traits like days to physiological maturity (1.84%), number of leaves per plant (6.89%), clove height (9.75%), bulb polar diameter (7.61%), and bulb equatorial diameter (9.88%) showed low genetic advance as percentages of the mean. For selecting the best individual, heritability estimates combined with genetic advancement are more helpful than the heritability value alone. For both the total bulb yield per hectare and the number of cloves per bulb, high heritability and high genetic advance were observed. The results of this study align with Haydar*et al.* (2007), Dhal and Brar (2013), Abebech (2013), Bhat *et al.* (2017), and Bayisa (2021) they reported high heritability and high genetic gain for number of leaves per plant, bulb yield per hectare and clove weight per bulb.

Comment [ss41]: Add recent references like Sharma et al. 2022-24 which suits the most for your results

Comment [ss42]: Spacing

Table4. Estimate of variability components for 14Garlic genotypes evaluated at Kulumsa

Traits	Range		Mean	δ^2g	δ^2p	δ^2e	PCV %	GCV %	H^2	GA	GAM
	Max	Min									

Comment [ss43]: USE SMALL h

DM	145.0	134.00	141.67	3.57	7.94	4.37	1.98	1.34	0.45	2.61	1.84
PH	83.20	62.60	70.76	21.21	7.39	6.12	7.39	6.51	0.78	8.36	11.81
NL	12.40	8.60	10.67	0.25	0.47	0.23	6.46	4.65	0.52	0.74	6.89
LW	2.20	1.20	1.68	0.05	0.08	0.02	16.39	13.58	0.69	0.39	23.18
LL	53.00	37.40	45.90	8.47	14.18	5.71	8.20	6.34	0.60	4.63	10.10
NCB	27.8	11.20	17.69	13.73	20.21	6.48	25.41	20.94	0.68	6.29	35.55
CW	4.2	1.40	2.23	0.16	0.42	0.26	29.06	17.81	0.37	0.50	22.49
CH	2.94	2.04	2.48	0.03	0.05	0.03	9.32	6.64	0.51	0.24	9.75
BPD	4.44	3.32	3.86	0.04	0.08	0.04	7.29	5.19	0.51	0.29	7.61
BD	5.02	3.64	4.26	0.07	0.12	0.05	7.98	6.19	0.61	0.42	9.88
TBY	12.76	3.79	7.97	27.13	30.85	1.37	30.85	27.13	0.77	3.92	49.13

Where: δ^2g =Genotypic variance, δ^2p =Phenotypic variance, PCV = phenotypic coefficient of variance, GCV = Genotypic coefficient of variation, H^2%= Heritability in broad sense, GA (5%) = genetic advance at 5% selection intensity, GAM (%) = genetic advance as percent mean, DM is Days to maturity, PH is plant height(cm), NL is number of leaf plants, LW is Leaf width, LL is leaf length(cm), NCB is Number of clove per bulb, CW is clove weight (g), CH is Clove height (cm), BPD is Bulb Polar diameter (cm), BD is bulb diameter (equatorial)(cm), TBY is total bulb yield (tons per hectare).

Comment [ss44]: Use small h

Comment [ss45]: Spacing

4. CONCLUSION AND RECOMMENDATION

Comment [ss46]: Remove as Conclusion is sufficient

The analysis of variance in the current experimental study showed that there were highly significant differences in each character's genotype. Total bulb yield showed highly significant variability among the genotypes, ranging from 4.78 to 12.72 t ha^{-1}, with a mean of 7.97 t ha^{-1}. In terms of total bulb yield, the genotypes G-043/19, G-005/19, G-045/19, G-009/19, G-134/19, G-010/19, and GOG-049/18 had mean performances higher than the mean of the standard check variety (HL), whereas the genotype GOG-070/18 produced lower yields. For every character under study, phenotypic coefficients of variation were generally greater than genotypic coefficients of variation, suggesting that environmental factors in addition to genetic factors influence how characters are expressed. The highest phenotypic coefficient of variation was found for cloves per bulb, clove weight, and bulb yield per hectare. Leaf weight was found to have a moderate PCV; on the other hand, days to maturity, plant height, number of leaves, leaf length, clove height, bulb polarity, and equatorial diameter were found to have low PCV. Both the total bulb yield per hectare and the number of cloves per bulb showed high GCV as a percentage of the mean, along with high heritability and high genetic advance. Additive genes control these characteristics, and improving them will be helpful for selection. This study suggests that selection would be beneficial in bringing out the greatest attributes in garlic due to its high PCV, GCV, heritability, and genetic gain. Since these traits additionally showed sufficient genetic variability, emphasis should be given to them when choosing genotypes during the yield improvement program as good selection criteria to improve bulb yield in garlic through breeding or selection.

Comment [ss47]: Make it more precise within 6-8 lines

REFERENCES

Comment [ss48]: Add newly cited references of Sharma et al. (5 in no. from 2022-2024) following strict guidelines of Journal

Abdlkader-Halmy, E.M.S., S.A. Abdal-Aziz, H.S. Abdel-Razzak, M.A. Wahab.allah and Al.garban. 2011. Evaluation of some agronomic traits and genetic relationships among developed garlic clones by RAPD markers and protein analysis. American-Eurasian.

Abebech T., 2013. Genetic variability and character association among bulb yield and yield related traits in garlic (Allium sativum L.) M. Sc. Thesis. Haramaya, Ethiopia

Allard, R.W. 1960. Principles of Plant Breeding. John Willey and Sons, Inc, New York, 227- 228.

Awale, D., Getachew, T. and Sentayew, A. 2011. Genetic variability and Association of Bulb Yield and Related Traits in Shallot (Allium cepa Var.Aggregatum Don.) In Ethiopia Int.J.Agric.Res, 6 (7):517-536.

Bayisa, K. 2021. Genetic Variability and Associations among Bulb Yield and Yield Related Traits of Garlic (Allium sativum L.) Genotypes at Bishoftu Agricultural Research Center, Ethiopia. M.Sc. Thesis, School of Graduate Studies of Haremaya University.

Belay F, Tekle G and Chernet S (2020) Evaluation of genotype × environment interaction effect on performance of garlic (Allium sativum L.) genotypes in Tigray region, Northern Ethiopia using AMMI and GGE biplot analysis. African Journal of Agricultural Research 16, 691–701

Benke, A.P.; Krishna, R.; Mahajan, V.; Ansari, W.A.; Gupta, A.J.; Khar, A.; Shelke, P.; Thangasamy, A.; Shabeer, T.P.A.; Singh, M.; et al. Genetic Diversity of Indian Garlic Core Germplasm Using Agro-Biochemical Traits and SRAP Markers. Saudi J. Biol. Sci. 2021, 28, 4833–4844.[CrossRef]

Bhatt, B, Soni, AK, Jangid, K and Kumar, S. A study on genetic variability, character association and path coefficient analysis in promising indigenous genotypes of garlic (Allium sativum L.). International Journal of Pure and Applied Bioscience. 2017; 5(1):679- 687.

Dejen, B., Mohammed, H., & Belay, B. (2021). Genetic divergence and cluster analysis for yield and yield contributing traits in lowland rice (*Oryza sativa* L.) genotypes at Fogera, Northwestern

Ethiopia. *International Journal of Advanced Research in Biological Sciences*, **8**(5), 1–11.**Google Scholar**

Dhal, R. K. and Brar, P. S. 2013. Genetic variability, correlation and path coefficient studies in garlic (Allium sativum L.). Vegetable Science, 40:102-104.

Dixit s, Dubey AK, Shukla IN, Singh l, Lal B. Genetic Variability, Heritability and Genetic Advance for Bulb Yield and Yield Developmental Traits in Garlic (Allium sativum L.). J Phytopharmacol 2021; 10(5):282-362. doi: 10.31254/phyto.2021.10514

EAA- Ethiopian Agriculture Authority (2021) Plant variety release, protection and seed quality control directorate report, crop variety register, Addis Ababa, Ethiopia.

Elsharkawy, G.A.; Hegazi, H.H.; Azab, E.; Gobouri, A.A.; Sayed, S.A. Assessment of Genetic Diversity among Egyptian Garlic Landraces Based on Morphological Characteristics and ISSR Markers. Eur. J. Hortic. Sci. 2021, 86, 579–589. [CrossRef]

Friesen, N.; Smirnov, S.V.; Shmakov, A.I.; Herden, T.; Oyuntsetseg, B.; Hurka, H. Allium Species of Section Rhizomatosa, Early Members of the Central Asian Steppe Vegetation. Flora Morphol. Distrib. Funct. Ecol. Plants 2020, 263, 151536. [CrossRef]

Getachew, T., Eshetu, D., & Tebikew, D. (2009). Guidelines for shallot and garlic production. Debre-Zeit Agricultural Research Center.**Google Scholar**

Gurpree SB, Hitesh K, Vikas G and Parmjit SB (2013) GGE biplot analysis for characterization of garlic (Allium sativum L.) germplasm based on agromorphological traits. International Journal of Plant Breeding 7, 106–110.

Hakim, L. 2008.Variability and correlation of agronomic characters of mung bean germplasm and their utilization for variety improvement. Indonesian Journal of Agricultural Science, 9 (1), 24-28

Haydar, N., Sharker, M.B., Ahmed, M.M., Hannan., M.A., Razvy, M., Hossain, A., Hoque and Karim, R. 2007. Genetic Variability and Interrelationship in Onion (Allium cepa L.). East Journal of Scientific Research, 2 (3-4): 132-134. Bangladesh.

Haydar, N., Sharker, M.B., Ahmed, M.M., Hannan., M.A., Razvy, M., Hossain, A., Hoque and Karim, R. 2007. Genetic Variability and Interrelationship in Onion (Allium cepa L.). East Journal of Scientific Research, 2 (3-4): 132-134. Bangladesh.

Hoogerheide, E. S. S., Azevedo Filho, J. A., Vencovsky, R., Zucchi, M. I., Zago, B. W., & Pinheiro, B. J. (2017). Genetic variability of garlic accessions as revealed by agro-morphological traits evaluated under different environments. *EmbrapaAgrossilvipastoril-Artigoemperiódicoindexado (ALICE)*, **16**(2), 1–10.**Google Scholar**

Ipgri, E. C. P., & Gr, A. (2001). *Descriptors for Allium (Allium spp.)*. International Plant Genetic Resources Institute.**Google Scholar**

Islam, M. A., Naher, M. S., Fahim, A. H. F., & Kakon, A. (2017). Study of the genetic diversity of garlic. *Journal of Scientific Achievements*, **2**(6), 6–8.**Google Scholar**

Johanson. H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. Agronomy Journal, 47:314-318

Kassahun, T. 2006. Variability and association among bulb yield and related traits in garlic (Allium sativum L.). M.Sc. Thesis, School of Graduate Studies of Alemaya University.

Khar, S, Kumar, S, Samnotra, RK, Kumar, M, Chopra, S, Kumar, M. and Gupta, S. Variability and correlation studies in garlic (Allium sativum L.) germplasm collected from different parts of Jammu. Indian Journal of Plant Genetic Resources. 2015; 28(2):229-236. 13.

Kumar, K., Ram, C.N., Yadav, G.C., Gautum, D.P, Kumar, P. and Kumar, R. 2017. Studies on variability, heritability and genetic advance analysis for yield and yield attributes of garlic (Allium sativum L.) International Journal of Current Research in Bioscience and Plant Biology, 4:123-129.

Kumar, K., Ram, C.N., Yadav, G.C., Gautum, D.P, Kumar, P. and Kumar, R. 2017. Studies on variability, heritability and genetic advance analysis for yield and yield attributes of garlic (Allium sativum L.) International Journal of Current Research in Bioscience and Plant Biology, 4:123-129.

Lawande, K.E., A., Khar Mahajan, P.S., Srinivas, V., Sankar and R.P., Singh. 2009. Onion and garlic research in India. J. Hortl. Sci., Vol. 4 (2): 91-119, 2009.

Panse, R., Jain, P.K., Gupta, A. and Singh S.D. 2013. Morphological variability and character association in diverse collections of garlic germplasm. African Journal of Agricultural Research, 8:2861-2869.

Parreño, R.; Rodríguez-Alcocer, E.; Martínez-Guardiola, C.; Carrasco, L.; Castillo, P.; Arbona, V.; Jover-Gil, S.; Candela, H. Turning Garlic into a Modern Crop: State of the Art and Perspectives. Plants 2023, 12, 1212. [CrossRef]

Pervin, M., Hassan, M.K., Hassan. K. and Hoque, A.K.M.A. 2014. Genetic variation of indigenous, improved and exotic Allium sativum L. Germplasm. Advances in Plants and Agricultural Research, 1:00011.

Sandhu, S., Brar, P.S. and Dhal, R.K. 2015. Variability of agronomic and quality characteristics of garlic (Allium sativum L.) ecotypes. SABRAO Journal of Plant Breeding and Genetics, 47:13-142.

SAS-Statistical Analysis System (2008) Institute Inc. SAS/STAT ®9.2 User″s Guide. Cary, NC: SAS Institute Inc.

Singh, K., Dubey, K. &Gupt, R. 2012. Studies on variability and genetic divergence in elite lines of garlic (Allium sativum L.). Journal of Spices and Aromatic Crops, 21:2, Pp.137- 144.

Sivasubramania, S. and Menon, M. 1973. Heterosis and inbreeding depression in the rice. Madras Agric. J., 60: 11-39.

Tesfaye, A. (2021). Genetic variability, heritability, and genetic advance estimates in garlic (*Allium sativum*) from the Gamo Highlands of Southern Ethiopia. *International Journal of Agronomy*, **2021**, 3171642. https://doi.org/10.1155/2021/3171642View**Web of Science®Google Scholar**

Tesfaye, A., Mijena, D. F., Zeleke, H., & Tabor, G. (2021). Genetic variability and character association for bulb yield and yield-related traits in garlic in Ethiopia. *African Crop Science Journal*, **29**(2), 293–308. https://doi.org/10.4314/acsj.v29i2.8View**Google Scholar**

Tsega Kassahun, Tiwari, Akhilesh and Woldetsadik Kebede Genetic variability among bulb yield and yield related traits in Ethiopian garlic (Allium sativum L.) germplasm. Pantnagar Journal of Research. 2011; 9(1):61-66

Tsega, K., Tiwari, A., Kebede, W. 2010. Genetic variability, correlation and path coefficients among bulb yield and yield traits in Ethiopian garlic germplasm. Indian J. Hort., 67(4):489-499.

Viana, J. P. G., Pires, C. D. E. J., Pinheiro, J. B., Valente, S. E. D. S., Lopes, Â. C. D. E. A., & Gomes, R. L. F. (2015). Divergênciagenéticaemgermoplasma de alho. *Ciência Rural*, **46**, 203–209. https://doi.org/10.1590/0103-8478cr20130988View**Web of Science®Google Scholar**

Volk, G. M., Henk, A. D., & Richards, C. M. (2004). Genetic diversity among US garlic clones as detected using AFLP methods. *Journal of the American Society for Horticultural Science*, **129**(4), 559–569. https://doi.org/10.21273/JASHS.129.4.0559View**CASWeb of Science®Google Scholar**