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Genetic Variability, Heritability and Genetic Advance in Garlic (Allium Sativum L.) Genotypes in Ethiopia

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Abstract

Garlic is the second most important bulbous allium species in the world after onion. It is also a popular vegetable in Ethiopia, used in various forms including flavoring food, generating income, and making traditional medicines. However, biotic and abiotic factors affect the genetic potential and the quality of garlic crops. Thus, the aim of this field trial was to assess the genetic variation, heritability, and genetic advance of garlic genotypes. Forty-nine (49) garlic genotypes were evaluated in a simple lattice design with two replications at Fogera National Rice Research and Training Center in Horticultural Research Site. The study revealed a significant genetic variation found in clove weight per bulb (26.41%), total fresh bulb yield per hectare (27.54%), bulb weight (21.1%), and clove number per bulb (24.71%). As well as a significant phenotypic variation observed in clove weight per bulb (39.99%), total fresh bulb yield per hectare (30.85%), bulb weight (31.62%), and clove number per bulb (27.85%). Total fresh bulb yield per hectare (81.42%), clove number per bulb (78.71%), and clove weight (43.62%) were characterized by high heritability and high genetic advance as a percent of the mean. A high genetic advance in fresh bulb yield per hectare, clove number per bulb, and bulb diameter are highly linked with the high heritability. These characteristics are therefore crucial for simple selection and helpful for future advantages aimed at improving garlic breeding.

Keywords: Bulb; Clove; Trait; Variation; Weight

Introduction

After onion, garlic is the most ancient vegetable to be produced, and it is the second-largest allium species worldwide. Besides onion, garlic is highly valued for its production, commercial use, medical properties, and culinary seasoning. It is also essential for cash as an income source, local medicine for health treatment, and spices as a flavoring agent in Ethiopia. Identifying crucial garlic genotypes in simple clonal selection and germplasm collection is important based on morphological diversity. Genotypic and phenotypic coefficients of variation, heritability, and genetic advance are essential way of tools for measuring the degree of variability in crop breeding programs. The selection of suitable genotypes in garlic depends on the genetic variability, heritability, and genetic advance among various traits [1].

Garlic production and productivity were declining year to year in many parts of Ethiopian garlic-growing regions due to variable weather conditions, including rainfall, wind, temperature, humidity, and edaphic factors, contribute to fungal diseases and soil-borne pathogens, including white root rot, leaf rust, aphids and lady bugs. 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. The Ethiopian Institute of Agricultural Research introduced new cultivars like Holeta, Chefe, Chelenko, Kuriftu, Qericho, Bishoftu Netch, and Tseday for Ethiopian growing environments, but their performance is lower than local planting material from this trial study areas of Libokemikem and Fogera districts. Further information is mandatory for garlic yield enhancement on genetic variability among garlic genotypes for variety development. Therefore, the study emphasizes the importance of estimating the entire genetic variability in garlic germplasm to enhance its production and productivity [2].

Materials and Methods

Overview of the research area

The study was carried out in the main rainy season on 2020/2021 at Fogera National Rice Research and Training Centre in Horticulture Research Station. Horticulture Research Station is located in Fogera district of South Gondar Zone of Ethiopia. It closes to the capital city of Fogera district of Woreta. The Station is Located at 11° 58′ N latitude and 37° 41′ E. It receives 1230 mm of rainfall annually and is located 1819 meters above sea level. The typical area temperatures are 12°C at the lowest and 28°C at the highest points. With a pH of 5.48, the soil is red clay [3].

Plant material and experimental design with agronomic management

Forty-nine (49) genotypes of garlic were collected from garlic growing areas of Ethiopia. The study was set up using two replications of a 7x7 simple lattice design. Before planting, the trial area was completely tilled and leveled. Ridges of 20 cm width and 15 cm height with a 40 cm furrow width were prepared. The spacing between double rows, rows, and plants was 60 cm, 20 cm, and 10 cm respectively.

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Healthy medium sized cloves were planted with the tip in an upright position and the basal part of the clove down to the soil surface. Cloves were planted on both sides of the ridge with 10 cm between plants (Table 1).

The plot size was 1.8 m2 (1.8 m x 1 m), and a plot had 60 plants on the three ridges (6 rows). NPS fertilizer as a source of nutrients (N = 38, P = 19, S = 7) was applied at a rate of 242 kg ha^{-1} during planting time, and Urea at a rate of 100 kg ha^{-1} was applied in two splits, the first half at complete emergence (10-15 days after planting) and the second at one and a half months after planting (45 days). All other recommended agronomic activities such as weeding, hoeing were handled uniformly at all experimental units based on the national recommendation [4].

Data collected

Data on growth morphology, phenological stages, yield, and yield-related parameters were collected during the cropping and post-harvest periods. Observations on bulb yield and yield-related traits were recorded on both at plot and plant basis, viz., plant height (cm), number of leaves per plant, pseudo stem length (cm), leaf width (mm), leaf length (cm), bulb diameter (mm), bulb weight (g), number of cloves per bulb, clove length (mm), clove diameter (mm), neck diameter of the plant (mm), days to maturity, clove weight (g), total soluble solid (%) bulb length (mm), and bulb yield per hectare (t/ha) [5].

Data analysis

Quantitative traits of plant height, number of leaves, pseudo stem length, leaf width, leaf length, diameter of the bulb, bulb weight, number of cloves, clove length, clove diameter, neck diameter of the plant, days to maturity, clove weight, total soluble solid, length of the bulb, and bulb yield per hectare were collected and tested against the normal distribution using Shapiro-Wilk's test before the analysis of variances. Analyses of variance (ANOVA) were made for all measured traits using SAS 9.4 PROC GLM procedures. Treatment means were tested for all significance traits after testing ANOVA assumptions. The difference between treatment means was compared by using LSD at 5% (P<0.05) and 1% (P<0.01) probability levels respectively [6]. The means and genetic parameters, including the Genotypic and Phenotypic variance, Genotypic and Phenotypic coefficient of variance, heritability (broad sense), expected genetic advance (GA), and genetic advances as a percent of the mean (GAM) were calculated by using the following formula;

$$Yj = \mu + \tau i + \beta j + \rho j + ł + \varepsilon j \quad (1)$$

Where μ= grand mean, = ith treatment effect, = jth block effect (nested with in replication), = jth replication effect, = effect of lth level of intra block error and = error term. The model for RCBD employed was: where μ= grand mean, = ith treatment effect, = jth block effect and = error term.

Estimation of variance components

The phenotypic and genotypic variability of each quantitative trait were estimated as phenotypic and genotypic variances and coefficients of variation. The phenotypic and genotypic coefficients of variations were computed using the formula suggested. Phenotypic coefficient of variation and Genotypic coefficient of variation estimated values are categorized as low (0-10%), moderate (10-20%), and high (>20%) [7].

Genotypic variance for a single location $(\sigma^2 g) = \frac{Msg - Mse}{r}$ (2)

Environmental variance $(\sigma^2 e) = \frac{Mse}{r}$ (3)

Phenotypic Variance $(\sigma 2p) = \sigma 2g + \sigma 2e$ (4)

Where σ2g = genotypic variance; Msg= mean square of genotype; Mse = mean square of error; r = number of replications; σ2e = Environmental variance; and σ2p = phenotypic variance.

Estimation of heritability

Broad sense heritability (H^2) for all characters was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage. Heritability values regarded as low (0-30%), moderate (31-60%) and high (60% and above). GA and GAM were calculated by the formulae described by.

$H^2 = \frac{\sigma 2g}{\sigma 2p}$ (5)

Where H2 = heritability in broad sense, σ2p = phenotypic variance and σ2g = Genotypic variance.

Expected genetic advance under selection (GA)

The expected genetic advance expressed under selection in a broad sense in the 5% selection intensity of the superior progeny was estimated by the following formulae described.

Table 1: Planting materials of 49 Ethiopian garlic genotypes.

S/No.	Genotype	S/No.	Genotype	S/No.	Genotype
1	G-067/18	17	G33-2	33	G29-1
2	G40-1	18	G36-1	34	G4-2
3	G38-2	19	G44-1	35	009/04
4	017/09	20	G22-2	36	G-061/18
5	G34-1	21	G17-1	37	G30-3
6	G16-1	22	G45-2	38	G44-2
7	G10-1	23	G-070/18	39	G37-3
8	G-028/18	24	025/02	40	G3-2
9	G-52/18	25	G14-2	41	G5-2
10	G3-1	26	G16-2	42	027/06
11	G50-1	27	G20-1	43	G-011/18
12	091/04	28	005/09	44	G35-1
13	G31-1	29	HL	45	G39-2
14	G11-1	30	G-044/18	46	G10-2
15	G24-1	31	G13-3	47	G1-1
16	G-007/18	32	G42-1	48	G18-2
				49	G14-1

$$GA = K * SDP * H2 \quad (6)$$

Where GA = Genetic advance; SDp = Phenotypic standard deviation on mean basis; H2= Heritability in the broad sense and K = the standardized selection differential at 5% selection intensity (K = 2.063).

Genetic advance as percent of mean (GAM)

Genetic advance as percent of the mean was calculated to compare the extent of the predicted advance of different traits to select genotypes based on the breeding objective. Genetic advance as percent of mean is categorized as low (0-10%), moderate (10-20%) and high (20% and above) [8].

$$\text{GAM} = \frac{\text{GA}}{\text{X}} \; x\ 100\ \% \quad (7)$$

Where GAM = Genetic advance as percent of mean; GA = Genetic advance and X = Mean value of the trait.

Results and Discussions

Garlic genotype variability

The analysis of variance (ANOVA) indicated highly significance ($P < 0.01$) difference among the traits of plant height, days to maturity, leaf number, leaf length, pseudo stem height, plant neck diameter, bulb length, bulb diameter, clove length, clove diameter, clove number, total soluble solid, bulb weight, clove weight, and total bulb yield. A significant difference at the $p < 0.05$ probability level was observed in leaf width (Table 2). These findings showed the presence of genetic variability among genotypes. A similar result was reported on leaf width. Similarly, highly significant ($p < 0.01$) variability was reported on plant height, days to physiological maturity, leaf number, leaf length, pseudo stem height, neck diameter, bulb length, bulb diameter, clove length, clove diameter, clove number, bulb weight, clove weight, and total bulb yield. Similar results on plant height, leaf number, maturity date, pseudo stem height, neck diameter, bulb weight, clove number, total bulb yield per hectare, and total soluble solids were reported [9].

Mean performance of genotypes

Genotypes showed a wide range of variability in all traits. The mean values indicated significant variation among traits. A range of variability was recorded in bulb diameter (24.3 to 42.78 mm), plant height (36.2 to 53.8 cm), bulb weight (6.48 to 22.64 g), and pseudo stem height (12.05 to 26 cm). On these traits, similar results have been reported by. These high ranges of variation among different genotypes can have a high contribution to breeding values for further improvement of desired traits.

Minimum and maximum mean values were recorded for all studied traits and genotypes. For example, genotype G37-3 has the most leaves (11.3), G50^{-1} has the smallest leaves (7.25), and genotypes 009/04 and G16-1 have the longest and shortest leaves, respectively [10,11]. The latest and earliest maturity dates were observed among genotypes. Genotype 009/04 had the highest bulb length (39.54 cm), while genotypes G-067/18 and G36-1 had the lowest. The largest bulb diameters were found in genotypes 009/04 and G36-1. The highest clove diameters were found in genotypes G-011/18 and G44-1. The G10-2 and G-028/18 genotypes had the highest and lowest total soluble solid values, respectively. G5-2 had the highest bulb weight and clove weight, while G5-2 and G36-1 had the highest and lowest bulb yields per hectare. Similar results were reported on the traits of highest leaf number for G49 was 10.63, the highest plant height for G29 was 74.6cm and leaf length for G49 was 43.57cm by from twenty five genotypes in the spring season [12,13].

Estimating of genetic parameters

Phenotypic and genotypic variance

High phenotypic coefficient of variation (>20%) in clove weight (39.99%), bulb weight (31.62%), total bulb yield per hectare (30.85%), clove number (27.85%), and pseudo stem height (21.72%). Similar results were reported. On clove weight, bulb weight, and clove number. While a moderately significant phenotypic coefficient of variation was observed in plant neck diameter (18.15%), leaf width (16.08%), clove diameter (14.00%), clove length (12.42%), bulb diameter (12.09%), leaf length (11.94%), total soluble solid (11.93%), and leaf number (10.68%). The phenotypic coefficient of variation showed minimum values for bulb length (9.71%), plant height (8.61%), and maturity date (3.39%) [14-16].

Table 2: Analysis of variance for 16 traits in garlic genotypes.

Traits in mean squares	Source of variation			Relative efficiency
	Replication (Df=1)	Genotypes (Df=48)	Error(Df=36)	
LN	0.32ns	1.32**	0.4	88.46
LW	0.02ns	0.03*	0.02	101.36
LL	5.81ns	13.53**	5.26	90.19
PSH	22.52ns	26.12**	10.14	95.06
PH	55.58*	22.29**	9.03	109.45
ND	0.013ns	0.03**	0.01	93.8
MD	167.18**	18.18**	9.02	101.95
BL	1.87ns	15.47**	5.07	87.91
BD	0.04ns	26.01**	9.21	90.67
CL	15.28ns	14.77**	5.11	90.61
CD	0.08ns	8.27**	2.87	92.23
CN	1.35ns	10.32**	1.23	93.88
TSS	2.53ns	15.71**	5.71	90.67
BW	0.54ns	27.24**	10.43	89.3
CW	0.001ns	0.02**	0.01	94.23
FBY	0.23ns	2.35**	0.24	98

LN- Number of leaves per plant, LW - Leaf width (mm), LL- Leaf length (cm), PSH - Pseudo stem length (cm), PH - Plant height (cm), ND- Neck diameter of bulb (mm), MD - Days to maturity, BL - Polar diameters of bulb (mm), BD - Equatorial diameter of bulb (mm), CL - Clove length (mm), CD - Clove widths (mm), CN - Number of cloves per bulb, TSS - Total soluble solid (%), BW - Average bulb weight (g), CW - Average clove weight (g), FBY - Fresh bulb yield per hectare (t/ha) and Df = degree of freedom

The range of genotypic coefficients of variation was 1.97% to 27.84%. Since the highest genetic coefficient of variation recorded in bulb yield (27.84%), clove weight (26.41%), clove number (24.71%), and bulb weight (21.12%) [17]. Moderate genetic variation was observed in pseudo stem height (14.42%) and plant neck diameter (13.71%). While low magnitudes were observed in clove diameter (9.75%), clove length (8.66%), bulb diameter (8.35%), leaf length (6.91%), leaf width (6.68%), plant height (5.61%), and maturity date (1.97%). Similar results were reported in high estimates of phenotypic and genotypic coefficients of variation for bulb yield per hectare. Similarly, high estimates of phenotypic and genotypic coefficients of variation for clove weight, total bulb yield, bulb weight, and clove number were observed [18,19].

Heritability and genetic advance

The range of most traits of heritability percentage in broad sense was 17.27% for leaf width and 81.42% for bulb yield, followed by clove number (78.71%), consistent results reported by. Moderate heritability was observed in plant neck diameter, leaf number, bulb length, clove length, total soluble solid, bulb weight, pseudo stem height, leaf length, clove weight, plant height, and maturity date, while Low heritability in the broad sense was estimated in leaf width (17.27%). High heritability for the above traits were least affected by environmental variations and that selection based on phenotypic performance would be reliable [20,21].

The range of genetic advance as a percent of the mean was 2.35% (maturity date) to 51.74%, (bulb yield) followed by clove number per bulb (45.17%), clove weight (34.93%), bulb weight (26.06%), and plant neck diameter (21.35%) [22]. The magnitude of moderate genetic advancement in various traits such as pseudo stem height (19.72%), clove diameter (13.99%), and clove length (12.43%), bulb diameter (11.88%), leaf number (11.60%), total soluble solid (14.77%), leaf length (10.83%), and bulb length (10.13%). A low genetic advance was observed for leaf width (5.72%), plant height (7.52%), and physiological maturity date (2.35%). A similar finding was reported by on total bulb yield, clove weight, and clove number and bulb weight [23].

The mean of high heritability with high genetic advance is more reliable indicator than heritability alone for genotype selection. Bulb yield (81.42% in heritability and 51.74% in genetic advance), clove number (78.71% in heritability and 45.17% in genetic advance), and clove weight (43.62% in heritability and 35.93% in genetic advance) all showed high heritability and high genetic advance as percent of the mean, with similar findings reported. Thus, High genetic advancement and high heritability make successful selection strategies, governed by additive gene action and further improved through mass selection [24,25].

Conclusions

For this study, significant variability was observed in the range and mean of traits across garlic genotypes. The result indicated a significant range among existing genotypes. High heritability and genetic advance were recorded for bulb yield, clove number, and clove weight. This result aids plant breeding researchers in understanding the genetic background of genotypes for further breeding improvement programs.

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References

1. Abera MW, Mehari AB (2018) The Significance of Garlic *(Allium sativum L.)* on the Livelihood of the Local Community. Journal of Food & Industrial Microbiology 4: 1-5.
2. Bhatt B, Soni AK, Jangid K, Kumar S (2017) A study on genetic variability and character association and path coefficient analysis in promising indigenous genotypes of garlic *(Allium sativum L.)*. Int J Pure App Biosci 5: 679-686.
3. Burton GN, Devane EM (1953) Estimating Heritability in Fall Fescue *(Festuca arundiancea L.)* from Replicated Clonal Materials. Agronomy Journal 45: 478-481.
4. Chatoo MA, Rashid R, Kamaluddin AA, Bhat FN (2018) Variability, Heritability and Genetic Advance in Garlic *(Allium sativum L.)*. Int J Pure App Biosci 6: 793-796.
5. Choudhary S, Choudhary B, Kumhar S (2017) Genetic variability in the garlic *(Allium sativum)* genotypes for growth, yield and yield attributing traits. Annals of Plant and Soil Research 19: 115-120.
6. Dubey BK, Singh RK, Bhonde SR (2010) Variability and selection parameters for yield and yield contributing traits in garlic *(Allium sativum L.)*. Indian Journal of Agricultural Sciences 80: 737-41.
7. Falconer DS, Mackay TFC (1996) Introduction to quantitative genetics.4th ed. Longman, London, UK.
8. Getahun D, Getaneh M (2019) Performance of garlic cultivars under rain-fed cultivation practice at South Gondar Zone, Ethiopia 14: 272–278.
9. Johanson HW, Robinson HF, Comstock RE (1955) Estimates of genetic and environmental variability in garlic. Agton J 47:314-318.
10. Khadi P, Hejjegar SHI (2022) Genetic variability, heritability and genetic advance in garlic *(Allium sativum L.)* genotypes.
11. Kumar K, Ram CN, Yadav GC, Gautum DP, Kumar P, et al. (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 4:123129.
12. Kumari S (2021) Electronic Journal of Plant Breeding Study on genetic parameters in garlic Allium for yield and quality traits 12: 477-484.
13. Rahim MA, Alam SM, Bin J, Rahman M, Rahman J, et al. (2019) Morphological characterization of garlic *(Allium sativum L.)* germplasm 2: 46-52.
14. Rakesh S, Nagaraju K, Komolafe O, Malik S (2016) Genetic variability, heritability and genetic advance in garlic genetic variability, heritability, and genetic advance in garlic genotypes.
15. Ranjitha MC, Vaddoria MA, Jethava AS (2018) Genetic Variability, Heritability and Genetic Advance in Garlic *(Allium sativum L.)* Germplasm 6: 401-407.
16. Shapiro SS, Wilk MB (1965) An analysis of variance test for normality (complete samples), Biometrika, 52: 591-611.
17. Sharma D, Chauhan A (2021) Genetic variability, heritability and genetic advance in garlic genotypes. Journal of Pharmacognosy and Phytochemistry 10: 1346-1348.
18. Shemesh-Mayer E, Kamenetsky-Goldstein R (2021) Traditional and novel approaches in garlic *(Allium sativum L.)* breeding. Advances in Plant Breeding Strategies: Vegetable Crops: Volume 8: Bulbs, Roots and Tubers 3-49.
19. Singh AK, Singh D (2010) Genetic variability, heritability, and genetic advance in marigold. Indian Journal of Horticulture 67: 132-136.
20. Singh G, Ram CN, Singh A, Prakash Shrivastav S, Kumar Maurya P, et al. (2018) Genetic Variability, Heritability and Genetic Advance for Yield and its Contributing Traits in Garlic *(Allium sativum L.)*. International Journal of Current Microbiology and Applied Sciences 7: 1362-1372.
21. Tabor G, Eshetu D, Tebikew D (2009) Guidelines for shallot and garlic. Debrezeit Agricultural Research Center, Debre Zeit Ethiopia 51pp.
22. Tesfaye A, Mijena DF, Zeleke H, Tabor G (1970) Genetic variability and character association for bulb yield and yield related traits in garlic in Ethiopia. African Crop Science Journal 29: 293-308.
23. Tsega K, Tiwari A, Woldetsadik K (2010) Genetic variability, correlation and path coefficient among bulbs yield and yield traits in Ethiopian garlic germplasm. Indian Journal of Horticulture 67: 489499.

24. Vatsyayan S, Dhall RK (2016) Genetic Variability Studies in Garlic *(Allium sativum L.)*, (December 2015).

25. Yeshiwas Y, Negash B, Walle T, Gelaye Y, Melke A, et al. (2018) Collection and characterization of garlic *(Allium sativm L.)* germplasm for growth and bulb yield at Debre Markos, Ethiopia. Journal of Horticulture and Forestry 10: 17-26.