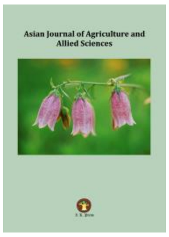

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Estimation of Variability Components among Garlic (*Allium sativum* L.) Germplasm at Kulumsa South Eastern Part of Ethiopia

Dasta Tsagaye [a*], Nimona Fufa [a] and Demis Fikre [a]

[a] *Kulumsa Agricultural Research Center, Vegetable Research Program, P.O. Box 489, Assella, Ethiopia.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Garlic (*Allium sativum* L.) is the most widely cultivated bulb crop after onion had major place in spices and medicinal use and grown in diverse areas, grown in sunny and dry areas in a moderately humid and dry environment. In Ethiopia, garlic is the most extensively farmed crop, and it is an essential cash crop for small land holder farmers since its unit price is substantially greater than most other vegetables produced. However, environmental factors affect the genetic potential and the quality of garlic crops. Thus, the aim current study was to estimate components of variation among one hundred twenty (120) garlic genotypes/accessions. The experiment was executed by alpha lattice design with two replications at Kulumsa Agricultural Research Center is found in Arsi, Zone Oromia Regional State, Ethiopia, is located 175km South East of Addis Ababa on the road

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*Corresponding author: E-mail: 6dasta2@gmail.com;

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from Adama to Asella. The result of study revealed that there was a significant genetic variation among garlic materials. During 2020 cropping season the highest genotypic coefficient of variation and phenotypic coefficients of variation 37.48% and 47.70% were observed respectively for weight of cloves and total yield tha^{-1}and moderately high heritability along with high genetic advance as percent of the mean were exhibited by shaft/pseodostem length. During 2021 cropping season the highest genotypic coefficient of variation and phenotypic coefficients of variation 29.10% and 41.73% were observed respectively for weight clove and total yield tha^{-1} and moderately high heritability along with high genetic advance as percent of the mean were exhibited by shaft length. Generally, the present study indicated that the presence of the genetic variability between germplasms to exploit the genetic improvement of the garlic crop through hybridization and simple selection methods.

Keywords: Genetic variation; genetic advance; heritability; phenotypic variation.

1. INTRODUCTION

"Garlic (*Allium sativum* L.) is the most widely cultivated bulb crop after onion had major place in spices and medicinal use which belongs to the family Amaryllidaceae (*Alliaceae*). Kazakhstan (Central Asia) is assumed as primary center of origin and Mediterranean and Caucasus zones are considered as secondary center of origin" [1]. The important countries that produce garlic are Spain, Egypt, France, Mexico, Brazil, India, China, Pakistan, Turkey and Sri Lanka.

"The word garlic comes from old English vernacular name garleac, which means spear leek. The gar means spear referring to spear shaped leaves and leac means leek" [2].

"Garlic (*Allium sativum* L.) botanically belongs to the Liliaceae family and Allium genus" [3]. "Bulb of the garlic contains several cloves, which are used for vegetative reproduction" [4]. "Garlic can be used as an antioxidant, antimicrobial, and reduction of cardiovascular diseases, anti-cancer and ant hypersensitive agent" [5,6]. "Garlic is grown in diverse areas, grown in sunny and dry areas in a moderately humid and dry environment" [7,8].

Ethiopia's garlic production and productivity in 2020 and 2021 were 18,344.46 and 15,979.54 hectares respectively, with 1,525,946.34 and 1,149,446.97 quintals harvested. In Ethiopia, garlic breeding improvement is weak due to the nature of the crop propagation method. Garlic can only be propagated via clonal methods since it is difficult to create new genetic variations. Ethiopia's garlic breeding program aims to release high-yielding varieties through clonal selection by utilizing collected garlic germplasm based on yield-wise characterizations to address production issues [9]. The Ethiopian Institute of Agricultural Research introduced new cultivars like Holeta, Chefe, Kuriftu, Bishoftu Netch, and Tseday for Ethiopian growing environments, but their performance is lower than local planting material. Further information is mandatory for garlic yield enhancement on genetic variability among garlic genotypes/accessions for varietal development.

"Study of genetic variability paves the way for any crop improvement programme" [10] and "also the detailed information related to genetic variability, genotypic and phenotypic coefficient of variation and heritability have better importance in the crop improvement programme of garlic" [11]. "The existing variability study can be a useful tool for increasing yield of the existing cultivar" [12]. The present investigation was carried out to estimate the extent variability (genotypic and phenotypic variation, heritability, and genetic advance along with the genetic gain) of growth and yield and traits among the one hundred twenty germplasm of garlic at Kulumsa to enhance its production and productivity.

2. METHODS AND MATERIALS

2.1 Description of the Study Area

"The experiment was conducted at Kulumsa Agricultural Research Center. Kulumsa Agricultural Research Center is found in Arsi, Zone Oromia Regional State, Ethiopia, is located 175km South East of Addis Ababa on the road from Adama to Asella. The geographical location of Kulumsa is 80 01' 10''N latitude and 390 09'13''E longitude and at an altitude of 2200 meter above sea level (m.a.s.l). The agro-ecology of the area is characterized by an average annual rain-fall of 850 mm, with short rain between March and April and long rain between June and September, and with annual mean minimum and maximum temperatures of 23.1^{o} C and 7.9 ^{o} C respectively. The soil types of the area are clay and silt loam with pH of 5.6" [13].

2.2 Planting Materials

One hundred twenty-eight garlic accessions (one hundred accessions were collected from the Bale, West Arsi and Arsi areas and 4 released varieties from the Kulumsa Agricultural Research Center).

2.3 Experimental Design and Field Management

The garlic accessions and released varieties were planted in an Alpha Lattice Design with two replicates in the 2020 and 2021 cropping season at Kulumsa highlands of Southern Eastern part of Ethiopia. The spacing between double rows, rows and plants was 60 cm, 40 cm and 20 cm. respectively. All agricultural management practices were carried out at the same time to all treatments such as weeding, watering, and hoeing. Fertilizers were also applied at the rate of 243 kg/ha NPS during planting and 130 kg/ha urea in split application once during planting and the second application was done after 45 days.

2.4 Data Collection

"Morphological traits were measured at deferent growth stages according to descriptors for garlic developed by the International Plant Genetic Resources Institute" [14]. The following data were recorded based on plant and plot basis: -Vigor, plant height (cm), neck thickness (cm), shaft length/pseodostem (cm), leaf width (cm), leaf length (cm), cloves number per bulb (no.), weight of cloves (g), clove height (cm), clove diameter (cm) and total yield (tha^{-1}). The bulb yield was recorded from the middle 4 rows of each plot and converted to tons per hectare.

2.5 Data Analysis

The variability function of the package in R software [15] was utilized to apply the data collected for each trait for variability estimation, using the methodology outlined in Gomez and Gomez [16]. The assumptions of ANOVA for each data point were made before the analysis, and pooled data analysis over years was carried out for all traits.

2.6 Estimation of Genetic Parameters

2.6.1 Variance components

Phenotypic and genotypic variances were estimated according to the method suggested by Singh and Chaudhary [17] as follows:

Environmental variance (σ^2e), σ^2e=MSe (error mean square)

Genotypic Variance (σ^2g) $\sigma^2g=\frac{\mathrm{MSg-MSe}}{\mathrm{r}}$

Where, r = number of replications, MSg = mean square due to genotypes,

MSe= mean square of error (Environmental variance) and l = location.

2.6.1.1 Heritability in broad sense

Broad sense heritability (H^2) values for all parameters were estimated based on the formula given by Falconer and Mackay [18] as follows:

$$H2 = \frac{\sigma^2\mathrm{g}}{\sigma^2\mathrm{p}} * 100$$

Where, H^2 = heritability in the broad sense, σ^2g = genotypic variance and σ^2p = phenotypic variance. Estimated heritability values was classified according to Singh [19] 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.

2.6.1.2 Genetic advance

The genetic advance expected under selection assuming selection intensity of the superior 5% of the plants was estimated in accordance with the methods illustrated by Allard [20]:

$$GA = K*(\sqrt{\sigma^2_p})*H^2$$

Where, GA = expected genetic advance, K = the standardized selection differential at 5% selection intensity (K=2.063), σ^2 p = is phenotypic standard deviation on mean basis and H^2 = heritability in the broad sense.

2.6.1.3 Genetic advance as percent of means (GAM)

Genetic advance as percentage over mean was worked as suggested by Johnson et al. [21]

GAM = $\frac{\mathrm{GA}}{\bar{x}} * 100$

Where,

GA = Genetic advance
$\bar{x}$ =Grand mean

Genetic advance as percent of mean was categorized as per the classified suggested by Johnson et al. [21]. 0-10% = Low, 10-20% = Moderate, >20% = High

2.6.1.4 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to Burton and Devane [22] based on the estimate of genotypic and phenotypic variance.

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

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

Environmental coefficient of variation (ECV %) = $\frac{\sqrt{\sigma 2 \ \mathrm{e}}}{\bar{x}}$ *100

Where, V_g = Genotypic variance, V_p = Phenotypic variance, Ve = Environmental 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 [23].

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

The analysis of variance for all studied characters, except number leaf's per plant which is non-significant (*p>0.01*), showed highly significant (p<0.01) differences among the garlic genotypes/accessions. This indicates to the existence of large variability among genotypes/accessions. Dixit [24] reported that the mean sum of squares due to genotypes were highly significant for all characters under study which indicated that the genotypes included in the study were a genetically diverse and a considerable amount of variability was present in the experimental material. The present study was in line with [25-27].

3.2 Estimation of Genetic Parameters

The present study indicated that, during 2020 cropping season the highest genotypic coefficient of variation (GCV) and phenotypic coefficients of variation (PCV) 37.48% and 47.70% were observed respectively for weight of cloves (g) and total yield tha^{-1}. The magnitudes of phenotypic and genotypic coefficient of variation were lowest for leaf length 6.99% and plant height 6.02% respectively. The PCV value of total yield tha^{-1} was higher than GCV value during 2020 cropping season. The present result revealed that, higher GCV were recorded for total yield t/ha (36.02), clove weight (37.48%), number of cloves per bulb (no.) (20.14%). Moderate GCV value were recorded for vigor of plant (14.97%), neck thickness (12.76%), shaft length (12.85%), leaf width (11.77%) and clove weight (10.26%). However, plant height (6.02%) and clove diameter (8.63%) had the lowest values. High PCV values were observed in total yield (47.70%), clove weight (40.65%), clove diameter (29.97%), neck thickness (23.99%), number of clove per bulb (21.81%) and vigor (20.87%). However, shaft length/pseudo-stem length (11.94%), leaf width (11.77%) and clove height (16.02%) had moderate values, whereas plant height (7.29%) and leaf length (6.99%) had low values (Table 1).

During 2021 cropping season the highest genotypic coefficient of variation (GCV) and phenotypic coefficients of variation (PCV) 29.10% and 41.73% were observed respectively for weight clove and total yield(t/ha). The magnitudes of phenotypic and genotypic coefficient of variation were lowest for leaf length 4.10 % during 2021 cropping season. The present result revealed that, during 2021, higher GCV were recorded for total yield t/ha (27.84), clove weight (29.10%) and neck thickness (23.99%). Moderate GCV value were recorded for number of cloves per bulb (15.94%) and cove height (10.26%). However, plant height (4.15%), leaf length (4.10%), and leaf width (7.05), vigor (7.45%) and clove diameter (8.63%) had the lowest values (Table 2).

During 2021 higher PCV were recorded for total yield t/ha (41.73%), clove weight (38.78%), cloves diameter (28.97%) and number of cloves per bulb (22.73%). Moderate PCV value were recorded shaft length (14.18%), leaf width (15.57%), neck thickness (12.75) and cove height (16.02%). However, plant height (7.36%) and leaf length (4.10%) had the lowest values

(Table 2). Azene (2021) reported that, the highest genotypic variance and phenotypic variance were for days to maturity, bulb weight, and bulb diameter (equatorial). Dixit et.al. [24] reported that “the phenotypic and genotypic coefficients of variation were higher for average weight of cloves bulb-1 (30.47 and 28.59, respectively), average weight of bulb (30.00 and 28.47) and plant height (20.49 and 20.07)”. Azene (2021) indicated that, all traits examined had a higher PCV than the GCV, suggesting an important role of the environment in the expression of traits. Among all traits examined, high-to-moderate PCV and GCV were observed for yield per plant (53.38%) and (46.8%), bulb diameter (equatorial) (46, 0%) and (45.7%), number of leaves (44.21%) and (42.8%), and bulb weight (42.75%) and (42.6%), respectively. The extent of phenotypic variation was highest because it is a product of environmental and genetic variance. The difference between PCV and GCV values were high for all traits indicating the presence of high environment was high effects on these traits. “The high-to-moderate values of PCV and GCV observed for the above traits in the present study indicated the existence of variability for the traits examined; and the high PCV and GCV traits mentioned above should allow reasonable scope for improvement by selection in the respective environments due to the modest genetic variability available in the germplasm collections evaluated” [27-29].

3.3 Estimation of Heritability and Genetic Advance as Percent of Mean

Important selection criteria, such as heritability and genetic advancement, are shown in Table 1 and 2. When anticipating the gain under selection, heritability estimates combined with genetic advancement are typically more useful than heritability estimates alone. Plant breeders frequently use heritability to measure the accuracy of a single field experiment or of a set of field trials. It is defined as the percentage of individual phenotypic variance in a population that may be attributed to heritable genetic factors. In the present investigation during 2020 cropping season, estimates of broad sense heritability (H^2) ranged from 0.08% to 94% for clove diameter and leaf width respectively. High heritability recorded for leaf width (0.94%), leaf length (0.80%), number of cloves per bulb (0.85%) and clove weight (0.85%), whereas plant height (0.68 %) and shaft length (0.74%) were moderately high; it was only vigor (0.51%), clove height (0.41%) and total yield (0.57%) had medium heritability. From the result of 2020 cropping season genetic advance as percent of mean (GAM) ranged from 5.12 to71.18 for clove diameter and weight cove respectively. High genetic advance as percent of mean (GAM) recorded for vigor (22.12), shaft length (22.77), leaf width (22.92), number of clove per bulb (38.3), weight of clove (71.18) and total yield (56.03), whereas plant height (10.23%), neck thickness (13.97), leaf length(11.56) and clove height (13.55) were moderately high; it was only clove diameter (5.12) had medium heritability. During 2020 cropping season, moderately high heritability along with high genetic advance as percent of the mean were exhibited by shaft/pseudo-stem length (Table 1) more or less similar results [30-32].

In the present investigation during 2021 cropping season, estimates of broad sense heritability (H^2) ranged from 0.08% to 0.56% for clove diameter and clove height respectively. Medium heritability recorded for number of cloves per bulb (0.0.47%), clove weight (0.56%), total yield (0.44%) and clove height (0.41%), whereas vigor (0.14%), plant height (0.32%), neck thickness (0.28%), shaft length (0.20%), leaf width (0.20%), leaf length (0.27%) and clove diameter (0.08%) were low. From the result of 2021 cropping season genetic advance as percent of mean (GAM) ranged from 4.34 to 44.90 for leaf length and weight cove respectively. High genetic advance as percent of mean (GAM) recorded for total yield (38.27), weight of clove (44.90) and number of clove per bulb (21.89), whereas plant height (4.82%), shaft length (5.91), and leaf length (4.34), clove diameter (5.12 and leaf width (6.58) were low high (Table 2). The results align with the observations made by Singh et al. [33,34].

During 2021 cropping season, moderately high heritability along with high genetic advance as percent of the mean were exhibited by shaft length. The traits having very high heritability indicated the relatively by small contribution of the environmental factors to the phenotype and then substantial improvement can be made using standard selection procedures. Johnson [21] reported that heritability estimates along with genetic advance would be more rewarding than heritability alone in predicting the consequential effect of selection to choose the best individual. Heritability in conjunction with genetic advance (GA) was found to be more effective and reliable in predicting the result and effect of selection. Heritability and genetic advance when estimated

Table 1. Estimate of variability components for garlic germplasm evaluated at Kulumsa during 2020 cropping season

Traits	**Range**		**Variance components**			**Coefficient of variation**					
	Max	**Min**	$\sigma^2 g$	$\sigma^2 p$	σ_e^2	**ECV (%)**	**PCV (%)**	**GCV (%)**	**H2 (%)**	**GA**	**GAM (%)**
Vigor	4.50	2.00	0.20	0.40	0.19	14.55	20.87	14.97	0.51	0.67	22.12
Plant height(cm)	82.00	57.00	17.01	24.99	7.98	4.12	7.29	6.02	0.68	7.01	10.23
Neck thickness (cm)	2.36	0.56	0.02	0.05	0.39	20.32	23.99	12.76	0.29	0.14	13.97
Shaft length/ Pseudostem (cm)	36.60	13.80	10.43	14.09	3.66	7.62	14.94	12.85	0.74	5.72	22.77
Leaf width(cm)	2.20	1.14	0.04	0.04	0.00	2.75	11.77	11.44	0.94	0.38	22.92
Leaf Length(cm)	60.60	35.00	7.95	9.90	1.96	3.12	6.99	6.26	0.80	5.20	11.56
Number of cloves per bulb (No.)	30.00	6.40	15.18	17.81	2.62	8.37	21.81	20.14	0.85	7.41	38.30
Weight of cloves (g)	98.58	10.22	81.44	95.82	14.37	15.74	40.65	37.48	0.85	17.14	71.18
Clove height (cm)	3.46	0.50	0.06	0.16	0.09	12.31	16.02	10.26	0.41	0.33	13.55
Cloves diameter(cm)	3.56	0.62	0.01	0.12	0.12	28.71	29.97	8.63	0.08	0.06	5.12
Total yield wt(t)/ha	22.05	0.52	6.28	11.02	4.74	31.27	47.70	36.02	0.57	3.89	56.03

Table 2. Estimate of variability components for garlic germplasm evaluated at Kulumsa during 2021 cropping season

Traits	**Range**		**Variance components**			**Coefficient of variation**					
	Max	**Min**	$\sigma^2 g$	$\sigma^2 p$	σ_e^2	**ECV (%)**	**PCV (%)**	**GCV (%)**	**H2 (%)**	**GA**	**GAM (%)**
Vigor	4.00	2.00	0.04	0.28	0.24	18.27	19.42	7.45	0.14	0.15	5.80
Plant height(cm)	83.75	53.00	8.31	26.12	17.80	6.08	7.36	4.15	0.32	3.35	4.82
Neck thickness (cm)	2.41	0.53	0.04	0.05	0.02	20.32	12.75	23.98	0.28	0.14	13.97
Shaft length/ Pseudostem (cm)	37.35	18.15	2.72	13.52	10.79	13.52	14.18	6.37	0.20	1.53	5.91
Leaf width(cm)	4.26	1.16	0.01	0.68	0.05	13.88	15.57	7.05	0.20	0.11	6.58
Leaf Length(cm)	61.20	27.20	3.60	13.26	9.68	6.66	4.10	4.10	0.27	2.03	4.34
Number of cloves per bulb (No.)	33.15	5.65	9.22	19.72	10.50	16.58	22.73	15.94	0.47	4.28	21.89
Weight of cloves (g)	51.12	4.63	47.45	84.42	36.97	25.66	38.78	29.10	0.56	10.64	44.90
Clove height (cm)	3.43	0.53	0.06	0.15	0.08	12.32	16.02	10.26	0.41	0.33	13.55
Cloves diameter(cm)	3.54	0.64	0.01	0.12	0.12	28.71	29.97	8.63	0.08	0.05	5.12
Total yield wt(t)/ha	14.96	1.27	2.49	5.59	3.11	31.08	41.73	27.84	0.44	2.17	38.27

together are more useful for predicting the genetic progress in selection as high heritability coupled with high genetic advance reflect preponderance of additive gene action. Mashhid [35] reported that in traits with high heritability, genotypic variance is more important than environmental variance and these characters could be considered and exploited for selection in earlier generations [36]. Whereas, in the traits with low heritability, influence of environmental factors is strong for their expression and genotype selection based on these characters should be continued to the next generations.

4. CONCLUSION

For this study, significant variation was observed in the range of traits across garlic genotypes/accessions. The result indicated a significant difference among genotypes. During 2020 cropping season the highest genotypic coefficient of variation and phenotypic coefficients of variation were observed respectively for weight of cloves and total yield tha^{-1}and moderately high heritability along with high genetic advance as percent of the mean were exhibited by shaft/pseodostem length. During 2021 cropping season the highest genotypic coefficient of variation and phenotypic coefficients of variation were observed respectively for weight clove and total yield (tha^{-1}) and moderately high heritability along with high genetic advance as percent of the mean were exhibited by shaft length. Generally, the present study indicated that the presence of the genetic variability between germplasm to exploit the genetic improvement of the garlic crop through hybridization and simple selection methods.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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