BAHIR DAR UNIVERSITY

COLLEGE OF AGRICUTLURE AND ENVIRONMENTAL SCIENCES

GRADUATE PROGRAM IN PLANT BREEDING

GENETIC VARIABILITY AND ASSOCIATION OF TRAITS IN GARLIC (*Allium sativum* L.) GENOTYPES IN FOGERA DISTRICT, NORTHWESTERN ETHIOPIA

MSc. Thesis

By

Mulat Getaneh Melese

October 2021

Bahir Dar, Ethiopia

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SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE (MSc.) IN PLANT BREEDING

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THESIS APPROVAL SHEET

As member of the Board of Examiners of the Master of Sciences (MSc.) thesis open defense examination, we have read and evaluated this thesis prepared by **Mr. Mulat Getaneh** entitled **"GENETIC VARIABILITY AND ASSOCIATION OF TRAITS IN GARLIC (***Allium sativum* **L.) GENOTYPES IN FOGERA DISTRICT, NORTHWESTERN ETHIOPIA**". We hereby certify that; the thesis is accepted for fulfilling the requirements for the award of the degree of Master of Sciences (MSc.) in Plant Breeding.

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DECLARATION

This is to certify that this thesis entitled with "**GENETIC VARIABILITY AND ASSOCIATION OF TRAITS IN GARLIC (*Allium sativum* L.) GENOTYPES IN FOGERA DISTRICT, NORTHWESTERN ETHIOPIA**" submitted in partial fulfillment of the requirements for the award of the degree of Master of Science in Plant Breeding to the Graduate Program of College of Agriculture and Environmental Sciences, Bahir Dar University by **Mr. Mulat Getaneh** (**ID. No. BDU1207117PR)** is an authentic work carried out by him under our guidance. The matter embodied in this project work has not been submitted earlier for award of any degree or diploma to the best of our knowledge and belief.

Name of the Student

Mulat Getaneh Signature_____ date _____

Name of the Supervisor

Alemu Abate (PhD) Signature_____ date_____

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ABBREVIATIONS AND ACRONYMS

ANOVA	Analysis of Variance
CSA	Central Statistical Agency
DZARC	Debrezeit Agricultural Research Center
EIAR	Ethiopian Institute of Agricultural Research
FAO	Food and Agricultural Organization
FAOSTAT	Food and Agriculture Organization of the United Nations Statistical Database
FNRRTC	Fogera National Rice Research and Training Center
GA	Genetic Advance
GAM	Genetic Advance as Percent of Mean
GCV	Genotypic Coefficient of Variation
GLM	General Linear Model
H^2	Heritability
IPGRI	International Plant Genetic Resource Institute
LSD	Least Significance Difference
Mse	Mean square of error
Msg	Mean square of genotype
PCA	Principal Components Analysis
PCV	Phenotypic Coefficient of Variation
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis System

GENETIC VARIABILITY AND ASSOCIATION OF TRAITS IN GARLIC (*Allium sativum* L.) GENOTYPES IN FOGERA DISTRICT, NORTHWESTERN ETHIOPIA

By

Mulat Getaneh

Advisor: Alemu Abate (PhD)

ABSTRACT

*Prior knowledge on genetic variability is required in crop improvement programs. Information on genetic variability in garlic genotypes is important for the genetic improvement. Garlic has been valued for food, culinary, income and medicinal purposes in the world. However, there is no sufficient information on garlic genetic variability and association of traits in Ethiopian garlic genotypes. Therefore, the present study was conducted to evaluate genetic variability among 49 garlic genotypes. The experiment was laid in 7x7 simple lattice design at FNRRTC on station during 2020/2021 cropping season. Both quantitative and qualitative traits were recorded and analyzed by SAS 9.4 version and Shannon-Wiener diversity index respectively. The analysis of variance showed highly significant ($p<0.01$) difference among the genotypes for almost all traits and leaf width showed significant ($p <0.05$) variations. Clove weight per bulb, total fresh bulb yield per hectare and clove number per bulb had high GCV and PCV values. Total fresh bulb yield per hectare (81.42% and 51.74%), clove number per bulb (78.71% and 45.17%) and clove weight (43.62% and 35.93%) had high heritability and genetic advance as percentage of mean values indicated in number respectively. Total fresh bulb yield per hectare had highly significant genotypic correlation coefficient with bulb weight per plant (r = 0.82***), pseudo stem height (r = 0.82***) and clove weight (r = 0.81***). Clove weight per bulb (r = 0.77***), pseudo stem height (r = 0.77***) and bulb weight per plant (r = 0.76***) had highly significant positive phenotypic association with total fresh bulb yield per hectare. Pseudo-stem height (0.42) and clove weight (0.39) had the highest phenotypic direct effect on total fresh bulb yield per hectare. The first two principal components were accounted for 74% of the overall variance. Cluster analysis showed the existence of two divergent groups with cluster-5 and cluster-4 (29.448). Since quantitative traits are polygenic and mainly affected by the environment, a one year experiment at one location does not reveal genotypes' variability in response to the environment. As a result, further trials in over years and locations will be required.*

Key words: *Bulb weight, Clover weight, Correlation, Genetic advance, Heritability*

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Chapter 1. INTRODUCTION

1.1. Background and Justification

Cultivated garlic is a sterile crop and is thus propagated through vegetatively. The genetic variation of garlic increases through spontaneous or induced mutations (Burba, 1993) and somaclonal variation (Novak, 1990). New cultivars are developed through clonal selection and introductions to different growing environments (Rubatzky and Yamaguchi, 1997). Garlic (*Allium sativum* L.) is a 2n = 16-diploid chromosome (Figliuolo *et al*., 2001). Botanically, garlic belongs to the family *Alliaceae* and the gnus *Allium.* Garlic is grouped under in essential vegetable crops of onions (*Allium cepa*), leek (*Alium ampeloprasum*) and shallots (*Alilium ascalonicum*) (Ipek *et al*., 2005).

Germplasm collection is the basic tool for identifying important genotypes based on clonal selection. The large extent of natural variation present among the genotypes in different traits is good scope for genetic improvement. Large variability gives a better opportunity to produce new forms of a crop. The degree of association between various traits and the direct effect of yield contributing traits on total bulb yield, variability parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advancement are important statistics for formulating an appropriate garlic breeding strategy. This aimed for exploiting the inherent variability of the original population of a crop (Singh *et al*., 2018). Clonal selection has been effective in altering garlic traits and regular treatments are vital for minimizing or removing viruses (Burba, 1997).

In Ethiopia, garlic bulb production period takes 3-6 months and during its production season, the amount of rainfall varies between 600 mm and 700 mm. The optimum garlic growing temperature lies between 12^{o}C and 24^{o}C. Garlic production is spread throughout the country under irrigation as well as rain-fed conditions in the center and highlands of Ethiopia (Martha Mebratu and Marie Mulie, 2019).

Garlic (*Allium sativum* L.) is the oldest cultivated vegetables and it is the second largest species in the world after onion (Benke *et al*., 2020a; Khandagale *et al*., 2020). It is grown and consumed around the world and is famous for its nutritional and medicinal properties (Fritsch and Friesen, 2002; Block, 2010). Garlic is the most useful medicinal plants in the world and used as conventional dietary supplements for diabetes. Garlic has verified for its anti-viral, anti-bacterial, anti-fungal, antioxidant, anti-atherosclerotic and anti-cancer properties (Tyagi *et al*., 2013).

Garlic (*Allium sativum* L.) is recognized in worldwide in terms of production, commercial, medicinal and food seasoning values along with common onion. Garlic has the characteristic of pungent odor and rich in sugar, protein, fat, calcium, potassium, phosphorous, sulphur, iodine fiber and silicon in addition to vitamins and many other substances that contribute significant nutritional value (Weldemariam Seifu, 2017). Garlic is essential for as a spice and flavoring agent for most dishes of Ethiopia (Melese Worku and Abay Bantihun, 2018).

Garlic is grown worldwide in an area of 1,468,811 ha, with production of 26,573,001tons and productivity of 18.09 t ha^{-1} (FAOSTAT, 2016/2017). China is the world leader in production (80%) followed by India (4.8%). However, the production and productivity of garlic is low in Ethiopia. Area coverage of garlic were 16,411.19 ha, 11,845.53 ha and 15,381.01 ha in 2014, 2015, and 2016, respectively. The total productions for the same years were 159,093.58, 107,743.5 and 138,664.3 tons of bulbs with productivity of 9.69, 9.10 and 9.02 t ha^{-1} respectively, in the main crop season (CSA, 2017/2018). Even in 2018 and 2019 the productivity of garlic in Ethiopia was 8.994 t ha^{-1} and 8.318 t ha^{-1} respectively (CSA, 2019/2020). Therefore, the major causes of low productivity in Ethiopia is poor yield potential of varieties coupled with susceptibility to pest and diseases.

1.2. Statement of the Problem

Garlic is a high value crop for home consumption and cash income in Ethiopia. It is produced under both rain fed and irrigation conditions. However, its production and productivity is very low. Due to lack of improved varieties coupled with susceptibility of pests and disease (onion

thrips, garlic rust, downy mildew, basal rot, white rot and purple blotch) and, the nature of propagation and inadequate planting materials (Getachew Tabor and Asfaw Zeleke, 2010; Mohamed Amin *et al*., 2014; Tewdrose Bezu *et al*., 2014).

In the Amhara region particularly in South Gondar zone of Fogera district, garlic is cultivated both under in rain-fed and irrigation conditions. However, lacks of improved varieties are the most serious bottleneck problem. Efforts were and are being made by research centers and universities to develop varieties through clonal selection but they were not further successful. Even to date, only few varieties are released at national level but the availability of planting materials dissemination of these varieties for the growers across the country is another challenge in the production system. Those released varieties from DZARC have been performed inferior to the local planting material at Libokemikem and Fogera district (Dessie Getahun and Mulat Getaneh, 2019).

Therefore, information on genetic variability among garlic genotypes and association of traits can contribute for enhancing the variety development. Hence, the present study was aimed for assessing genetic variability and association of traits among garlic genotypes to quantify potential variability for the development or identification of improved varieties.

1.3. Objectives of the Study

1.3.1. General objective

To assess the variability and associations of traits in the Ethiopian collected garlic genotypes

1.3.2. Specific objectives

To estimate genetic variability of garlic genotypes using both quantitative and qualitative traits;
To determine the association among bulb yield and yield related traits;
To identify the traits having major contribution to the total variation among the genotypes and
To identify promising genotypes of garlic for future breeding programs.

Chapter 2. LITERATURE REVIEW

2.1. Origin, Genetics and Distribution of Garlic

Cultivated garlic (*Allium sativum* L.) is a sterile plant with major variation in morphological and physiological characteristics. The primary center of origin is the northwestern side of the Tien Shan Mountains of Central Asia because several fertile clones of primitive garlic type were discovered in this area (Etoh and Simon, 2002). The secondary center is the Mediterranean of Caucasus zones (Vavilov, 1951). Now a day, this crop is cultivated in many areas around the world due to high ecological flexibility and successful trade (Hong and Etoh, 1996). The crop originated from its progenitor, *Allium longicuspis* Regel in West to Middle Asia and was transported from there to the Mediterranean and other cultivation areas (Maab and Klaas, 1995). Vvedensky (1944) also suggested that all domesticated garlic originated from the wild species *Allium longicuspis,* originally spread from southern Turkmenia to Tien Shan and now restricted to central Asia and it is distributed by trade and colonization to other parts of the world (Tindal, 1986).

Cultivated garlic in various regions of the world has accumulated mutations in order to adapt different climatic conditions (Etoh and Simon, 2002). Garlic has been used for over 5000 years in China and India and in Egypt since 2000 B.C. Garlic is the world's most common cultivation of *Alliums* and ranks second next to onion (Voigt, 2004). Garlic is a vegetative propagation species which exhibits high morphological diversity. Furthermore, its clones have unique adaptations to various agro-climatic regions. Garlic the oldest known horticultural crops originated from Central Asia (centric in Kyrgyzstan, Tajikistan, Turkmenistan, and Uzbekistan) (Paredes *et al*., 2008).

2.2. Botanical Description and Taxonomy of Garlic

Commercial garlic is a distinctive apomictic obligatory crop (Etoh, 1985). Thus, through the domestication process it has a long history of vegetative propagation by bulbs or bulbils and spread to multiple agro-climate environments (Manjunathagowda *et al*., 2017). Whether garlic

has become sterile since the beginning of its production is unknown but sterility in garlic is certainly as a result of the evolution and domestication (Etoh, 1985). Garlic sets flowers rose in an umbel but did not set the seeds due to underdeveloped gametophytes, which may cause male and female sterility (Benke *et al*., 2020b).

The garlic plant consists of edible fleshy cloves covered in a thin white or pink coat. It has leaves, stems, and seeds that are edible on the head. It is easy to grow and it can evolve throughout the year. The leaves are flat, long and thin. It is cultivated both tropical and temperate climates. In well-drained soil, garlic plant grows well and needs a period of cool and moist growth. It is propagated by means of cloves obtained from the bulbs and is ready for harvest when the top turns brown or yellowish. It is best kept in well-ventilated spaces (Ourouadi *et al*., 2016).

2.3. Economic and Culinary Importance

All over the world garlic is highly valued for its medicinal and culinary interest. A variety of therapeutic uses for this botanical were promoted by early men of medicine like Hippocrates, Pliny, and Aristotle. Nowadays, it is widely used as a seasoning or spice in many cultures. Garlic is also the second most used additive. Diseases that can be prevented or avoided by the therapeutic acts of garlic include Alzheimer's disease, cancer, cardiovascular disease (including atherosclerosis, strokes, hypertension, thrombosis, and hyperlipidemias), diseases of babies, dermatological treatments, stress and infections. Some studies points the potential benefits of garlic to diabetes, drug addiction, and osteoporosis (Bongiorno and Health, 2014).

Garlic (*Allium sativum*) is commonly used as a flavoring in cooking, but it has also been used as a medicine in ancient and modern thought, it has been used to prevent and treat a wide type of diseases and ailments. One of fresh garlic extract 's key active substance allicin, whose ready permeability across phospholipid membranes may contribute to its potential biological activity and contain sulfur compounds, which are thought to bring some of the health benefits. Currently, Garlic is commonly used for several heart and blood system related conditions, including atherosclerosis (hardening of the arteries), high cholesterol, heart attack, cardiac disease, and hypertension. Garlic is also used by some people today to avoid lung cancer, cancer of the heart,

cancer of the breast, cancer of the stomach, cancer of the rectum; cancer of the colon. Garlic bulb is an important ingredient in seasoning and is used in countless cuisines around the world. Clonal lines within this species are extremely variable in bulb size and color (Nair *et al*., 2013).

Garlic has sulfur compounds that are responsible for heavy odor, distinctive taste and nutritional benefits (Salomon, 2002). Garlic is flavoring many forms of dishes including vegetable soup, meat, salad, tomato mix, spaghetti, sausages, and pickles (Brewster, 1994). Garlic is consumed in various ways as green and blenched tops, as fresh and cooked form (Rabinowitch and Brewster, 1990). Bread and butter derived from garlic have various uses in cooking and food preparations in homes and restaurants (Nonnecke, 1989).Garlic is best medicinal plants for antibacterial and antiseptics (Keusgen, 2002).

2.4. Garlic Production and Productivity in Ethiopia

Garlic is used as a spice or a condiment in Ethiopia. It is primarily used in various dishes for flavoring and seasoning vegetables. It has many medicinal properties as well (Abreham *et al*., 2014). Garlic cultivation in Ethiopia was 19412.49 ha with production and productivity were 1780000 tons and 9.18 t ha^{-1} respectively (CSA, 2018). According to CSA (2019) garlic cultivation in Ethiopia was 21754.49 ha of land with the production and productivity were about 195740.045 tons with 8.994 t ha^{-1}. In 2019/2020, in Ethiopia garlic cultivation was 18344.47 ha with the production and productivity was 152594.634 tons with 8.318 t ha^{-1} in the main cropping season (CSA, 2019/2020). Garlic cultivation in Amhara region was 6857.43 with production and productivity about 53592.361 tons and 7.815 t ha^{-1} respectively. And garlic cultivation in North Gondar zone was 344.75 with production and productivity were 2859.28 tons and 8.294 t ha^{-1} respectively (CSA, 2019/2020).

2.5. Genetic Variability and Diversity of Garlic

There are more than 800 species in the genus *Allium* (Li *et al*., 2010). The most widely grown *Allium sativum* species in the world are onion (*Allium cepa* L.), shallot (*Alliumcepa* var. *ascalonicum* L.), garlic (*Allium sativum* L.) and leek (*Allium Ampeloprasum* L.) (Stearn, 1992).

The mode of garlic clone propagation allows the production of uniform crop that preserves quality traits such as flavor and the nutritive properties of the crop. For its adaptation in different climatic and bio-geographic regions over a long history of cultivation shows large variations in bulb size, shape and color, clove number and size, peeling capacity, maturity date, flavor, and pungency, bolting capacity, inflorescence number and size of top sets and flowers (Meredith, 2008). Large morphological variations in cultivated garlic or clonal lineages such as in leaf number, bulb size and structure (such as clove arrangement, number, and size), floral scape length and inflorescences (Kamenetsky *et al*., 2005), (Buso *et al*., 2008).

Taxonomic studies categorize the Central Asian Longicuspis group as the most primitive within the genus and modern biochemical and molecular studies suggest that this group still retains the highest level of intraspecific variation. Thus, the Longicuspis community is the most significant source of genetic variation within the species and therefore needs careful consideration to ensure the use of its specific features in future enhancement programmes. However, this precious gene pool is currently under severe extinction threat because of the very rapid replacement of traditional land races with modern sativum group cultivars. An international initiative will be imperative in the very near future (Rina, 2007).

Garlic is propagated exclusively by cloves on a vegetative basis and its scope of development over breeding methods is inadequate. Garlic shows wide-ranging morphological and agronomic variations in plant height, days to flowering, clove number and size, days to harvest, dormancy, and adaptation to agro-climate conditions (Lu *et al.,* 2001, Singh *et al*., 2013). Garlic shows large morphological and agronomic variations in colour, bulb size, plant height, flowering, clove number and size, harvesting days, storability capacity resistance, dormancy and adaptation to agro-climatic situations (Mario *et al.*, 2008). Lack of sexuality in garlic limits the variability that is useful for breeding for economically important traits such as tolerance to biotic and abiotic stress, earliness, yield and quality (Kamenetsky, 2007).

2.6. Association of Traits

Correlations are the measures of associations among two traits that measure the magnitude and direction of one trait on another (Singh *et al*., 2013). Correlation is either due to pleiotropic gene action or linkage or both. The correlation coefficient reveals the essence of the relationship between the various traits. To determine the inter-relationship between the characters, the correlation coefficient between yield and its attributes was calculated at the genotypic and phenotypic levels. It offers in detail on the type, degree and direction of selection pressure that should be applied for practical purposes. High magnitude indicates the existence of a linear relationship between the studied traits. For the direction, when signs are equal, positive, or negative; it is understood that the two traits are benefited or harmed by the same causes of variations; however, opposite signs of correlation determines an increase in one trait greatly decrease the other trait (Singh *et al*., 2011; Chotaliya and Kulkarni, 2017).

The most relevant causes of association are either due to the action or linkage of the pleiotropic gene or both. Genotypic and environmental effects are included in the phenotypic correlation, providing details between the measurable characters. Phenotypic correlations provide data on the relationship between two characters while genotypic correlation provides a measure of the genetic association between the characters and is typically used in selection while a genotype plays a major role in achieving the higher yield coupled with better quality as a genetic and environmental way. The association between components of yield and other quantitative characteristics helps to explain the interdependence of characteristics (Ganie and Jan, 2013)

Phenotypic variability increases under different environmental conditions while genetic variability remains constant and more beneficial to a plant breeder for selection or hybridisation. Yield is very complex features governed by many yield-contributing components and is strongly influenced by environmental factors, so heritability estimates and genetic advancement are helpful for selection. It is necessary to estimate the correlation coefficient between the characters contributing to yield to understand the direction of selection and optimize yield. The path coefficient is an effective way to deal with the causes of direct and indirect selection interaction and measures the relative importance of each causal factor (Singh *et al*., 2018).

Correlation is an association which refers to the strength of relationship between two-variables. There is a high or strong correlation between two or more variables which indicates a strong relationship with each other while a weak or low correlation implies that the variables are weakly related. Correlation coefficients can range from -1.0 to +1.0. The value of -1.0 represents a perfect negative correlation while a value of +1.0 represents a perfect positive correlation. A value of zero is no relationship between the variables (Singh and Singh, 2010).

In order to explain cause and effect relationships between characteristics associated with yield, correlation coefficients are only insufficient while path coefficient analysis enables a deeper understanding of correlations between different characters by breaking down coefficients of correlation associated with the main character into direct and indirect effects (Hossain *et al*., 2015). Analysis of the path coefficient provides an efficient means of partitioning correlation coefficients into unidirectional and alternate paths, enabling a critical analysis of the factors that create a correlation. Wright (1921) provided the definition of path analysis but the method was first used by (Dewey and Lu, 1959).

Analysis of path coefficient is simply a standardized partial regression coefficient which divides the coefficient of correlation into measures of direct and indirect impact on the independent variable. In other words, the direct and indirect contribution of the different independent characters to the dependent character is calculated. It also predicts residual effects. Path coefficient analysis is useful in indirect selection. Total fresh bulb yield was taken as a dependent variable in garlic bulb and the rest characters were considered as an independent variable. The study of the path coefficient divides the overall correlation coefficient of different characteristics into direct and indirect effects on the total yield of the bulb in such a way that the number of direct and indirect effects is equal to the total correlation of the genotypes. As a significant crop, garlic needs commitment to genetic enhancement (Dewey and Lu, 1959).

Correlation coefficients show a simple relationship between variables. In a biological environment the relationship could be extremely complex. As a result, it is critical to investigate the relationship between variables in depth. Path coefficient analysis is a powerful method that

allows for partitioning of a given relationship into its components. In other words, it considers not just the relationship between component characters and dependent characters but also their relationship with other components. As a result, it aids in a deeper understanding of the causal system by allowing the overall correlation coefficient to be divided into direct and indirect effects of different characters (Panse, 2013). Acording to Gizachew Atinafu *et al*. (2021) significant positive correlation of total bulb yield per hectare was observed in maturity date, plant height, number of clove per bulb and bulb weight in garlic.

2.7. Genetic Divergence and Clustering

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Cluster analysis is a multivariate techniques which classify a sample of genotypes based on a set of measured variables into a number of different groups such that similar objects are placed in the same group. Clustering is defined as the process of organizing genotypes or individuals into groups whose members are similar in some ways (Chahal and Gosal, 2002). Cluster analysis is used to arrange a set of variables into clusters. Its objective is to sort genotypes into groups or clusters, so the degree of association would be strong between members of the same cluster and weak between members of different clusters.

Divergence analysis is a technique used to categorize genotypes into one group as similar as possible and the other into different ones. Ecuadorean distance (ED) was used to classify the different genotypes into different groups. One of the most common and efficient methods of statistical multivariate analysis for grouping genotypes is cluster analysis. Hence, the extent of diversity among selected genotypes is estimated by genetic divergence analysis. Clustering shows as a dendrogram dissimilarity representing the closest accessions in homogeneous groups. Studying of percent contribution in garlic showed that plant height was found for highest contribution followed by length of leaf, number of cloves per bulb and total soluble solids for total divergence among the available genotypes of garlic. While number of leaves per plant, bulb yield per plant, diameter of bulb, contributed very low towards the divergence (Mishra, 2018).

2.8. Principal Component Analysis

Principal component analysis (PCA) is multivariate methods that identify the variables having a large amount of contribution to the total variation. In the study of association between attributes, principal component analysis helps to classify the most important characters. At each axis of differentiation, the principal component analysis (PCA) reflects the importance of the largest contributor to the total variation (Sharma, 1998). PCA helps to categorize genotypes in to similar groups and understand the most essential traits that explain much of the variability among the studied genotypes. Traits with large absolute value close to unity with the first principal components can influence clustering more than those with lower absolute value closer to zero (Chalal and Gosal, 2002).

The first step in PCA is to see an Eigen value which defines the amount of total variation that is displayed on the PC axis. The first PC summarizes most of the variability present in the original data relative to all remaining PCs. The second PC explains most of the variability not summarized by the first PC and uncorrelated with the first and so on. Principal component analysis (PCA) has various applications such as the study of genetic divergence between genotypes which allows the identification and selection of the most promising genotypes for cultivation and improvement as well using in evaluating the relative importance of characters in the total variation among genotypes (Jollife, 1986).

The results showed that more than 75% of diversity of the total 131 garlic germplasm is present in first 4 principal components out of 12 and they had Eigen values recorded more than one. The first PC explained characters viz., plant height, pseudo stem height and diameter, polar or equatorial diameter of bulb, bulb weight per plant and number of cloves per bulb positively related to total bulb yield. In case of PC2, characters like Plant height, Pseudo stem height, equatorial diameter of bulb and number of cloves per plant showed positive correlation. Bi-plot shows that there is a lot of variability present in the studied genotypes (Rakesh, 2018)

Chapter 3. MATERIALS AND METHODS

3.1. Description of the Study Area

The experiment was carried out at Fogera National Rice Research and Training Center (FNRRTC) on-station in 2020/2021 during the rainy season. FNRRTC is located near to Woreta town in Fogera district at the South Gondar Administrative Zone of Amhara Region, Ethiopia. It is 60 km away to the North from Bahir Dar, and 625 km from Addis Ababa. Woreta lies in the latitude 11° 58′ N, and longitude 37° 41′ E. It has an altitude of 1819 m above sea level and obtains 1230 mm annual rainfall. The minimum and maximum mean area temperatures are 12 ºC and 28 ºC, respectively. The soil is red clay with pH value of 5.48 (Dessie Getahun and Birhanu Habtie, 2017).

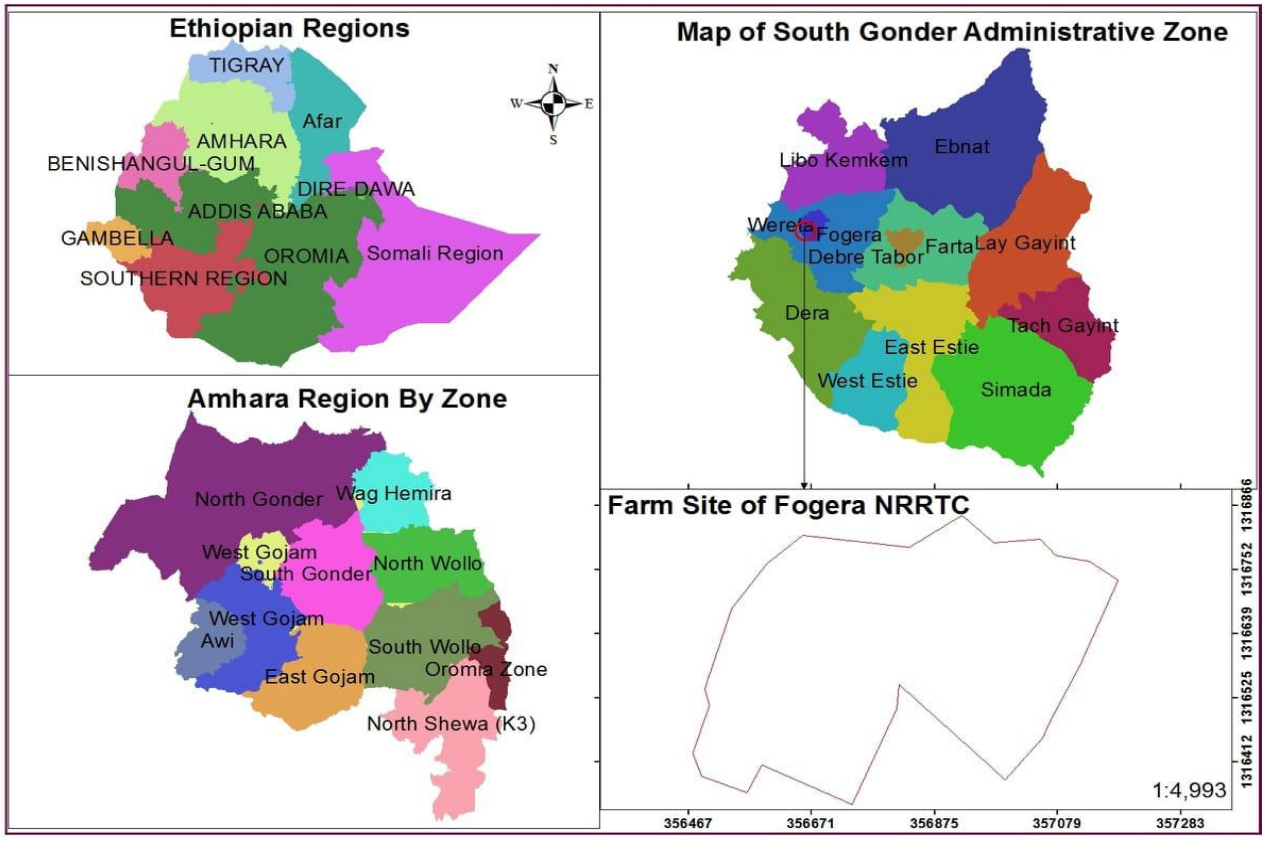


Figure 3. 1. Map description of the study area

3.2. Experimental Materials

Forty-nine (49) genotypes of garlic were used for the study. Thirty-nine (39) garlic genotypes were obtained from FNRRTC which were collected from the North and South Gondar administrative zones. The remaining ten (10) local collected genotypes were obtained from Debrezeit Agricultural Research Center (DZARC) (Appendix table 1).

3.3. Experimental Design and Agronomic Management

The experiment was laid in 7x7 simple lattice designs with two replications. The experimental area was thoroughly plowed and leveled before planting. Ridges of 20 cm width and 15 cm height with 40 cm furrow width were prepared. The spacing between double rows, rows and plants were 60 cm - 20 cm - 10 cm respectively. The planting materials or cloves were planted with the tip in upright position and the basal part of the clove down to the soil surface. Cloves or bulb splits were planted on both sides of the ridge at 10 cm between plants.

The plot size was 1.8 m^2 (1.8 m x 1 m), and a plot had 60 plants on the three ridges (6 rows) one meter long and 1.8 m wide. NPS fertilizer as a source of nutrients (N = 38: P = 19: S = 7) were applied at a rate of 242 kg ha^{-1} during planting and Urea at the rate of 100 kg ha^{-1} were applied in two splits, the first half at complete emergence (10 - 15 days after planting) and the second were applied at one and a half months after planting (45 days). All other recommended agronomic activities such as weeding, hoeing, etc. were handled timely and uniformly (Getachew Tabor *et al.,* 2009).

3.4. Data Collected

Data on growth morphology, phenological stages, yield and qualitative parameters were collected during the cropping season and in the post-harvest. Observations on bulb yield and yield related traits were recorded on both plot and plant basis as mentioned below. All other traits were recorded based on the standard descriptors for garlic developed by the International Plant Genetic Resources Institute (IPGRI, 2001).

3.4.1. Phenological data

Days to physiological maturity: physiological maturity was recorded when 75% of the leaves of the plants in each plot become yellow, dry and/or shown senescence.

3.4.2. Growth and yield related data

Plant height (cm): plant height was measured in centimeter from the soil surface to the tip of matured leaf in the plant at physiological maturity by a ruler.

Leaf number per plant (count): The number of leaves per plant was counted from 5 randomly selected plants at physiological maturity. The mean number of leaves was calculated by dividing total number of leaves observed from five plants by five.

Leaf length (cm): The length of five leaves per plant (from upper, medium, and lower) was measured at physiological maturity by using a ruler and the average leaf length was taken.

Average bulb weight per plant (g): the average mature bulb weight per plant was recorded after weighting five bulbs from each plot of the central rows and dividing by the number of plants.

Bulb neck diameter (cm): The average neck thickness was measured at the middle narrow point of the bulb neck from five randomly taken plants from the middle three rows in each plot using graduated caliper.

Bulb diameter or Equatorial diameter (mm): bulb diameter was measured from randomly taken five bulbs at the widest point in the middle portion of the bulb using graduated caliper

Pseudo stem height (cm): five randomly selected plants was taken from each central row of a plot and measured from the plant base up to the tip portion of pseudo stem height

Bulb length or Polar diameter (mm): bulb length was measured from randomly taken five bulbs at the basal end point from the bottom scar of the bulb to the tip point of the bulb using graduated caliper.

Clove diameter or Equatorial diameter (mm): clove diameter was measured from randomly taken five cloves at the widest point in the middle portion of the clove using graduated caliper

Number of clove/bulbs (count): The cloves were counted from 5 plants and their average was taken as a number of cloves per plant

Clove length or Polar diameter (mm): clove length was measured from randomly taken five bulbs at the basal end point from the bottom scar of the bulb to the tip point of the clove using graduated caliper

Bulb weight per plant (g): an average bulb weight per plant was measured from five randomly taken bulbs after the bulb was cured or exposed for seven days by sunlight.

Clove weight per bulb (g): an average clove weight per bulb was measured from ten randomly taken cloves of five randomly taken composite splitting bulbs when the bulbs were cured or exposed for seven days by sunlight.

Yield of bulb per hectare (t): weighted per plot bulb yield and converted into yield per hectare.

3.4.3. Qualitative traits

Leaf color: the leaf color under deep (light, green), yellowish, and brown measured by leaf color chart (LCC) per plot was scored.

Bulb color: the bulb color under white, cream, white stripes, light violet, violet and dark violet measured by bulb color chart (BCC) per plot was scored.

Clove color: the split cloves color under white, yellow, and light brown, brown, red and violet measured by clove color chart (CCC) was scored.

Foliage attitude: The foliage shapes under erect, intermediate, and prostrate were scored.

3.4.4. Quality traits

Total soluble solid (brix %): was recorded by randomly five bulb tissues, and crushed the bulb and drop the juice on Table Refracto-meter to determine the TSS percent.

3.5. Data Analysis

3.5.1. Shannon-Wiener diversity analysis

Shannon's diversity index (H) is an index that is used to categorize the species diversity in a certain community. Shannon's diversity index is an account for both richness and evenness present in the species also used for a wide diversity of fields. It is also known as phylogenetic indices or phylogenetic metrics, which is a numerical estimation that indicates how many types of variation are present in a community and simultaneously can consider the phylogenetic relations among the individuals and was calculated (Shannon,1948) using the formula as follows: $H = -\sum pi \ln (pi)$; $E = H/Hmax$; $Hmax = \ln (N)$; (i = trait grade, pi = the frequency of the sample within a certain grade and ln = natural logarism, E = equability or evenness). A low H indicates extremely unbalanced phenotypic classes for an individual trait and a lack of genetic diversity (Perry and Mclntosh, 1991).

The Shannon diversity index was calculated using the qualitative traits of garlic among the genotypes studied. The Shannon diversity index was derived using species richness (the number of species in the community) and abundance (the total number of species in the sample). A high Shannon diversity index indicates that the community has high species diversity. On the other hand, little Shannon diversity index indicates low species richness in the community (Maniruzzaman, 2006) and (Konopiński, 2020).

3.5.2. Analysis of variance

Using Shapiro Wilk's test (Shapiro and Wilk, 1965), the data was tested for its normal distribution before moving to analysis. Analyses of variance (ANOVA) on all measured characters were performed using SAS software 9.4 proc GLM procedures. Treatment means were tested for significance after testing in ANOVA assumptions by least significance difference (LSD) at 5% probability level. Relative efficiency of using lattice over RCBD was checked to be effective for traits unless relative efficiency of using lattice over RCBD was ineffective, ANOVA was carried out based on RCBD design.

The model for simple lattice design employed was: $Yij = \mu + \tau i + \beta j + \rho j + yl + \varepsilon ij$ where μ= grand mean, τi = i^{th} treatment effect, βj = j^{th} block effect (nested with in replication), ρj = j^{th} replication effect, yl = effect of l^{th} level of intra block error and εij = error term. The model for RCBD employed was: $yij = \mu + \tau i + \beta j + \varepsilon ij$ where μ= grand mean, τi = i^{th} treatment effect, βj = j^{th} block effect and εij = error term.

Based on the relative efficiency principles in randomized complete block and simple lattice design when a value of relative efficiency is less than 100% indicates that the RCBD is a more efficient design than the lattice design, a value close to 100% indicates that the two designs produce comparable results and a value of relative efficiency is greater than 100% indicates that the lattice design is more efficient as compared to RCBD. Hence, based on the above relative efficiency principles, randomized complete block design (RCBD) is effective on relative efficiency less than 100% traits for by reducing experimental error, coefficient of variation, and error mean square for yield (Raza and Masood, 2009).

Table 3. 1. Skeleton of ANOVA for simple lattice design

Source of variation	Degrees of freedom (*df*)	Sum of squares	Mean squares	Computed F
Replication	r – 1	SSR	MSR	MSR/MSE
Genotype (unadj.)	$k^2 – 1$	SSG (unadj.)		
Genotype (adj.)	$k^2 – 1$	SSG (adj.)	MSG (adj.)	MSG/MSE
Blocks within replication (adj.)	r(k-1)	SSB (adj.)	MSB (adj.)	MSB/MSE
Intra-block error	(k-1) (rk-k-1)	SSE	MSE	
Total	$rk^2 – 1$	SSTot		

Where, r = Number of replications; K^2 = Number of treatments; and k = Number of plots in a block; MSR= mean square of replications; SSG (unadj.) = sum square of unadjusted genotypes; MSG (unadj.) = mean square of unadjusted genotypes; SSG (adj.) = sum square of adjusted genotypes; MSG (adj.) = mean square of adjusted genotypes; SSB (adj.) = sum square of adjusted blocks; MSB (adj.) = mean square of adjusted blocks; SSE = sum square of error; MSE = mean square of error and SSTot = sum square of total treatments.

Table 3. 2. Skeleton of ANOVA for RCBD design

Source of variation	Degree of freedom	Sum of squares	Mean squares	Computed F	Tabular F	
					5%	1%
Replication	r-1	SSR	SSR/r-1	MSR/MSE		
Treatment	t-1	SST	SST/t-1	MST/MSE		
Error	(t-1) (r-1)	SSE	SSE/(t-1) (r-1)			
Total	tr-1	SSTot				

Where, r = number of replications; t = number of treatments; SSR = sum square of replications; SST = sum square of treatment; SSE = sum square of error; SSTot = sum square of total treatments.

Estimation of mean, components of variance, phenotypic, genotypic, and environmental coefficient of variation, heritability, genetic advance and genetic advance as percentage of mean: The mean of different characters were calculated by the following method: mean = $\frac{\Sigma xi}{n}$, Where Σxi = the sum of all the observation for i^{th} character and N = Number of observations. Range was recorded by observing the lowest and the highest mean values for each character.

3.5.3. Estimating of genetic parameters

Genetic parameters were estimated by utilized the respective mean square values using the formulae given by Burton (1952), Johnson *et al*. (1955b) and Singh and Chaudhary (1999). Environmental variance (σ^2e) = MSE, Genotypic variance (σ^2g) = $\frac{MSg - MSe}{r}$ Phenotypic variance (σ^2p): $\sigma^2p = \sigma^2g + \sigma^2e$, phenotypic coefficient of variation (PCV) = $\frac{\sqrt{\sigma^2 p}}{\overline{X}} * 100$, Genotypic coefficient of variation (GCV) = $\frac{\sqrt{\sigma^2 g}}{\overline{X}} * 100$, PCV and GCV categorized as low (0-10%), moderate (10-20%) and high (20% and above) as given by Deshmukh *et al*. (1986).
Heritability is the ability of a particular trait that transmitted from one generation to another. The magnitude of heritability indicates which genotype can be recognized by its phenotypic expression. Higher heritability for a particular trait will have a chance for improving genotypes

by selection. Heritability (H^2) (broad sense) = (σ^2g / σ^2p)*100, where σ^2g is the genotypic component of variance and $\sigma^2 p$ is the phenotypic component of variance. According to Singh (2001) heritability values regarded as low (0-30%), moderate (31-60%) and high (>60%). GA and GAM were calculated by the formulae described by Johnson *et al.* (1955b).

Genetic advance (GA) = K ∗δP ∗ H, where GA = expected genetic advance, δp = phenotypic standard deviation on mean basis, H= Heritability in broad sense, K = selection differential (where k = 2.06 at 5% selection intensity). Genetic advance as percent of mean (GAM) $= \frac{GA}{\overline{X}} * 100$; where GA= genetic advance and $\overline{X}$ refers to the mean of the trait to be evaluated. Genetic advance as percent of mean is categorized as low (0-10%), moderate (10-20%) and high (>20%) as given by Johnson *et al*. (1955a).

3.5.4. Correlation and path coefficient analysis

Phenotypic and genotypic correlations between yield, yield related and quality traits were estimated using SAS proc candisc procedure (SAS, 2011). Phenotypic correlation coefficient between character x and y; rpxy $= \frac{\text{COV pxy}}{\sqrt{\sigma^2\text{px}.\sigma^2\text{py}}}$; where COV pxy = phenotypic covariance between character x and y, $\sigma^2 px$ = phenotypic variance for character x and σ^2py = phenotypic variance for character y. Phenotypic correlation coefficient between character x and y was tested for their significance by the formulae t = r/SE (rp) where, rp= phenotypic corelation; SE (r_p) = standard error of phenotypic correlation. SE (r_p) = ($\sqrt{1 - r^2}$p)/ (n-2); where, n number of genotypes tested, r_p is phenotypic correlation coefficient. Genotypic correlation coefficient between character x and y; rgxy = $\frac{\text{COV } gxy}{\sqrt{\sigma^2\text{gx}.\sigma^2\text{gy}}}$; where, rgxy = genotypic correlation coefficient between character x and y. COV gxy = genotypic covariance between character x and y. $\sigma^2 gx$ = genotypic variance for character x. $\sigma^2 gy$ = genotypic variance for character y. Genotypic correlation coefficient was tested with the formulae $t = rgxy/\ SErgxy$; $where\ SErgxy = (\sqrt{1 - r^2 gxy})/2\text{H}\ x$ * Hy**.** SErgxy = Standard error of genotypic correlation coefficient between character X and Y. Hx = heritability for character x and Hy = heritability for character y.

Both phenotypic and genotypic correlation coefficients split into direct and indirect effects on grain yield. Path coefficient analysis was done using proc IML SAS procedure. $Rij = Pij + \sum r_{ik} P_{kj}$ where, r_{ij} = mutual association between the independent character (i) and dependent character, grain yield (j) as measured by the correlation coefficients. P_{ij} = components of direct effects of the independent character (i) as measured by the path coefficients and $\sum r_{ik} p_{kj}$ = summation of components of indirect of a given independent character (i) on a given dependent character (j) via all other independent characters (k). The contribution of the remaining unknown factor was measured as the residual factor (P_R), which was calculated as; $P_R = \sqrt{(1 - \sum r_{ij} p_{ij})}$; the magnitude of P_R indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary, 1999). The path coefficient were to be rated based on the scales given below; > 1.0 = very high, 0.30 – 0.99 = high, 0.2 – 0.29 = moderate, 0.1 – 0.19 = low. If P_R value is small (for instance, nearly zero) the dependent character considered (yield) is fully explained by the variability in the independent characters, whereas higher P_R value indicates that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent character (yield). Traits showed significant genotypic correlation coefficients with yield were considered for path analysis.

3.5.5. Cluster analysis and genetic divergence

The cluster analysis was performed based on the unweighted pair group method using arithmetic average (UPGMA) and following the algorithm and sequential, agglomeration, hierarchic, and non-overlapping (SAHN) method. Clustering method of Euclidean distance matrixes follows the average linkage method by XLSTAT Statistical Software2018 (Addinsoft, 2018). Genetic distance of genotypes were estimated using Euclidean Distance (ED) calculated from quantitative traits after standardization (subtracting the mean value and dividing it by the standard deviation) as established by as follows; where; EDjk=distance between genotypes j and k; Xij and Xik = phenotype traits values of the ith traits for genotypes j and k, respectively; and n=number of phenotype traits used to calculate the distance. The calculated average distance (ED)

was used to estimate which genotypes are closest or distant to others. The genetic divergence values obtained for pairs of clusters were considered as the calculated values of Chi- square ($\chi 2$) and were tested for significance at (1% and 5%) probability levels against the tabulated value of $\chi 2$ for 'P' degree of freedom, where P is the number of parameters considered (Singh and Chaudhary, 1985).

3.5.6. Principal component analysis

The principal component analysis (PCA) was done with subsequent Pearson correlation coefficients applied to construct a dendrogram to observe the groupings and relatedness among the genotypes. The trait mean data of the test genotypes were used for principal components analysis in order to identify the major traits accounting for much of the gross observed variability among the genotypes. Principal components were estimated based on the pre- standardized original data using the XLSTAT statistical software 2018 (Addinsoft, 2018). The first PCA value (Y1) is given by the linear combination of the variables X1, X2…Xp. Y1 = a11X1+a12+…a1pXp. The second principal component was calculated in the same way, Y2=a21X1+a22X2+…a2pXp. This continues until a total of principal components have been calculated equals to the original number of variables. At this point, the sum of variances of all the principal components is equals to the sum of the variances of all of the variables. Principal components having Eigen value greater than one were considered as significant and presented in the result.

Chapter 4. RESULTS AND DISCUSSION

4.1. Variability of Garlic Genotypes

The analysis of variance (ANOVA) showed that the genotypes showed highly significance ($P < 0.01$) difference for the traits of 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, total soluble solid, bulb weight, clove weight and total bulb yield (Tables 4.1 and 4.2). In addition, leaf width showed significance difference ($p < 0.05$) among genotypes. This finding indicates the presence of genetic variability among genotypes. Similar result was reported on leaf width by Azene Tesfaye *et al*. (1970). 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, total bulb yield by Singh and Singh (2010); Singh *et al*. (2013); Rahim *et al*. (2019). Choudhary *et al*. (2017) also reported similar findings on plant height, leaf number, maturity date, pseudo stem height, neck diameter, bulb weight, clove number, total bulb yield per hectare and total soluble solid.

Table 4. 1. Mean squares for three traits of garlic genotypes using simple lattice design

Traits	Rep	Genotype adjusted	Block within rep adjusted	Intra block error	RE
	(1)	(48)	(12)	(36)	
LW	0.02ns	0.03*	0.02	0.02	101.36
PH	55.58*	22.29**	17.11	9.03	109.45
MD	167.18**	18.18**	12.02	9.02	101.95

*Note: ** = Significant at 1% probability level and * = Significant at 5% probability level; LW = leaf width; PH = plant height; MD = days to 75% of physiological maturity date and RE = relative efficiency.*

Table 4. 2. Mean squares for 13 traits in garlic using RCBD

Traits	Rep (1)	Genotype (48)	Error	RE
LN	0.32ns	1.32**	0.40	88.46
LL	5.81ns	13.53**	5.26	90.19
PSH	22.52ns	26.12**	10.14	95.06
ND	0.013ns	0.03**	0.01	93.8
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
TBY	0.23ns	2.35**	0.24	98

*Note: ** = Significant at 1% probability level and * = Significant at 5% probability level; LN= leaf number; LL = leaf length; PSH = pseudo stem height; ND = neck diameter; BL= bulb length; BD = bulb diameter; CL = clove length; CD = clove diameter; CN = clove number; TSS = total soluble solid; BW = bulb weight; CW = clove weight; TBY = total bulb yield; RE = relative efficiency; RCBD = randomized complete block design and Rep = replication.*

4.2. Mean Performance of Genotypes

Genotypes revealed a wide range of variability in all traits (Table 4.3). The mean values also revealed that genotypes showed significant variation among traits. An extended 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 had been reported by Choudhary *et al*. (2017); Ranjitha *et al*. (2018) and Nguyen (2020). These high ranges of variation among different genotypes can have high contribution for breeding values for further improvement of desired traits. The genotype G37-3 had high number of leaves (11.3) while G50-1 had the fewest leaves (7.25). In the range of leaf width, genotype G37-3 had the broadest leaf (1.34 cm) while G-007/18 had the narrowest leaf (0.81 cm). In the range of leaf length, genotype of 009/04 and G16-1 had the longest (31.27 cm) and shortest (19.63 cm) leaf respectively. In the case of pseudo stem height, the longest and shortest pseudo stem lengths were found in the G5-2 (26 cm) and HL (12.05 cm) genotypes. The highest plant height was recorded in the genotype 009/04(53.8 cm) while the lowest plant height was observed in the genotype G16-1(36.2 cm). Neck diameter was statistically significant for all genotypes, with genotype 017/09 was the largest (1.03 cm) and genotype G16-1 was the lowest (0.47 cm). The physiological maturity date was found to be significant in all genotypes. The most recent and earliest physiological maturity dates were 017/09, 009/04, G-044/18, G-007/18 and HL (114 days) and G14-1 and G17-1 (102 days) respectively. Similar results were reported by Nguyen, (2020) pseudo stem height, plant height, neck diameter, bulb diameter and bulb weight.

The highest bulb length was recorded in genotype 009/04 (39.54 cm) while the lowest bulb length was recorded in the genotype G-067/18 and G36-1 (27.81cm). Of all genotypes, genotypes 009/04(42.79 mm) and G36-1(24.3 mm) had the largest and smallest bulb diameters respectively. G18-2 (32.14 mm) and HL (19.74 mm) genotypes had the longest and shortest clove lengths respectively. G14-2 genotypes had the largest (22.9 mm) clove diameters of all genotypes. On the other hand, G36-1 had the smallest (13.17 mm) clove diameter. Genotypes G-011/18 (13.7) and G44-1 (5.6) had the highest and lowest clove numbers from all genotypes respectively. The highest and lowest total soluble solid values were found in the G10-2 (32.06 brix) and G-028/18 (21.02 brix) genotypes respectively. The genotype G5-2 had the highest bulb

weight (22.64 gm) and the genotype G36-1 had the lowest bulb weight (6.48 gm) per plant. The genotype G14-2 had the highest clove weight (0.61 gm) while the genotype G-007/18 had the lowest clove weight (0.13 gm). G5-2(5.98 t ha^{-1}) and G36-1(1.55 t ha^{-1}) genotypes recorded the highest and lowest fresh bulb yields per hectare respectively. Similar results were reported on the traits of leaf number, plant height, leaf length, clove number, bulb diameter, bulb weight and total bulb yield by Rahim *et al*. (2019); Nguyen (2020).

Table 4. 3. Ranges, means, standard errors of means and coefficient of variation for 16 quantitative traits of garlic genotypes

Traits	Range	Mean ± SE	CV (%)
LN	7.25-11.3	8.67±0.09	7.736
LW	0.805-1.335	1.08±0.02	11.556
LL	19.63-31.265	25.67±0.31	9.407
PSH	12.05-26	19.61±0.43	16.659
PH	36.2-53.8	45.94±0.45	6.541
ND	0.465-1.025	0.71±0.01	12.271
MD	102.5-114	108.84±0.43	2.759
BL	27.81-39.55	33.01±0.32	7.274
BD	24.3-42.78	34.71±0.42	9.182
CL	19.74-32.14	25.38±0.32	9.351
CD	13.17-22.9	16.85±0.24	10.465
CN	5.6-13.7	8.63±0.24	13.264
TSS	21.02-32.065	27.44±0.33	9.144
BW	6.475-22.635	13.72±0.44	24.909
CW	0.1335-0.6055	0.35±0.01	21.354
TBY	1.5625-5.971	3.69±0.11	13.412

LN = leaf number; LW = leaf width; LL = leaf length; PSH = pseudo stem height; PH = plant height; ND = neck diameter; MD = maturity date; BL = bulb length; BD = bulb diameter; CL= clove length; CD = clove diameter; CN = clove number; TSS = total soluble solid; BW = bulb weight; CW = clove weight; TBY = total bulb yield; CV = coefficient of variation and SE = standard error of the mean

4.3. Variability in Qualitative Traits

Results showed that green leaf color accounted for more than half of the genotypes (61.22%) followed by light green leaf color (22.45%) and the rest genotypes had dark leaf color (16.22%). Erect intermediate and prostrate of foliage attitudes accounted for 12.24%, 61.22 %, and 26.54% of the genotypes respectively. White, cream, beige and light violate of bulb color were found in 12.24%, 28.57%, 51.02%, and 8.17% of genotypes respectively. Light brown, brown and violate of clove color were found in 46.94%, 34.69 % and 18.37% of the genotypes respectively. Similar result was reported by Wang *et al*. (2014). The Shannon's diversity indexes (H) of garlic qualitative traits ranged from the lowest (monomorphic) of 0.91 for plant habit to the higher of 1.16 (polymorphic) for bulb color.

Table 4. 4. Estimate of frequency, proportion and Shannon-Weiner diversity index (H) of qualitative traits of 49 Ethiopian garlic genotypes

Traits	Descriptions	Code	Frequency of Genotypes	Proportion / Percentage	Shannon-Weiner diversity index (H)	Evenness (E)
Plant habit /type	Erect	1	6	16.22	0.91	0.66
	Intermediate	2	30	61.22		
	Spreading/prostrate	3	13	22.25		
Leaf color	Green	1	30	61.22	0.93	0.67
	Light green	2	11	26.54		
	Dark green	3	8	12.24		
Bulb color	White	1	6	12.24	1.16	0.84
	Light yellow/cream	2	14	28.57		
	Light red/beige	3	25	51.02		

	Purplish red/light	4	4	8.17		
Clove color	Light brown	1	23	46.94	1.03	0.75
	Brown	2	17	34.69		
	Violate	3	9	18.37		

4.4. Estimating of Genetic Parameters

4.4.1. Phenotypic and genotypic variance

Phenotypic coefficient of variation ranged from 3.39% to 39.99%. High phenotypic coefficient of variation (>20%) was observed for clove weight (39.99%) followed by 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 by Rakesh *et al*. (2016); Nguyen (2020) on clove weight, bulb weight and clove number. Moderate magnitude of phenotypic coefficient of variation (10-20%) was observed for 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 minimum values of phenotypic coefficient of variation were observed for bulb length (9.71%), plant height (8.61%) and maturity date (3.39%). The phenotypic coefficient of variation alone does not represent the genetic variability of genotypes; thus it is important to work out genotypic variation (Table 4.5).

The data has recorded in a wide range of genotypic coefficient of variation of traits ranged from 1.97%- 27.84%. Total bulb yield (27.84%) had the highest genetic coefficient of variation followed by clove weight (26.41%), clove number (24.71%) and bulb weight (21.12%). Moderate (10-20%) genetic coefficient of variation was observed for pseudo stem height (14.42%) and neck diameter (13.71%). Low (<10%) magnitude of genotypic coefficient of variation was observed for clove diameter (9.75%), clove length (8.66%), bulb diameter (8.35%), total soluble solid (8.15%), leaf length (7.92%), leaf number (7.82%), bulb length (6.91%), leaf width (6.68%), plant height (5.61%) and maturity date (1.97%). Similar results were reported by

Singh *et al*. (2013); Rakesh *et al*. (2016), Vatsyayan and Dhall (2016); Bhatt *et al*. (2017); Kumar *et al*. (2017) in high estimates of phenotypic and genotypic coefficient of variation for total bulb yield per hectare. Similarly high estimates of phenotypic and genotypic coefficient of variation for clove weight, total bulb yield, bulb weight and clove number were observed by (Kumari ,2021; Sharma and Chauhan, 2021).

4.4.2. Heritability and genetic advance

Estimation of heritability for traits studied in (table 4.5). Most traits in the study showed high heritability percentage. The heritability values for broad sense heritability ranged from 17.27% for leaf width to 81.42% for total bulb yield. Total bulb yield (81.42%), clove number (78.71%). Moderate heritability was recorded in neck diameter (57.1) followed by leaf number (53.62%), bulb length (50.65%), clove length (48.59%), clove diameter (48.48%), bulb diameter (47.71%), total soluble solid (46.69%), bulb weight (44.6%), pseudo stem height (44.08%), leaf length (44.02%) clove weight (43.62%), plant height (42.36%) and physiological maturity date (33.69%). Low heritability in broad sense was estimated in leaf width (17.27%) (Table 4.5). High heritability for the above traits explained that they were least effected by environmental variations and selection based on phenotypic performance would be reliable. The findings were in consistent with the findings of Tsega *et al*. (2010).

In this study, genetic advance as percent of mean ranged from 2.35% for days to physiological maturity to 51.74% for total bulb yield (Table 4.5). The highest genetic advance as percent of mean was recorded by total bulb yield (51.74) followed by clove number per bulb (45.17%), clove weight (35.93%), bulb weight (29.06%) and neck diameter (21.35%). Moderate genetic advance recorded for 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 (11.47%), leaf length (10.83%) and bulb length (10.13%). Low genetic advance observed for leaf width (5.72%), plant height (7.52%) and physiological maturity date (2.35%). Similar finding was reported by Chatoo *et al*. (2018) on total bulb yield, clove weight, and clove number and bulb weight. High heritability combined with a high genetic advance as present of mean is typically more useful than heritability alone in predicting improvement under selection (Johnson *et al*.,

1955a). Total bulb yield (81.42% and 51.74%), clove number (78.71% and 45.17%), and clove weight (43.62% and 35.93%) all showed high heritability and genetic advance as percent of mean in the current study with similar findings observed on clove number, clove weight and total bulb yield Yebirzaf (Yeshiwas *et al*., 2018; Sharma and Chauhan, 2021). Thus, high genetic advance combined with high heritability provides the most successful situation for selection. Thus, these traits are genetically governed by additive gene action and they can be further improved through mass selection (Dubey *et al*., 2010).

Table 4. 5. Estimates of genetic coefficient of variation parameters for sixteen quantitative traits

Traits	σ^2g	σ^2p	σ^2e	GCV (%)	PCV (%)	ECV (%)	H^2 (%)	GA	GAM (%)
LN	0.46	0.86	0.40	7.82	10.68	7.28	53.62	1.02	11.80
LW	0.01	0.03	0.02	6.68	16.06	11.56	17.27	0.06	5.72
LL	4.13	9.39	5.26	7.92	11.94	8.93	44.02	2.78	10.83
PSH	7.99	18.13	10.14	14.42	21.72	16.24	44.08	3.87	19.72
PH	6.63	15.66	9.03	5.61	8.61	6.54	42.36	3.45	7.52
ND	0.01	0.02	0.01	13.71	18.15	11.88	57.10	0.15	21.35
MD	4.58	13.60	9.02	1.97	3.39	2.76	33.69	2.56	2.35
BL	5.20	10.27	5.07	6.91	9.71	6.82	50.65	3.34	10.13
BD	8.40	17.61	9.21	8.35	12.09	8.74	47.71	4.12	11.88
CL	4.83	9.94	5.11	8.66	12.42	8.90	48.59	3.16	12.43
CD	2.70	5.57	2.87	9.75	14.00	10.05	48.48	2.36	13.99
CN	4.55	5.78	1.23	24.71	27.85	12.85	78.71	3.90	45.17
TSS	5.00	10.71	5.71	8.15	11.93	8.71	46.69	3.15	11.47
BW	8.40	18.84	10.43	21.12	31.62	23.54	44.60	3.99	29.06
CW	0.01	0.02	0.01	26.41	39.99	20.83	43.62	0.13	35.93
TBY	1.06	1.30	0.24	27.84	30.85	13.30	81.42	1.91	51.74

Note: σ^2g = genotypic variance; σ^2p = phenotypic variance; σ^2e environmental variance; GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; H^2 = broad sense heritability; GA = Genetic Advance; GAM = genetic advance as percent of mean; LN = leaf number; LW = leaf width; LL = leaf length; PSH = pseudo stem height; PH = plant height; ND = neck diameter; MD = maturity date; BL = bulb length; BD = bulb diameter; CL= clove length; CD = clove diameter; CN = clove number; TSS = total soluble solid; BW = bulb weight; CW = clove weight; TBY = total bulb yield.

4.5. Correlations of Traits

4.5.1. Genotypic correlation among the sixteen traits

The present study in genotypic correlation, total bulb yield per hectare showed significant positive correlation with leaf number (0.39), leaf width (0.65), leaf length (0.72), pseudo stem height (0.82), plant height (0.75), neck diameter (0.43), bulb length (0.76), bulb diameter (0.81), clove length (0.7), clove diameter (0.63), bulb weight (0.82) and clove weight (0.81) (Table 4.6). Similar results were found by Prajapati *et al*. (2016); Bhatt *et al*. (2017), (Chotaliya and Kulkarni (2017) on the traits of total bulb yield, leaf length, pseudo stem height, plant height, neck diameter, bulb weight and clove weight.

Similarly, traits that revealed positive and significant correlation among themselves were found in clove weight with leaf width (0.52), leaf length (0.59), pseudo stem height (0.77), plant height (0.54), maturity date (0.44), bulb length (0.65), bulb diameter (0.69), clove length (0.78), clove diameter (0.7), clove number (0.35) and bulb weight (0.74). Bulb weight was positively correlated with leaf number (0.55), leaf width (0.75), leaf length (0.76), pseudo stem height (0.76), plant height (0.75), neck diameter (0.56), bulb length (0.71), bulb diameter (0.81), clove length (0.8) and clove diameter). Clove number with leaf number (0.35), neck diameter (0.42), and maturity date (0.61). Clove diameter was positively correlated with leaf number (0.29), leaf width (0.55), leaf length (0.61), pseudo stem length (0.67), plant height (0.53), bulb length (0.63), and bulb diameter (0.69) and clove length (0.68) but negatively correlated with physiological maturity date. Clove length with leaf number (0.44), leaf width (0.62), leaf length (0.75), pseudo stem length (0.64), plant height (0.7), neck diameter (0.46), bulb length (0.68) and bulb diameter but negatively correlated with pseudo stem height. Bulb diameter was positively correlated with leaf number (0.39), leaf width (0.64), leaf length (0.7), pseudo stem height (0.78), plant height (0.63), neck diameter (0.43) and bulb length (0.79) but negatively correlated with physiological maturity date. Bulb length was positively correlated with leaf number (0.44), leaf width (0.66), leaf length (0.66), pseudo stem height (0.6), plant height (0.6) and neck diameter (0.45). Physiological maturity date was positively correlated with leaf number (0.3) and neck diameter (0.43) but negatively correlated with pseudo stem height. And plant neck diameter with leaf

number (0.42), leaf width (0.61), and leaf length (0.72) and plant height (0.71). Plant height with leaf number (0.64), leaf width (0.71), leaf length (0.84) and pseudo stem height (0.61). Plant pseudo stem height with leaf width (0.54) and leaf length (0.59). Besides leaf length with leaf number (0.71) and leaf width (0.8) with leaf number (0.66). Similar findings reported by Ganie and Jan (2013); Sable (2020) on leaf number, leaf width, leaf length, pseudo stem length, plant height, neck diameter, bulb length, bulb diameter, clove length, clove diameter, bulb weight, and clove weight and these traits could aid in the garlic genetic improvement program. And similar findings was reported by Yebirzaf Yeshiwas *et al*. (2018) on the traits plant height, leaf number, bulb weight, clove weight and bulb diameter were strong significant correlation with total bulb yield.

4.5.2. Phenotypic correlation coefficients among the sixteen traits

Phenotypic correlation is the outcome of both genotypic and environmental effects that offers information among visible traits. Leaf number was positively correlated with leaf width (0.56), leaf length (0.62), pseudo stem height (0.31), plant height (0.57), neck diameter (0.59), and bulb length (0.34) bulb diameter (0.34), clove length (0.39), clove diameter (0.24), clove number (0.3), bulb weight (0.52) and total bulb yield (0.36). Leaf width has been found to be positively associated with leaf length (0.7), pseudo stem height (0.52), plant height (0.58), neck diameter (0.47), bulb length (0.57), bulb diameter (0.57), clove length (0.53), clove diameter (0.47), bulb weight (0.72), clove weight (0.48) and total bulb yield (0.56). Leaf length has shown positively correlated with pseudo stem height (0.55), plant height (0.74), bulb length (0.57), neck diameter (0.59), bulb diameter (0.65), clove length (0.65), clove diameter (0.47), bulb weight (0.73), clove weight (0.5) and total bulb yield (0.66). Pseudo stem height was positively correlated with plant height (0.52), bulb length (0.53), and bulb diameter (0.71), clove length (0.6), and clove diameter (0.62), total soluble solid (0.31), bulb weight (0.74), clove weight (0.73) and total bulb yield (0.77). Similar findings were reported by Sharma *et al*. (2016). But physiological maturity date and clove number were negatively correlated. Plant height has been found to be positively correlated with neck diameter (0.62), bulb length (0.47), bulb diameter (0.55), clove length (0.56), clove diameter (0.42), clove number (0.21), bulb weight (0.65) and clove weight (0.47) as well as total bulb yield (0.66). Neck diameter has been linked to physiological maturity date

(0.43), bulb length (0.35), bulb diameter (0.35), clove length (0.35), clove number (0.38), bulb weight (0.47) and total bulb yield (0.4). The Physiological maturity date has shown positively correlated with clove number (0.55) while negatively correlated with bulb length, bulb diameter, clove length, clove diameter, total soluble solid, leaf length, bulb weight, clove weight and total bulb yield. Similar agreements were reported by Benke *et al*. (2020a) on physiological maturity date. Bulb length was positively correlated with bulb diameter (0.71), clove length (0.61), and clove diameter (0.49), bulb weight (0.62), clove weight (0.59) and total bulb yield (0.67).

Bulb diameter was positively correlated with clove length (0.65), clove diameter (0.6), total soluble solid (0.25), and bulb weight (0.74), and clove weight (0.65) and total bulb yield (0.75). Clove length has shown positively correlated with clove diameter (0.61), bulb weight (0.75), clove weight (0.74) and total bulb yield (0.65). Clove diameter was positively correlated with total soluble solid (0.25), bulb weight (0.58), clove weight (0.67) and total bulb yield (0.58). Clove number was negatively correlated with clove weight and total bulb yield. This indicates that many of number of cloves per bulb can not necessarily increase bulb weight. Bulb weight has shown positively correlated with clove weight (0.71) and total bulb yield (0.76). Clove weight was positively correlated with total bulb yield (0.77). Low phenotypic value might be due to significant relations of genotypes with environments. Total bulb yield revealed positive and significance genotypic and phenotypic correlations with plant height, number of leaves per plant, pseudo stem height and bulb weight. Similar findings were reported by Dubey *et al*. (2010) and Tsega *et al*. (2010) on plant height, pseudo stem height and bulb weight to the total bulb yield.

Table 4. 6. Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients

	LN	LW	LL	PSH	PH	ND	MD	BL	BD	CL	CD	CN	TSS	BW	CW	TBY
LN		0.56***	0.62***	0.31**	0.57***	0.59***	0.19ns	0.34**	0.34**	0.39***	0.24*	0.30**	-0.04ns	0.52***	0.19ns	0.36**
LW	0.66***		0.70***	0.52***	0.58***	0.47***	-0.05ns	0.57***	0.57***	0.53***	0.47***	-0.06ns	0.07ns	0.72***	0.48***	0.56***
LL	0.71***	0.80***		0.55***	0.74***	0.59***	0.01ns	0.57***	0.65***	0.65***	0.47***	0.07ns	0.10ns	0.73***	0.50***	0.66***
PSH	0.27ns	0.54***	0.59***		0.52***	0.11ns	-0.48***	0.53***	0.71***	0.60***	0.62***	-0.31**	0.31**	0.74***	0.73***	0.77***
PH	0.64***	0.71***	0.84***	0.61***		0.62***	0.08ns	0.47***	0.55***	0.56***	0.42***	0.21*	0.02ns	0.65***	0.47***	0.66***
ND	0.72***	0.61***	0.72***	0.17ns	0.71***		0.43***	0.35**	0.35**	0.35**	0.15ns	0.38***	-0.16ns	0.47***	0.16ns	0.40***
MD	0.30*	-0.04Ns	0.02Ns	-0.47**	0.01ns	0.43**		-0.25**	-0.27**	-0.29**	-0.41***	0.55***	-0.21*	-0.15ns	-0.41***	-0.20*
BL	0.44**	0.66***	0.66***	0.60***	0.60***	0.45**	-0.24ns		0.71***	0.61***	0.49***	-0.15ns	0.07ns	0.62***	0.59***	0.67***
BD	0.39**	0.64***	0.70***	0.78***	0.63***	0.43**	-0.29*	0.79***		0.65***	0.60***	-0.15ns	0.25**	0.74***	0.65***	0.75***
CL	0.44**	0.62***	0.75***	0.64***	0.70***	0.46**	-0.28ns	0.68***	0.70***		0.61***	-0.15ns	0.03ns	0.75***	0.74***	0.65***
CD	0.29*	0.55***	0.61***	0.67***	0.53***	0.22ns	-0.40**	0.63***	0.69***	0.68***		-0.46***	0.25**	0.58***	0.67***	0.58***
CN	0.35**	-0.02ns	0.07Ns	-0.28*	0.25ns	0.42**	0.61***	-0.13ns	-0.15ns	-0.15ns	-0.44**		-0.28**	0.01ns	-0.37**	-0.07ns
TSS	-0.10ns	0.08ns	0.07Ns	0.42**	-0.05ns	-0.28*	-0.32*	0.10ns	0.25ns	0.01ns	0.27ns	-0.32ns		0.16ns	0.16ns	0.14ns
BW	0.55**	0.75***	0.76***	0.76***	0.75***	0.56***	-0.15ns	0.71***	0.81***	0.80***	0.66***	0.05ns	0.14ns		0.71***	0.76***
CW	0.18ns	0.52**	0.59***	0.77***	0.54***	0.22ns	-0.44**	0.65***	0.69***	0.78***	0.70***	-0.35**	0.17ns	0.74***		0.77***
TBY	0.39**	0.65***	0.72***	0.82***	0.75***	0.43**	-0.23ns	0.76***	0.81***	0.70***	0.63***	-0.04ns	0.14ns	0.82***	0.81***	

*Note: *, **/*** significance at 0.05 and 0.01 probability levels, respectively; LN = leaf number; LW = leaf width; LL = leaf length; PSH = pseudo stem height; PH = plant height; ND = neck diameter; MD = maturity date; BL = bulb length; BD = bulb diameter; CL= clove length; CD = clove diameter; CN = clove number; TSS = total soluble solid; BW = bulb weight; CW = clove weight; TBY = total bulb yield.*

4.6. Path Coefficient Analysis

4.6.1. Genotypic direct and indirect relationships

In this study, path coefficient analysis was performed for understudied characters using genotypic and phenotypic correlation coefficients with total bulb yield per hectare as the dependable variable, to see the causal factor and to identify the components that are responsible for producing total bulb yield per hectare and the rest of the characters were considered as independent variable. As a result, the path coefficient analysis divides the overall correlation coefficient of various traits into direct and indirect effects on total bulb yield with the number of direct and indirect effects equal to the total genotypic correlation. The direct and indirect genotypic effects of traits on bulb yield are discussed in (table 4.7). Along with the genotypic path coefficient study, pseudo stem height (0.41), clove weight (0.39) and bulb length (0.25) all had a strong and positive direct effect on bulb yield and were found to be the most significant While bulb diameter (0.07), maturity date (0.07), leaf width (0.04), clove diameter (0.02) and bulb weight (0.01) had a very low or negligible and positive direct effect on bulb yield. The clove length, leaf number, total soluble solid and neck diameter had the greatest negative direct effect on bulb yield per hectare. Consistent results have been reported by Ganie and Jan (2013); Panse (2013) on high direct effect of clove weight and bulb weight for total bulb yield.

Characters like pseudo stem height, clove weight and bulb length was the most significant determinants of total bulb yield. The high indirect effect also revealed that clove length, bulb diameter, and leaf length and bulb weight were the most influential traits on total bulb yield per hectare. As a result, direct selection of high direct effect traits convoyed by high indirect value traits is likely to increase bulb yield per hectare. The bulb yield per hectare was determined in part by an overall observation of path coefficient analysis of bulb yield with its components, namely pseudo stem height, clove weight, and bulb length.

4.6.2. Phenotypic direct and indirect relationships

The phenotypic path coefficient study showed pseudo stem height (0.42), clove weight (0.39), bulb length (0.18), clove number (0.17) and plant height all had a significant and positive direct impact on total bulb yield per hectare whereas leaf number, neck diameter and clove length had significant and negative indirect effect on bulb yield per hectare (Tables (4.8). The residual (unexplained) variation in the path analysis came out were 0.11 based on genotypic correlations and 0.17 based on phenotypic correlations among the traits studied for all the genotypes. This residual variation signified that there was still unexplained and unaccounted variations left among the genotypes which could not have explained by the sixteen traits studied. To explain the same, some more morphological, and biochemical characters would have been studied. Similar results found by Dejen Bikis *et al*. (2021); Chotaliya and Kulkarni (2017) on bulb length, plant height and pseudo stem height for the total bulb yield.

Thus, path analysis revealed that increase in clove weight and number of cloves per bulb reflected in an increase in total bulb yield. Also, selection for higher clove weight per plant may lead to increase in total bulb yield. Moreover, increase in leaf and clove number results in decrease in total bulb yield. Leaf number, clove length, total soluble solid and leaf width were negative direct effect on total bulb yield both in phenotypically and genotypically path coefficients. Similar results were found by Kuma *et al.* (2017) on leaf number, clove length and leaf width. Similar findings were reported by Ghodhani and Singh (2000); Dubey *et al*. (2010); Panse (2013) on high positive direct contribution of clove weight and bulb length on total bulb yield. And on the other hand Singh *et al. (*2011) on indirect positive contribution of plant height, number of leaves per plant, number of cloves per bulb were appreciable for the total bulb yield.

Table 4. 7. Genotypic path coefficient analysis direct (diagonal and bold) and indirect effects of traits on bulb yield of garlic

	LN	LW	LL	PSH	PH	ND	MD	BL	BD	CL	CD	CN	TSS	BW	CW	rg
LN	**-0.12**	0.03	0.09	0.11	0.07	-0.02	0.02	0.11	0.03	-0.08	0.00	0.06	0.01	0.01	0.07	0.39**
LW	-0.08	**0.04**	0.10	0.22	0.08	-0.02	0.00	0.16	0.04	-0.11	0.01	0.00	-0.01	0.01	0.20	0.65***
LL	-0.08	0.04	**0.12**	0.24	0.09	-0.02	0.00	0.17	0.05	-0.14	0.01	0.01	-0.01	0.01	0.23	0.72***
PSH	-0.03	0.02	0.07	**0.41**	0.07	0.00	-0.03	0.15	0.05	-0.12	0.01	-0.05	-0.04	0.01	0.30	0.82***
PH	-0.07	0.03	0.10	0.25	**0.11**	-0.02	0.00	0.15	0.04	-0.13	0.01	0.05	0.00	0.01	0.21	0.75***
ND	-0.08	0.03	0.09	0.07	0.08	**-0.03**	0.03	0.11	0.03	-0.08	0.00	0.08	0.02	0.01	0.08	0.43**
MD	-0.03	0.00	0.00	-0.19	0.00	-0.01	**0.07**	-0.06	-0.02	0.05	-0.01	0.11	0.03	0.00	-0.17	-0.23ns
BL	-0.05	0.03	0.08	0.24	0.07	-0.01	-0.02	**0.25**	0.05	-0.12	0.01	-0.02	-0.01	0.01	0.25	0.76***
BD	-0.05	0.03	0.08	0.32	0.07	-0.01	-0.02	0.20	**0.07**	-0.13	0.01	-0.03	-0.02	0.01	0.27	0.81***
CL	-0.05	0.03	0.09	0.26	0.08	-0.01	-0.02	0.17	0.05	**-0.18**	0.01	-0.03	0.00	0.01	0.31	0.70***
CD	-0.03	0.02	0.07	0.27	0.06	-0.01	-0.03	0.16	0.05	-0.12	**0.02**	-0.08	-0.02	0.01	0.27	0.63***
CN	-0.04	0.00	0.01	-0.11	0.03	-0.01	0.04	-0.03	-0.01	0.03	-0.01	**0.18**	0.03	0.00	-0.14	-0.04ns
TSS	0.01	0.00	0.01	0.17	-0.01	0.01	-0.02	0.02	0.02	0.00	0.00	-0.06	**-0.08**	0.00	0.06	0.14ns
BW	-0.06	0.03	0.09	0.31	0.08	-0.01	-0.01	0.18	0.05	-0.15	0.01	0.01	-0.01	**0.01**	0.29	0.82***
CW	-0.02	0.02	0.07	0.31	0.06	-0.01	-0.03	0.16	0.05	-0.14	0.01	-0.07	-0.01	0.01	**0.39**	0.81***

Note: residual = 0.11; rg = genotypic correlation; LN = leaf number; LW = leaf width; LL = leaf length; PSH = pseudo stem height; PH = plant height; ND = neck diameter; MD = maturity date; BL = bulb length; BD = bulb diameter; CL= clove length; CD = clove diameter; CN = clove number; TSS = total soluble solid; BW = bulb weight; CW = clove weight; TBY = total bulb yield.

Table 4. 8. Phenotypic path coefficient analysis of direct (diagonal and bold) and indirect effects of traits on bulb yield of garlic

	LN	LW	LL	PSH	PH	ND	MD	BL	BD	CL	CD	CN	TSS	BW	CW	rp
LN	**-0.11**	-0.01	0.05	0.13	0.06	0.05	0.02	0.06	0.04	-0.03	0.01	0.05	0.00	-0.04	0.07	0.36**
LW	-0.06	**-0.03**	0.06	0.22	0.06	0.04	-0.01	0.10	0.06	-0.04	0.02	-0.01	0.00	-0.05	0.19	0.56***
LL	-0.07	-0.02	**0.08**	0.23	0.08	0.05	0.00	0.10	0.07	-0.05	0.02	0.01	0.00	-0.05	0.20	0.66***
PSH	-0.03	-0.01	0.05	**0.42**	0.05	0.01	-0.05	0.10	0.08	-0.05	0.03	-0.05	-0.01	-0.05	0.29	0.77***
PH	-0.06	-0.01	0.06	0.22	**0.10**	0.05	0.01	0.08	0.06	-0.04	0.02	0.04	0.00	-0.05	0.18	0.66***
ND	-0.07	-0.01	0.05	0.05	0.06	**0.09**	0.05	0.06	0.04	-0.03	0.01	0.07	0.00	-0.03	0.06	0.40***
MD	-0.02	0.00	0.00	-0.20	0.01	0.04	**0.10**	-0.04	-0.03	0.02	-0.02	0.09	0.00	0.01	-0.16	-0.20*
BL	-0.04	-0.01	0.05	0.23	0.05	0.03	-0.03	**0.18**	0.08	-0.05	0.02	-0.02	0.00	-0.04	0.23	0.67***
BD	-0.04	-0.01	0.06	0.30	0.06	0.03	-0.03	0.13	**0.11**	-0.05	0.03	-0.03	-0.01	-0.05	0.25	0.75***
CL	-0.04	-0.01	0.05	0.25	0.06	0.03	-0.03	0.11	0.07	**-0.08**	0.03	-0.02	0.00	-0.05	0.29	0.65***
CD	-0.03	-0.01	0.04	0.26	0.04	0.01	-0.04	0.09	0.07	-0.05	**0.05**	-0.08	-0.01	-0.04	0.26	0.58***
CN	-0.03	0.00	0.01	-0.13	0.02	0.03	0.06	-0.03	-0.02	0.01	-0.02	**0.17**	0.01	0.00	-0.14	-0.07ns
TSS	0.00	0.00	0.01	0.13	0.00	-0.01	-0.02	0.01	0.03	0.00	0.01	-0.05	**-0.02**	-0.01	0.06	0.14ns
BW	-0.06	-0.02	0.06	0.31	0.07	0.04	-0.02	0.11	0.08	-0.06	0.03	0.00	0.00	**-0.07**	0.28	0.76***
CW	-0.02	-0.01	0.04	0.31	0.05	0.01	-0.04	0.11	0.07	-0.06	0.03	-0.06	0.00	-0.05	**0.39**	0.77***

Note: residual = 0.17; rp = phenotypic correlation; LN = leaf number; LW = leaf width; LL = leaf length; PSH = pseudo stem height; PH = plant height; ND = neck diameter; MD = maturity date; BL = bulb length; BD = bulb diameter; CL= clove length; CD = clove diameter; CN = clove number; TSS = total soluble solid; BW = bulb weight; CW = clove weight; TBY = total bulb yield.

4.7. Genetic Divergence Analysis

4.7.1. Cluster analysis

The principal component analysis clearly explained that some of the studied genotypes were diverse from others while many others are similar and positioned near to each other on biplot. But clear-cut grouping of these genotypes not occurred by PCA. So to differentiate the genotypes on the basis of similarity and differences, they were subjected to cluster analysis among the phenotypic traits. The 49 garlic genotypes considered in the present study were grouped into five clusters (Figure 4.1 and Table 4.9). The variation observed among the genotypes based on morphological traits can show variability among the existing garlic genotypes. The first number of clusters (cluster-1 = 19) had the largest (38.78%) and the fourth cluster (cluster-4 = 1) had the smallest (2.04%) number of genotypes considered respectively.

4.7.2. Cluster distances and means of garlic genotypes

The cluster means showed the average result of all traits in each cluster. Cluster means also showed significant differences for all the studied traits as shown in (Table 4.9). Highest mean value for maturity days, plant height, bulb diameter, bulb length, total soluble solid, leaf length and clove length was seen in cluster-1. Cluster-2 contains the highest value for maturity, plant height, bulb diameter, bulb length, leaf length and clove length. Cluster-3 had fourteen genotype, was characterized by highest mean for maturity days and followed by plant height, bulb diameter, bulb length, total soluble solid, clove length, leaf length and bulb weight. Cluster -4 contained one genotype, was characterized by highest mean for maturity days and followed by plant height, bulb diameter, bulb length, total soluble solid, clove length and leaf length. Clusters with single genotype indicated their independent identity and importance due to various unique characters possessed by them. A similar finding was reported by Singh *et al*. (2014) on single genotypes clustered in one class from nineteen garlic genotypes. Cluster 5 had three genotypes. This cluster is characterized by highest cluster mean for maturity days followed by plant height, bulb diameter, bulb length, total soluble solid, clove length, leaf length and pseudo stem height. Similar results have been reported for total soluble solid, total bulb yield, clove weight and

maturity days Singh *et al*. (2014). Also similar findings reported by Islam *et al*. (2020) on bulb diameter, bulb length, clove length and plant height.

Table 4. 9. The distribution of 49 garlic genotypes into two clusters based on Euclidean distance

Cluster number	Number of Genotypes	Name of genotypes
1	19	G50-1, G38-2, G44-1, G1-1, G39-2, G3-2, G13-3, G44-2, G29-1, G-070/18, G14-1, 091/04, G35-1, G40-1, G24-1, G10-2, G17-1, G42-1 and G10-1
2	12	G-52/18, HL, G-007/18, G36-1, G33-2, G34-1, G-067/18, G-028/18, G31-1, G11-1, G-044/18 and G-011/18
3	14	G14-2, G30-3, G-061/18, G45-2, G22-2, G20-1, G4-2, G5-2, 005/09, G3-1, 027/06, G18-2, G16-2 and 025/02
4	1	G16-1
5	3	017/09, 009/04 and G37-3

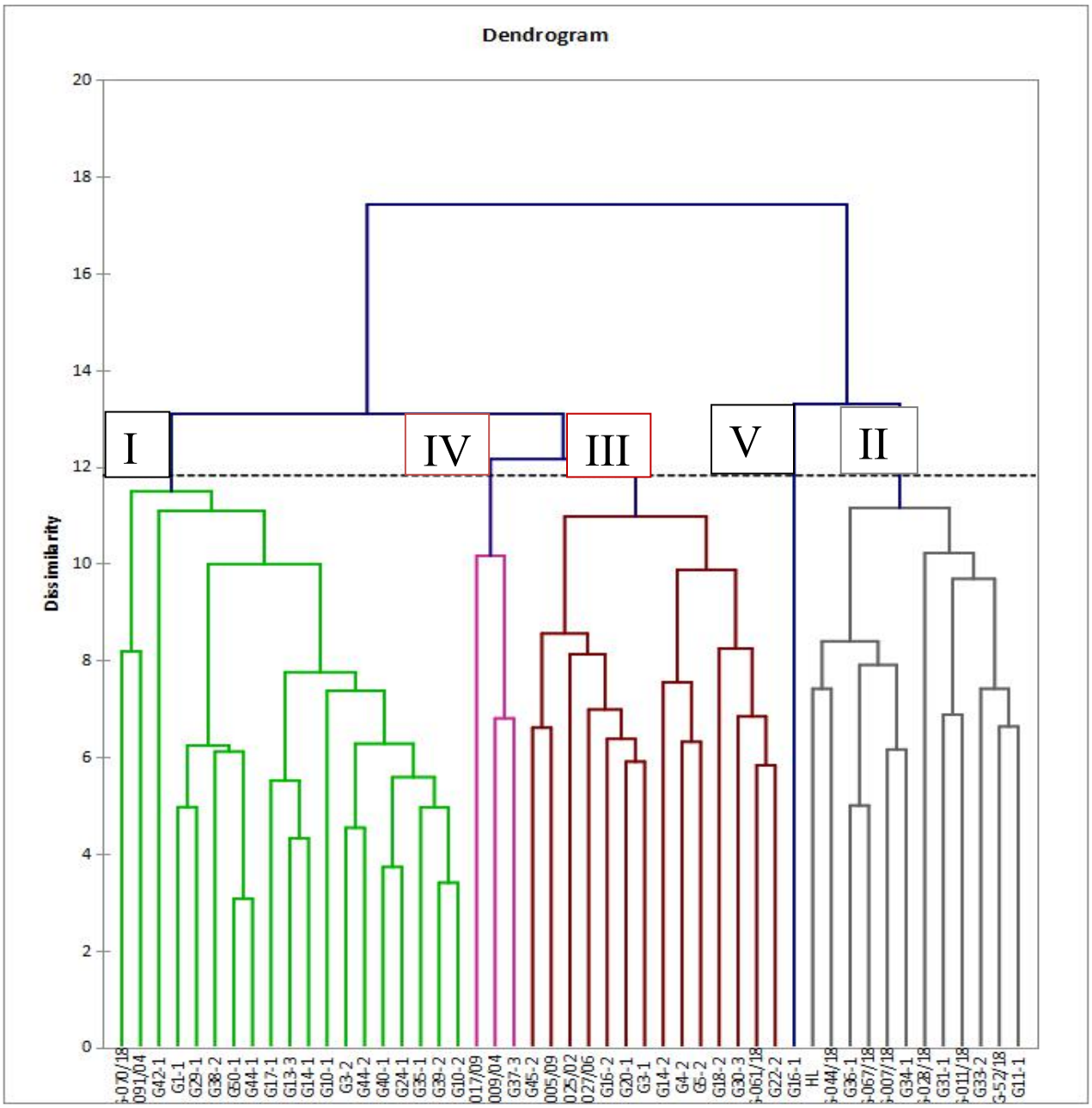


Figure 4. 2. Dendrogram showing relationships among 49 garlic genotypes

Table 4. 10. Cluster mean for sixteen traits in 49 genotypes of garlic

Traits	Cluster-1	Cluster-2	Cluster-3	Cluster-4	Cluster-5
LN	8.30	8.43	8.96	8.70	10.63
LW	1.05	0.99	1.16	0.94	1.30
LL	24.91	23.68	27.75	19.63	30.69
PSH	20.61	14.79	22.56	15.07	20.17
PH	44.67	43.65	49.31	36.20	50.60
ND	0.64	0.71	0.76	0.47	0.98
MD	106.32	112.46	108.29	107.00	113.50
BL	33.34	30.21	34.17	28.36	38.29
BD	35.15	30.49	37.08	28.63	39.78
CL	25.03	22.79	27.74	19.81	28.86
CD	17.31	14.46	18.04	13.77	18.97
CN	7.43	10.23	8.83	6.80	9.47
TSS	28.66	25.52	27.62	27.34	26.54
BW	13.00	9.97	17.19	8.40	18.96
CW	0.36	0.23	0.44	0.22	0.39
TBY	3.65	2.48	4.74	2.13	4.40

Note: LN = leaf number; LW = leaf width; LL = leaf length; PSH = pseudo stem height; PH = plant height; ND = neck diameter; MD = maturity date; BL = bulb length; BD = bulb diameter; CL= clove length; CD = clove diameter; CN = clove number; TSS = total soluble solid; BW = bulb weight; CW = clove weight; TBY = total bulb yield.

The divergences between pairs of inter clusters and intra-cluster distance were non-significant except the inter cluster distance of cluster-5 and cluster-4 were significant ($p<0.05$). Regarding the inter-cluster distance, the maximum distance was found between cluster-5 and cluster-4 (29.448), followed by cluster-4 and cluster-3 (24.01) and cluster-5 and cluster-2 (19.25). The minimum distance (9.92) was obtained between cluster-3 and cluster-1 followed by the genetic distance between cluster-2 and cluster-1 (10.61).

The significant inter- cluster distance between clusters indicates the presence of wider genetic diversity among garlic genotypes. The extent of diversity present in the studied genotypes implied the opportunity of garlic improvement through clonal selection and hybridization depending on the nature of gene action governing the desired traits. The intra cluster values were lower than the inter cluster values, indicating that the genotypes with in the clusters were both homogeneous between clusters. As a result, it is advised that genotypes be chosen based on large cluster distances which could lead to a broad spectrum of beneficial genetic diversity for improving bulb yield. In the present study, a cross which involves genotypes from cluster-5 and cluster-4 might be rewarding for the improvement of garlic through heterosis breeding and vital to develop superior inbred lines from the segregating generations.

Table 4. 11. Intra (bold diagonal) and inter Euclidean distance among genotypes

Clusters	1	2	3	4	5
1	**6.27**				
2	10.61ns	**6.77**			
3	9.92ns	13.14ns	**6.71**		
4	17.27ns	13.58ns	24.01ns	**0.00**	
5	15.94ns	19.25ns	8.62ns	29.448*	**5.21**

*Note: *; ns; significance at 5% probability level and ns = non significance at 5% probability level respectively from chi square table ($\chi 2$ = 24.966 and 30.578 at 5% and 1% probability level) respectively.*

4.8. Principal Components Analysis

Principal component analysis identify plant traits that contribute the most to the observed variation within a set of genotypes and it has a practical application in the parental selection lines for breeding purpose (Ahmadizadeh and Felenji, 2011). The principal components contributed the most to the overall variability of the forty-nine genotypes. The cumulative variance of 74% by the first two principal components with Eigen values more than 1.0 which is indicated that the identified traits within this axis showed great influence on the phenotype of the cultivars and could effectively be used for selection among them (Table 4.12). Bulb weight (0.31), total bulb yield (0.30), bulb diameter (0.30), leaf length (0.30), clove length (0.29) were the first principal components with positive and high values followed by pseudo stem height (0.28), leaf width (0.28), bulb length (0.28), clove weight (0.27), clove diameter (0.26) and clove number (0.2). Physiological maturity (0.46), clove number (0.46), neck diameter (0.4), leaf number (0.34), and plant height (0.19) were the main contributing traits in the second principal component with strong and positive component loading.

Table 4. 12. Principal component analysis, Eigen value and total variability explained by the six teen traits of garlic genotypes

Traits	Eigen vectors	
	P1	P2
LN	0.20	0.34
LW	0.28	0.12
LL	0.30	0.15
PSH	0.28	-0.22
PH	0.29	0.19
ND	0.20	0.40
MD	-0.08	0.46
BL	0.28	-0.03
BD	0.30	-0.08
CL	0.29	-0.03
CD	0.26	-0.20
CN	-0.03	0.46
TSS	0.05	-0.30
BW	0.31	0.03
CW	0.27	-0.21
TBY	0.30	-0.04
Eigenvalue	8.67	3.09
Variability (%)	54.20	19.34
Cumulative %	54.20	73.54

Note: LN = leaf number; LW = leaf width; LL = leaf length; PSH = pseudo stem height; PH = plant height; ND = neck diameter; MD = maturity date; BL = bulb length; BD = bulb diameter; CL= clove length; CD = clove diameter; CN = clove number; TSS = total soluble solid; BW = bulb weight; CW = clove weight; TBY = total bulb yield.

To check the diversity among the selected genotypes they were plotted on biplot regarding the first two PCs that had Eigen value greater than one and contributing 74% variability. Genotypes that are closely located on biplot, perceived as similar when rated on the given attributes. The genotypes far from the point of origin are more diverse from the others. According to Dehghani *et al*. (2008), the correlation between any two traits is approximated by the cosine of the angle between their vectors.On biplot, genotypes G16-1, G14-2, 017/09, G007/18 and G-011/18 clogged far away from the origin and were considered as diverse from the others. The remaining genotypes G20-1, 091/04, 027/06, G16-2, G40-1, 005/09, G30-3, G5-2, G22-2, G18-2, G4-2, G23-3 and G10-1 were clustered together and closer to the origin as well hence, these genotypes are less diverse and have less breeding value and these genotypes could directly select for total bulb yield improvement (Figure 4.2).

A strong positive association showed between maturity date, clove number; neck diameter, leaf number whereas, relatively positive association with plant height, leaf length, leaf width, bulb weight, clove length, total bulb yield, bulb diameter, bulb length and low magnitude positive association with clove diameter, clove weight, pseudo stem height and total soluble solid. Therefore, the bi-plot gave more opportunity to assess which genotypes were good for which traits that would help as baseline information for garlic improvement.

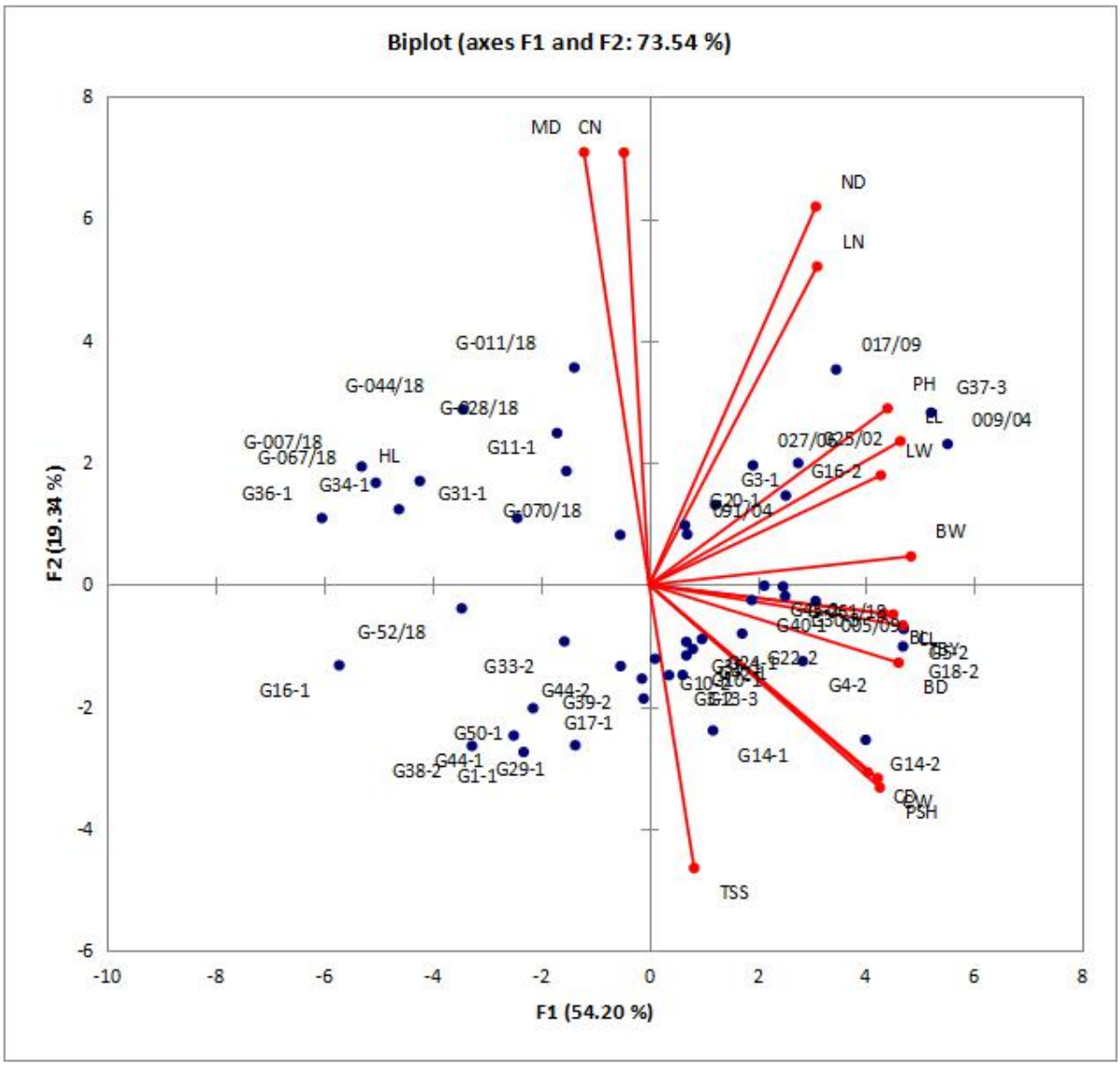


Figure 4. 3. Bi plot of PC1 and PC2 showing relationships of genotypes by traits

Note: The light-black dot color represents genotypes (n=49) and the red color represents the traits under study.

Chapter 5. CONCLUSIONS AND RECOMMENDATIONS

5.1. Conclusions

Analysis of variance (mean squares) revealed that highly significant ($p < 0.01$) variation for all traits of 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, total soluble solid, bulb weight, clove weight, total bulb yield in addition to significance ($p < 0.05$) difference in leaf width indicating larger variability in the existing genotypes.

Clove weight (39.99%) had the highest phenotypic coefficient of variation, followed by, bulb weight (31.62%), total bulb yield per hectare (30.85%) and clove number (27.85%). Total bulb yield had the highest genotypic coefficient of variation (27.84%), followed by clove weight (26.41%), and clove number (24.71%) and bulb weight (21.12%). Total bulb yield (81.42%) had the highest heritability, followed by clove number (78.71%) and neck diameter (57.1%), and total bulb yield (51.74) had the highest genetic advance as a percent of mean, followed by clove number (45.17%) and clove weight (35.93%).

Correlations with total bulb yield showed bulb weight ($r = 0.82$), pseudo stem length ($r = 0.82$), clove weight ($r = 0.81$), bulb diameter ($r = 0.81$), bulb length ($r = 0.76$), plant height ($r = 0.75$), leaf length ($r= 0.72$), clove length ($r = 0.7$), leaf width (0.65), and clove diameter (0.63) were all strongly positively associated with total bulb yield in genotypic correlation. In phenotypic association, clove weight ($r = 0.77$), pseudo stem height ($r = 0.77$), bulb weight ($r = 0.76$), bulb diameter ($r = 0.75$), bulb length ($r = 0.67$), leaf length ($r = 0.66$), plant height ($r = 0.66$), clove length ($r = 0.65$), clove diameter ($r = 0.58$) and leaf width ($r = 0.56$) had very high significance and were strongly positive correlated.

Path coefficient analysis showed that highest consideration for their relative importance of various yield contributing characters should be given to pseudo stem height, clove weight, bulb length, clove number and plant height all had a strong and positive direct impact on bulb yield and were found to be the most significant yield components in garlic.

The cluster analysis of the 49 garlic test genotypes based on unweighted pair group method with arithmetic means (UPGMA) clustering method from Euclidean distances matrix estimated from 16 quantitative traits gave 5 major clusters. The principal components analysis revealed that two principal components with Eigen-values greater than one accounted for 74% of the gross variability observed for 16 traits of 49 garlic genotypes. The first principal component alone explained 54% of the total variation, while Principal component two explained 20% of the gross observed variation among the test garlic genotypes.

5.2. Recommendations

The result will be helpful for researchers to comprehensively understand the genetic background of these studied garlic genotypes and more easily select the target genotypes, especially those with high total bulb yield. Bulb weight, pseudo stem height, clove weight, bulb diameter, bulb length, plant height, leaf length, clove length, leaf width, and clove diameter all showed a positive and important relationship with bulb yield. Total bulb yield, clove number, and clove weight are illustration of traits with high heritability and high genetic advance as a percent of mean that can be used for trait enhancement by direct and indirect choices. Furthermore, genotypes with high inter-cluster (cluster-5 and cluster-4) distance can be hybridization. However, one season experiment would not realize genotypes' variability in response of environment because quantitative traits are polygenic and profoundly influenced by the environment. Thus, further experiment on these genotypes in over seasons is required. Moreover, the genotypes such as G5-2, G18-2, G30-3, G3-2, 005/09 and, 091/04 having the highest total bulb yield can be utilized for further breeding improvement program.

6. REFERENCES

Abreham Mulatu, Bizuayehu Tesfeye and Essubalew Getachew. 2014. Growth and bulb yield of garlic varieties affected by nitrogen and phosphorus application at Mesqan Woreda, South Central Ethiopia. Sky Journal of Agricultural Research. 3(11): 249-255.

Addinsoft. 2018. XLSTAT statistical and data analysis solution. New York, USA. https://www.xlstat.com.

Ahmadizadeh M. and Felenji H. 2011. Evaluation diversity among potato cultivars using agro-morphological and yield components in fall cultivation of Jiroft area. American- Eurasian Journal of Agriculture and Environmental Science. 11(5): 655-662

Azene Tesfaye, Mijena D. F., Zeleke, H. and Getachew Tabor. 1970. 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.v29i2.8

Benke A. P., Khar A., Mahajan V., Gupta A. and Singh M. 2020a. Study on dispersion of genetic variation among Indian garlic ecotypes using agro morphological traits. Indian Journal of Genetics and Plant Breeding. 80(1): 94–102. https://doi.org/10.31742/IJGPB.80.1.12

Benke A.P., Nair A., Krishna R., Anandhan S., Mahajan V. and Singh M. 2020b. Molecular screening of Indian garlic genotypes (*Allium sativum* L.) for bolting using DNA based Bltm markers. Veg. Sci. 47 (1):116–120

Bhatt B., Soni A. K., Jangid, K and 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(1): 679-686

Block E. 2010. *Garlic and Other Alliums*: The Lore and the Science. Cambridge, UK: Royal Society of Chemistry Publishing.

Bongiorno P. and Health I. S. 2014. Journal of Complementary and Integrative Medicine Potential Health Benefits of Garlic (*Allium sativum*): A Narrative Review. (January 2008). https://doi.org/10.2202/1553-3840.1084

Brewster J. 1994. Onions and other vegetable alliums. Horticultural research international, Wellesbourne, Warwick, UK University press, Cambridge. (3): 83-125.

Burba J. L. 1993. Producción de “Semilla” de Ajo. Asociación Cooperadora EEA, La Consulta, Argentina.

Burba, J. L. 1997. Obtencion de nuevas culivares de ajo. 50 Temas Sobre Prod. de Ajo. 2:49–53.

Burton G. W.1952. Quantitative inheritance in grasses in proceedings of the 6th international grassland congress. A case study. Ames, Iowa, USA. Pp. 277-283.

Buso G. S., Paiva M. R., Torres A. C., Resende F. V., Ferreira M. A., Buso J. A. and Dusi A. N. 2008. Genetic diversity studies of Brazilian garlic cultivars and quality control of garlic-clover production. Genet. Mol. Res. 7: 534–541.

Chahal, G.S. and Gosal S.S. 2002. Principles and procedures of plant breeding: biotechnological and conventional approaches. Alpha Science Int'l Ltd. 399-412.

Chatoo M.A., Rashid R., Kamaluddin A.A. and Bhat F.N. 2018. Variability, Heritability and Genetic Advance in Garlic (*Allium sativum* L.). Int. J. Pure App. Biosci. 6(2):793-796.

Chotaliya P. and Kulkarni G. U. 2017. Character Association and Path Analysis for Quantitative Traits in Garlic (*Allium sativum* L.). International Journal of Current Microbiology and Applied Sciences. 6(8): 175–184. doi: 10.20546/ijcmas.2017.608.025.

Choudhary S., Choudhary B. and 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(1): 115-120.

CSA (Central Statistical Agency). 2017. Agricultural Sample Survey 2016/2017. Report on area and production of major crops (Private Peasant Holdings, Meher season). Addis Ababa, May 2017. Statistical Bulletin. 584, Vol. I.

CSA (Central Statistical Agency). 2018. The Federal Republic of Ethiopia Central Statistics Authority Agricultural Sample Survey 2018/2019 (2011 E. C), Report on Area and Production of Major Crops (Private Peasant Holdings, Meher season). Addis Ababa, June, 2019. 589 Statistical Bulletin. 589, Vol. I.

CSA (Central Statistical Agency). 2019. The Federal Republic of Ethiopia Central Statistics Authority Agricultural Sample Survey 2019/2020 (2012 E. C), Report on Area and Production of Major Crops (Private Peasant Holdings, Meher season). Addis Ababa, April 2020. Statistical Bulletin. 587, Vol. I.

Dehghani, D., Omidi, H. and Sabaghnia, N. 2008. Graphic analysis of trait relations of canola (*Brassica napus* L.) using biplot method. Agronomy J. 100:760-764.

Dejen Bekis, Hussein Mohammed and Dessie Getahun. 2021. Interrelationship of Agronomic Traits with Bulb Yield of Garlic (*Allium sativum* L.) Genotypes. Fogera National Rice Research and Training Center, Hawassa University and Ethiopian Institute of Agricultural Research, Ethiopia. World Research Journal of Agricultural Sciences. 8(1): 285-291.

Deshmukh S., Basu M.S and Reddy P.S. 1986. Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of ground nut. Indian jour. Agri. Sci. 56: 515-518

Dessie Getahun and Birhanu Habtie. 2017. Growth and Yielding Potential of Hot Pepper Varieties under Rain-Fed Production at Woreta, Northwestern Ethiopia. International Journal of Research Studies in Agricultural Sciences. 3(3). https://doi.org/10.20431/2454-6224.0303002

Dessie Getahun and Mulat Getaneh. 2019. Performance of garlic cultivars under rain-fed cultivation practice at South Gondar Zone, Ethiopia. 14(5): 272–278. https://doi.org/10.5897/AJAR2018.13757

Dewey J.R. and Lu K.H. 1959. A correlation and path co-efficient analysis of components of crested wheat seed production. Agron. J. 51: 515-518.

Dubey B. K., Singh R. K. and Bhonde S. R. 2010. Variability and selection parameters for yield and yield contributing traits in garlic (*Allium sativum* L.). Indian Journal of Agricultural Sciences. 80(8): 737-41.

Etoh T. 1985. Studies on the sterility in garlic (*Allium sativum* L). Mem. Fac. Agric. Kagoshima Univ. 21: 77–132.

Etoh T. and Simon PW. 2002. Diversity, fertility and seed production of garlic. In: Rabinowitch HD and Currah L. (Eds). Allium crop sciences recent advances. CABI, Walling ford, UK. Pp 101–117

Figliuolo G., Candido V., Logozzo G., Micolis V. and Zeuli PLS. 2001. Genetic evaluation of cultivated garlic germplasm *Allium sativum* L and Aampeloprasum L. Euphytica. 121: 325-334.

Fritsch R.M. and Friesen N. 2002. Evolution, domestication and taxonomy in allium crop science. In: Rabinowitch HD and Currah L. (Ed). Allium crop science recent advances. CAB International D. Walling ford, UK. Pp 5–30.

Ganie S. A. and Jan N. 2013. Character association and path analysis in garlic (*Allium sativum* L.) for yield and its attributes. 11(1): 45–52.

Getachew Tabor, Eshetu Derso and Tebikew Desalegne. 2009. Guidelines for shallot and garlic. Debrezeit Agricultural Research Center, DebreZeit Ethiopia. Pp 51.

Getachew Tabor and Asfaw Zeleke. 2010. Achievements in shallot and garlic research. Report No.36. Ethiopian Agricultural Research Organization, Addis Ababa Ethiopia

Gizachew Atinafu, Fasil Tadesse Tewlolede, Yenenesh Asfaw, Getachew Tabor, Fekadu Gebertensaye Mengistu and Deseta Fekadu. 2021. Morphological characterization and evaluation of garlic (*Allium sativum* L.) accessions collected from Northern Highlands of Ethiopia. ACST. 9: 474.

Godhani P.V. and Singh S. P. 2000. Genetic variability, correlation and path coefficient studies in garlic (*Allium Sativum* L.). In: Kirti Singh, Lawande K E, Pandey U B, Lallan Singh and Bhonde S R (Eds). Approaches for sustainable development of onion and garlic. Proceedings of the National Symposium on Onion and Garlic Production and Post Harvest Management Challenges and Strategies . Pp 95-98.

Hong C.J. and Etoh T. 1996. Fertile clones of garlic (*Allium sativum* L.) abundant around the Tien Shan Mountains. Breed Sci. 46:349–353.

Ipek M., A. Ipek S.G. Almquist and Simon P.W. 2005. Demonstration of linkage and development of the first low-density genetic map of garlic based on AFLP markers. Theor. Appl. Genet. 110:228-236.

IPGRI. 2001. Descriptors for Allium (Allium spp.). International Plant Genetic Resources Institute, Rome, Italy

Islam MA., Naher MS., Fahim AHF and Kakon A. 2020. Study of the Genetic Diversity of Garlic. Journal of Scientific Achievements. 2 (6): 6-8.

Johanson H.W., Robinson H.F. and Comstock R.E. 1955a. Estimates of genetic and environmental variability in garlic Agton J. 47:314-318.

Johnson H.W., Robinson H.F. and Comstock R.F.1955b. Genotypic and phenotypic correlation in garlic and their implication in selection. Agronomy Journal. 47: 477-483.

Jollife I.T.1986. Principal component analysis. New York, Springer.

Kamenetsky R. 2007. Garlic: botany and horticulture. Hort. Rev. John Wiley and Sons, Inc. 33: 123-172.

Kamenetsky R., London, Shafir I., Khassanov F., Kik, C., Van, Heusden A.W., Vrielink-Van Ginkel M., Burger-Meijer K., Auger J., Arnault I., Rabinowitch, H.D. 2005. Diversity in fertility potential and organo-sulphur compounds among garlics from Central Asia. Biodivers Conserv. 14(2): 281–295.

Keusgen M. 2002. Health and Alliums In: Rabinowitch, HD, Currah L (Eds.). Allium crop science: Recent advances. CAB International, Wallingford, UK. Pp. 357-378.

Konopiński M. K. 2020. Shannon diversity index: A call to replace the original Shannon's formula with unbiased estimator in the population genetics studies. doi: 10.7717/peerj.9391.

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.

Kumari S. 2021. Electronic Journal of Plant Breeding Study on genetic parameters in garlic (Allium for yield and quality traits. 12(May): 477–484.

Li Q., Zhou, S., He X., Yu Y., Zhang Y. and Wei X. 2010. Phylogeny and biogeography of Allium (Amaryllidaceae: Allieae) based on nuclear ribosomal internal transcribed spacer and chloroplast rps16 sequences, focusing on the inclusion of species endemic to China.709–733. https://doi.org/10.1093/aob/mcq177

Lu G. Y., Fan, Z. C. and Du, H. F. 2001. Relationship between ecotypes of garlic (*Allium sativum* L.) germplasms and introductions, Northwest Sci-Tech University of Agriculture and Forestry. 29(4): 5559.

Maab H. I. and Klaas, M. 1995. Infraspecific differentiation of garlic (*Allium sativum* L.) by isozyme and RAPD markers. Theoretical and Applied Genetics. 91(1): 89–97. https://doi.org/10.1007/BF00220863

Maniruzzaman K. M. 2006. Comment, Regional Development Dialogue. 27(1): 212–214.

Mario P. C., Viviana, B. V. and Marya, I. A. 2008. Low genetic diversity among garlic accessions detected using RAPD. Chilean Journal of Agricultural Research. 68: 3-12.

Martha Mebratu and and Marie Mulie. 2019. Intra row spacing effect on growth performance of garlic (*Allium Sativum* L.) at WolaitaS odo Southern Ethiopia.

Melese Worku Abera and Abay Bantihun Mehari. 2018. The Significance of Garlic (*Allium sativum* L.) on the Livelihood of the Local Community. Journal of Food & Industrial Microbiology. 4(1): 1–5. https://doi.org/10.4172/2572-4134.1000123

Meredith T. 2008. *The Complete Book of Garlic*: A Guide for Gardeners, Growers and Serious Cooks. Timber Press, Portland

Mishra, S. S., Ram, C. N., Chakravati, S. K., Vishwakarma, M. K., Singh, P. K. and Singh, V. B. 2018. Genetic Divergence Studies in Garlic (Allium sativum L.) through Morphological Features. International Journal of Current Microbiology and Applied Sciences. 7(12): 1013–1020. https://doi.org/10.20546/ijcmas.2018.712.126

Mohammed Amin, Shiberu Tadele and Thangavel Selvaraj. 2014. White rot (ScelerotiumcipivorumBerk)-an aggressive pest of onion and garlic in Ethiopia: an overview. Journal of Agricultural Biotechnology and Sustainable Development. 6(1): 6 - 15.

Nair A., Khar A., Hora A., and Malik, C. 2013. Garlic: Its Importance and Biotechnological Improvement. LS: International Journal of Life Sciences. 2(1): 72. https://doi.org/10.5958/j.2319-1198.2.1.010

Nguyen M. P. 2020. Feasibility of Edible Coating, Storage Temperature and Packaging forthe Rancidity ad Proteolytic Activity of Dry-Salted Snakeskin Gourami, Trichopodus pectoralis. Bioscience Biotechnology Research Communications. *13*(1): 23–29. https://doi.org/10.21786/bbrc/13.1/5

Nonnecke I.1989. Vegetable Production, New York. Pp. 657. www.omafra.gov.on.ca/english/crops/facts/09-011w.htm

Novak F. J. 1990. Allium tissue culture. In: Rabinowitch H. D. and Brewster J. L.(Eds.). Onions and allied crops. 1: 233–250.

Ourouadi. S., Moumene H., Zaki N., Boulli A.-A., Ouatmane A. and Hasib A. 2016. Garlic (*Allium Sativum*): A Source of Multiple Nutraceutical and Functional Components (Review). (November), 13.

Panse R., Jain P. K., Gupta A., and Sasode D. S. 2013. Morphological variability and character association in diverse collection of garlic germplasm. African Journal of Agricultural Research. 8(23): 2861–2869. https://doi.org/10.5897/AJAR12.551

Paredes C.M., Becerra V.V. and González A.M. I. 2008. Low Genetic Diversity Among Garlic (*Allium sativum* L.) Accessions Detected Using Random Amplified Polymorphic DNA (RAPD). Chilean Journal of Agricultural Research. 68(1): 3–12. https://doi.org/10.4067/s0718-58392008000100001

Perry M.C. and Mclntosh M.S. 1991. Geographical patterns of variation in the USDA soybean germplasm collection: I. Morphological traits. Crop Science. 31:1350-13. https://doi.org/10.2135/cropsci1991.0011183X003100050054x

Prajapati S., Tiwari A., Jain P. K., Mehta A. K. and Sharma H. L. 2016. Evaluation and characterization of garlic (*Allium sativum* L.) genotypes. JNKVV, Jabalpur thesis.

Rabinowitch H. D. and Brewster J.L. 1990. Onions and Allied Crops. CRC press, Boca Raton. Florida. 2: 320.

Rahim M. A., Alam S. M. Bin J. Rahman M. and Rahman J. 2019. Morphological characterization of garlic (*Allium sativum* L.) germplasm. 2(2): 46–52. https://doi.org/10.2478/mjhr-2019-0014

Rakesh S. Nagaraju K. Komolafe O. and Malik S. 2016. Genetic variability, heritability and genetic advance in garlic genetic variability, heritability and genetic advance in garlic genotypes', (November).

Rakesh Sharma V., Sunil Malik, Mukesh Kumar and Anil Sirohi. 2018. Morphological Classification of Genetic Diversity of Garlic (Allium sativum L.) Germplasm for Bulb and Yield-Related Traits Using Principal Component Analysis.Int.J.Curr.Microbiol.App.Sci. 7(6): 2016-2022. doi: https://doi.org/10.20546/ijcmas.2018.706.238

Ranjitha M. C., Vaddoria M. A., and Jethava A. S. 2018. Genetic Variability, Heritability and Genetic Advance in Garlic (*Allium sativum* L.) Germplasm. 6(4): 401–407.

Raza I. and Masood M. A. 2009. Efficiency of lattice design in relation to randomized complete block design in agricultural field experiments', Pakistan J.Agric.Res.Vol, 22(3–4).

Rina Kamenetsky. 2007. Garlic: Botany and Horticulture Department of Ornamental Horticulture. TheVolcani Center, Bet Dagan, 50250, Israel. (Vol. 33).

Rubatzky V. E. and M. Yamaguchi. 1997. *World vegetables*: Principles, Production and Nutritive Values 2nd ed., Chapman and Hall. New York.

Sable S. V., Deshmukh D. T., Ghawade S. M. and Rawat, S. S. 2020. Genetic Variability and Correlation Studies in Garlic (*Allium sativum* L.). International Journal of Current Microbiology and Applied Sciences. 9(5). https://doi.org/10.20546/ijcmas.2020.905.040

Salomon R. 2002. Virus diseases in garlic and the propagation of virus free planting. In: Rabinwitch, H.D. and L. Currah (Eds.). Allium crop sciences: Recent advances. CAB International, Wallingford, UK. Pp. 311-327.

Shannon C. E. 1948. A mathematical theory of communication. Bell System Technical Journal. 27(3): 379–423.

Shapiro S. S. and Wilk M. B. 1965. An analysis of variance test for normality (complete samples), Biometrika. 52: 591–611.

Sharma D. and Chauhan A. 2021. Genetic variability, heritability, and genetic advance in garlic genotypes. 10(2): 1346–1348.

Sharma J.R. 1998. Statistical and Biometrical Techniques in Plant Breeding. New Age International (P) Limited Publishers, New Delhi.

Sharma R.V., Komolafe O., Malik S., Mukesh Kumar and Sirohi A. 2016. Character association and path analysis in garlic (Allium sativum L.) International Quarterly Journal of Life science. 11(3):1931-1935.

Singh A. K. and Singh D. 2010. Genetic variability, heritability, and genetic advance in marigold. Indian Journal of Horticulture. 67(1):132–136.

Signh B.D. 2001. Plant Breeding Principles and methods. Kalyani publishers. New Delhi, India. Pp 896.

Singh G., Ram C. N., Singh A., Prakash Shrivastav S., Kumar Maurya P., Kumar P. and om, S. 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(2): 1362–1372. https://doi.org/10.20546/ijcmas.2018.702.165

Singh R., Dube, B., and Gupta R. 2014. Intra and Inter Cluster Studies for Quantitative Traits in Garlic (*Allium sativum* L). SAARC Journal of Agriculture: 11(2): 61–67. https://doi.org/10.3329/sja.v11i2.18402

Singh R.K. and Chaudhary B.D. 1999. Biometrical Methods in Quantitative Genetics Analysis. Kalyani Publishers. New Delhi, India. Pp 318.

Singh R.K. and Chaudhary BD. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers. New Delhi. Revised. Ed, 318.

Singh R.K., Dubey B.K., Bhonde S.R. and Gupta R.P. 2011. Correlation and path coefficient studies in garlic (*Allium sativum* L.). Journal of Spices and Aromatic Crops. 20: 83-85.

Singh S. R., Ahmed N. A., Lal S., Asima Amin., Mudasir Amin., Ganie S. A. and Nusrat J. 2013. Character association and path analysis in garlic (Allium sativum L.) for yield and its attributes. SAARC J. Agriculture. 11(1): 45-52

Singh, G. Kumar,H. Gupta, V. and Singh, P. 2013. GGE Biplot analysis for characterization of garlic (*Allium sativum* L.) germplasm based on agro-morphological traits. International Journal of Plant Breeding. 7(2):106-110.

Stearn W. T. 1992. How Many Species of Allium Are Known. Curtis's Botanical Magazine. 9(4): 180–182. https://doi.org/10.1111/j.1467-8748.1992.tb00096.x

Tewodros Bezu, FikreyohannesGedamu, NigussieDechassa and Mulatua Hailu. 2014. Registration of 'Chelenko I ' Garlic (Allium sativum L.) Variety.East African Journal of Sciences. 8(1):71-74

Tindal H. D. 1986. Vegetable in the Tropics. Macmillan Education Limited, Houdmills.

Tsega Kassahun, Tiwari Akhilesh., Woldetsadik, Kebede. 2010. Genetic variability, correlation and path coefficient among bulbs yield and yield traits in Ethiopian garlic germplasm. Indian Journal of Horticulture. 67: 489499.

Tyagi S., Chirag, P.J., Poonam D., Dhruv M., Ishita S., Labu, Z.K., Gupta A.K. and Patel K.N. 2013. Importance of garlic (*Allium sativum*): an exhaustive review. Journal of Drug Discovery and Therapeutics. 1(4): 23-27.

Vatsyayan, S., Brar, P.S. and Dhall, R.K. 2016. Genetic variability studies in garlic (Allium sativum L.). Vegetable Science. 42(2): 96-97.

Vavilov, N.I. 1951. The origin, variation, immunity and breeding of cultivated plants. Bot. 13:1–364.

Voigt, C. 2004. Garlic Trial in Northeastern Illinois. Dept. of Natural Resources and Environmental Sciences, University of Illinois.11:65-374

Wang H., Li X. and Shen D. 2014. Diversity evaluation of morphological traits and allicin content in garlic (*Allium sativum* L.) from China. Pp. 243–254. doi: 10.1007/s10681-014-1097-1.

Weldemariam Seyifu. 2017. Evaluation of Different Mulching Practices on Garlic (*Allium sativum* L.) Growth Parameters under Irrigated Condition. 7(9): 25–31.

Wright S. 1921. Correlation and causation. J. Agric. Res. 20: 557-585.

Yebirzaf Yeshiwas, Belete Negash, Tegibew Walle, Yohaness Gelaye, Abayneh Melke and Kassahun Yissa. 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(3), 17–26. https://doi.org/10.5897/jhf2017.0500

7. APPENDICES

Appendix table 1. Description of forty-nine (49) garlic genotypes with their sources

S/No.	Genotype	Source	Place of collection	
			Zone	District
1	G-067/18	DZARC	East Shewa	Gimbichu
2	G40-1	FNRRTC	South Gondar	Libokemikem
3	G38-2	FNRRTC	South Gondar	Libokemikem
4	017/09	DZARC	South Gondar	Libokemikem
5	G34-1	FNRRTC	North Gondar	Maksegnit
6	G16-1	FNRRTC	South Gondar	Libokemikem
7	G10-1	FNRRTC	South Gondar	Libokemikem
8	G-028/18	DZARC	East Shewa	Gimbichu
9	G-52/18	DZARC	East Shewa	Gimbichu
10	G3-1	FNRRTC	South Gondar	Libokemikem
11	G50-1	FNRRTC	South Gondar	Libokemikem
12	091/04	DZARC	East Shewa	Gimbichu
13	G31-1	FNRRTC	South Gondar	Farta District
14	G11-1	FNRRTC	South Gondar	Libokemikem
15	G24-1	FNRRTC	South Gondar	Libokemikem
16	G-007/18	DZARC	East Shewa	Gimbichu
17	G33-2	FNRRTC	South Gondar	Farta district
18	G36-1	FNRRTC	South Gondar	Libokemikem
19	G44-1	FNRRTC	South Gondar	Libokemikem
20	G22-2	FNRRTC	South Gondar	Libokemikem
21	G17-1	FNRRTC	South Gondar	Libokemikem
22	G45-2	FNRRTC	South Gondar	Libokemikem
23	G-070/18	DZARC	East Shewa	Gimbichu
24	025/02	DZARC	East Shewa	Gimbichu
25	G14-2	FNRRTC	South Gondar	Libokemikem
26	G16-2	FNRRTC	South Gondar	Libokemikem
27	G20-1	FNRRTC	South Gondar	Libokemikem
28	005/09	FNRRTC	South Gondar	Farta District

29	HL	DZARC	East Shewa	
30	G-044/18	DZARC	East Shewa	Gimbichu
31	G13-3	FNRRTC	South Gondar	Libokemikem
32	G42-1	FNRRTC	South Gondar	Libokemikem
33	G29-1	FNRRTC	South Gondar	Libokemikem
34	G4-2	FNRRTC	South Gondar	Libokemikem
35	009/04	DZARC	East Shewa	Gimbichu
36	G-061/18	DZARC	East Shewa	Gimbichu
37	G30-3	FNRRTC	South Gondar	Libokemikem
38	G44-2	FNRRTC	South Gondar	Libokemikem
39	G37-3	FNRRTC	South Gondar	Libokemikem
40	G3-2	FNRRTC	South Gondar	Libokemikem
41	G5-2	FNRRTC	South Gondar	Libokemikem
42	027/06	DZARC	East Shewa	Gimbichu
43	G-011/18	DZARC	East Shewa	Gimbichu
44	G35-1	FNRRTC	North Gondar	Maksegnit
45	G39-2	FNRRTC	South Gondar	Libokemikem
46	G10-2	FNRRTC	South Gondar	Libokemikem
47	G1-1	FNRRTC	South Gondar	Libokemikem
48	G18-2	FNRRTC	South Gondar	Libokemikem
49	G14-1	FNRRTC	South Gondar	Libokemikem

Appendix table 2. Mean performance of 49 genotypes of garlic for 16 characters

genotypes	LN	LW	LL	PSH	PH	ND	MD	BL	BD	CL	CD	CN	TSS	BW	CW	TBY
G-067/18	8.3 f-i	0.94 g-k	21.94 i-l	12.5 kl	40.4 jkl	0.81 c-h	114 a	27.81 o	27.48 no	21.2 mno	13.51 mn	9.4 d-j	26.95 b-k	7.79 nop	0.27 i-p	1.96 rs
G40-1	8.6 d-i	1.21 a-f	26.395 b-i	23.0 a-e	48 a-g	0.75 d-l	109 a-d	33.35 c-m	36.68 b-j	25.21 c-n	18.02 b-g	9.5 d-j	30.75 a-d	17.37 a-h	0.41 b-i	4.42 c-g
G38-2	7.4 hi	0.96 f-k	21.315 kl	17.5 d-l	39.3 kl	0.54 opq	104 de	31.38 h-o	33.35 d-n	22.99 i-o	15.83 d-n	7.3 j-p	30.47 a-d	11.83 f-p	0.31 g-n	2.29 o-s
017/09	10. abc	1.31 ab	29.885 abc	16.8 e-l	49.6 abc	1.04 a	114 a	37.725 abc	35.67 b-k	28.74 a-e	18.88 bcd	9.7 d-i	23.58 jkl	17.93 a-f	0.37 d-j	4.1 e-k
G34-1	8.2 f-i	0.96 e-k	21.555 jkl	12.6 kl	41.9 f-l	0.66 g-p	114 a	29.55 k-o	30.39 k-o	22.73 k-o	13.91 k-n	10.7 b-f	29.2 a-g	9.43 l-p	0.16 nop	2.17 p-s
G16-1	8.7 c-h	0.94 g-k	19.63 l	15.1 i-l	36.2 l	0.47 q	107 b-e	28.36 no	28.63 mno	19.81 o	13.78 lmn	6.8 k-p	27.34 a-j	8.4 mnop	0.22 j-p	2.13 qrs
G10-1	8.95 c-g	1.07 b-j	29.1 a-f	19.2 b-j	45.6 c-k	0.61 l-q	107 b-e	33.335 c-m	33.59 d-m	27.23 b-k	17.87 b-h	6.5 l-p	29.82 a-e	13.07 c-o	0.41 b-i	3.71 g-l
G11-1	9.2 c-f	1.31 ab	25.835 c-k	15.9 f-l	45.8 c-k	0.72 d-n	110.5 abc	31.2 i-o	30.97 i-n	22.98 i-o	14.46 i-n	9.7 d-i	25.97 d-k	10.83 i-p	0.27 i-p	2.54 m-s
G31-1	8.6	0.91	24.085	18.5	46.7	0.69	112.5	30.355	30.29	23.2	15.33	12.4	30.62	10.39	0.28	3.21

	d-i	jk	g-l	c-k	b-j	d-p	ab	j-o	k-o	i-o	e-n	ab	a-d	i-p	h-p	j-o
091/04	8.6	1.02	24.135	16.7	47.2	0.69	107.5	37.935	35.15	26.29	17.83	12.6	22.37	13.67	0.42	5.15
	d-i	c-k	g-l	e-l	a-i	d-p	bdce	ab	b-k	b-l	b-i	ab	kl	c-o	b-h	a-d
G50-1	7.25	1.01	24.225	19.0	40.1	0.61	109	32.265	33.04	24.89	16.39	5.8	29.77	10.1 j-p	0.33	3.11
	i	c-k	g-l	b-j	jkl	l-q	a-d	g-o	d-n	d-n	b-n	p	a-e		f-l	k-q
G3-1	9.0	1.15	27.36	22.2	46.3	0.73	112.5	32.255	35.84	26.46	14.36	12.3	27.42	16.11	0.51	4.89
	c-g	a-j	a-h	a-f	b-j	d-n	ab	g-o	b-k	b-l	j-n	ab	a-j	b-k	a-d	b-e
G-52/18	7.4	0.91	21.995	15.6	42	0.63	110.5	33.36	31.98	21.04	14.59	8.6	26.3	10.58	0.3	3.19
	hi	ijk	i-l	g-l	e-l	j-q	abc	c-m	h-n	no	h-n	f-l	c-k	i-p	g-o	j-o
G-028/18	8.5	1.15	24.69	15.2	47.5	0.74	110	29.06	30.73	24.98	15.13	12.1	21.02	14.72	0.29	2.82
	e-i	a-j	e-k	h-l	a-h	d-m	abc	mno	j-n	d-n	f-n	abc	l	b-m	g-o	l-r
G24-1	8.6	1.11	26.055	22.6	46.2	0.7	109	32.075	37	23.76	18.13	7.6	29.97	15.87	0.41	4.27
	d-i	a-j	b-i	a-e	b-i	d-o	a-d	g-o	a-i	f-o	b-g	i-p	a-e	b-l	b-i	d-i
G-007/18	7.9	0.81	21.39	13.5	40.7	0.63	114	29.335	31.91	23.59	13.24	13.7	24.44	9.675	0.14	1.86
	f-i	k	kl	jkl	i-l	k-q	a	l-o	h-n	g-o	n	a	g-l	k-p	p	rs
G33-2	8.3	1.03	24.62	17.9	42.9	0.63	109	31.88	32.16	25.48	17.05	5.6	24.12	10.8	0.38	3.15
	f-i	c-k	f-k	c-l	d-k	k-q	a-d	g-o	g-n	b-n	b-l	p	i-l	i-p	d-i	j-p
G36-1	8.0	0.91	21.975 i-l	13.5	42.1	0.57	114	27.81	24.29 o	22.32	13.16 n	8.6	24.33 h-l	6.475 p	0.18 m-p	1.56
	f-i	h-k		jkl	e-l	m-q	a	o		l-o		f-l				s

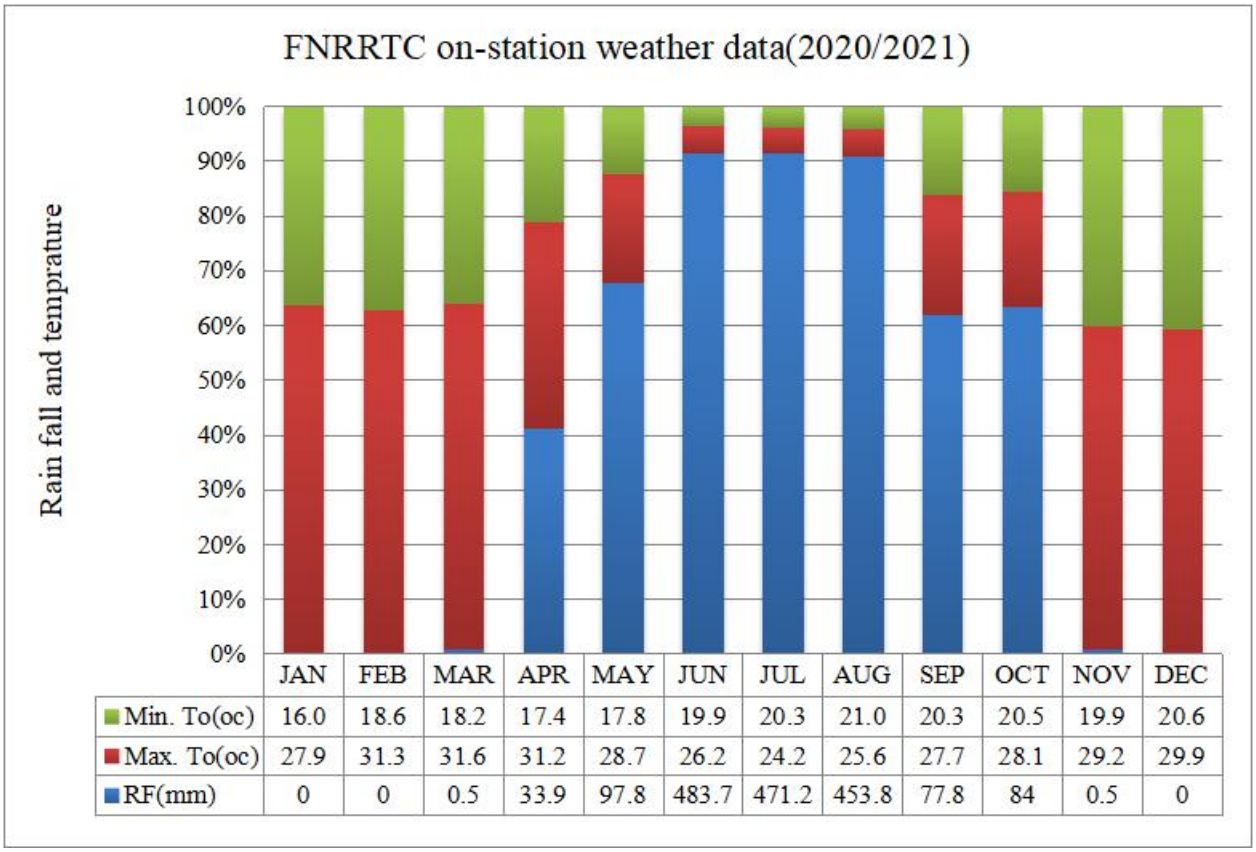
G44-1	7.7	1.00	23.57	19.1	40.7	0.53	107	31.64	31.87	23.4	16.73	5.6	30.17	10.14	0.34	2.73
	g-i	d-k	h-l	b-j	i-l	pq	b-e	h-o	h-n	i-o	b-m	p	a-d	j-p	e-k	l-r
G22-2	8.8	1.22	27.305	20.6	49.5	0.69	104	34.36	34.09	28.03	17.09	6.9	27.49	14.58	0.4	4.11
	c-g	a-d	a-h	a-i	a-d	d-p	de	b-j	c-m	a-g	b-l	k-p	a-j	b-m	b-i	e-j
G17-1	8.8	1.1	24.915	19.3	44.6	0.62	102.5	34.335	35.22	25.33	18.02	6.4	28.7	11.32	0.35	3.29
	c-g	a-j	d-k	b-j	c-k	k-q	e	b-j	b-k	c-n	b-g	l-p	a-i	g-p	e-j	i-n
005/09	8.9	1.23	26.625	25.4	49.6	0.76	110.5	35.11	39.09	24.25	19.13	7.8	28.57	16.34	0.42	5.78
	c-g	a-d	b-h	ab	abc	c-l	abc	a-i	a-d	e-o	bcd	h-p	a-i	a-j	b-h	ab
G20-1	8.8	1.09	28.125	20.6	48.6	0.69	112.5	31.725	35.53	24.92	17.46	10	26.39	13.43	0.38	4.29
	c-g	a-j	a-h	a-i	a-e	d-p	ab	h-o	b-k	d-n	b-j	c-h	b-k	c-o	c-i	d-h
G16-2	9.7	1.17	29.325	20.8	49.4	0.82	110.5	32.555	36.66	27.99	17.89	10.6	29.28	16.79	0.35	4.86
	b-e	a-i	a-d	a-i	a-d	b-g	abc	g-n	b-j	a-h	b-h	b-g	a-f	a-i	e-k	b-e
G14-2	8.1	1.17	28.115	22.3	48.4	0.66	107	35.15	38.39	29.52	22.9	6.1	30.5	19.09	0.61	4.79
	f-i	a-g	a-h	a-f	a-f	f-p	b-e	a-i	a-f	abc	a	nop	a-d	abc	a	b-f
025/02	10.6	1.19	28.245	23.2	52.5	0.83	110.5	33.85	33.3	25.59	19.76	11.3	29.02	17.79	0.34	4
	ab	a-g	a-g	a-d	ab	b-f	abc	b-l	d-n	b-m	ab	bcd	a-h	a-g	e-l	e-k
G-070/18	8.5	1.07	26.325	19.5	45.8	0.71	107.5	35.835	35.74	22.69	14.37	11.6	26.38	11.79	0.3	3.84
	e-i	b-j	b-i	b-j	c-k	d-n	b-e	a-h	b-k	k-o	j-n	a-d	b-k	f-p	g-o	f-k

G45-2	8.6	1.12	26.71	21.4	48.1	0.78	111	33.87	40.11	28.2	18.55	7.4	26.69	16.09	0.42	4.03
	d-i	a-j	a-h	a-i	a-g	c-k	abc	b-k	abc	a-f	b-e	j-p	b-k	b-k	b-h	e-k
HL	7.8	0.99	24.305	12.1	41.1	0.79	114	31.055	32.31	19.74	14.84	8.3	23.64	7.295	0.17	2.34
	g-i	d-k	g-k	l	h-l	c-j	a	i-o	f-n	o	g-n	h-n	jkl	op	nop	n-s
G-044/18	9.2	0.94	24.59	12.4	44.7	0.78	114	30.9	28.97	23.45	14.79	10	22.27	10.44	0.2	1.89
	c-f	g-k	f-k	kl	c-k	c-k	a	i-o	l-o	h-o	g-n	c-h	kl	i-p	k-p	rs
G13-3	8.3	1	25.13	21.2	45.6	0.73	104	33.03	37.56	25.99	17.85	7	26.93	14.56	0.41	3.98
	f-i	d-k	d-k	a-i	c-k	d-n	de	f-m	a-h	b-l	b-i	k-p	b-k	b-m	b-i	e-k
G42-1	8.9	1.04	24.7	22.1	44.7	0.64	107	33.185	36.09	28.29	18.27	5.7	21.15	14.18	0.48	3.84
	c-g	c-k	e-k	a-f	c-k	i-p	b-e	d-m	b-k	a-f	b-f	p	l	b-n	a-f	f-k
G29-1	8.4	0.92	24.05	22	42.6	0.56	104	30.41	32.84	24.4	17.62	6.2	29.82	12.59	0.39	3.21
	e-i	h-k	g-l	a-g	e-l	n-q	de	j-o	e-n	e-n	b-j	m-p	a-e	d-p	c-i	j-o
G4-2	8.8	1.14	27.57	22.9	46.6	0.73	106	35.79	38.96	27.28	17.53	7.8	31.15	19.07	0.48	4.56
	c-g	a-j	a-h	a-e	b-i	d-n	dce	a-h	a-d	b-j	b-j	h-p	ab	a-d	a-e	c-g
009/04	10.6	1.27	31.265	22.2	53.8	0.92	114	39.545	42.79	28.71	19.09	8.9	28.48	18.43	0.41	4.79
	ab	abc	a	a-f	a	abc	a	a	a	a-e	bcd	e-k	a-i	a-e	b-i	b-f
027/06	9.2	1.12	26.8	22.5	49.7	0.8	112.5	32.95	35.32	27.35	17.21	11.1	23.45	18.37	0.38	4.79
	c-f	a-j	a-h	a-e	abc	c-i	ab	f-m	b-k	b-i	b-k	b-e	jkl	a-e	d-i	b-f
G5-2	8.8	1.2	28.52	26	48.2	0.79	107	37.125	39.12	29.58	17.16	8.4	29.3	22.64	0.54	5.98

	c-g	a-f	a-g	a	a-f	c-k	b-e	a-f	a-d	abc	b-l	g-m	a-f	a	ab	a
G3-2	8.2	1.06	25.62	21.2	47.4	0.68	107	33.67	34.89	23.98	17.28	5.8	28.02	10.88	0.43	4.94
	f-i	b-k	c-k	a-i	a-h	e-p	b-e	b-l	b-l	f-o	b-k	p	a-j	h-p	b-g	b-e
G37-3	11.3	1.34	30.915	21.6	48.4	0.98	112.5	37.59	40.88	29.13	18.96	9.8	27.57	20.54	0.4	4.39
	a	a	ab	a-h	a-f	ab	ab	a-e	ab	a-d	bcd	d-i	a-j	ab	b-i	c-g
G44-2	8.3	1.02	25.505	22.2	46.1	0.65	106	31.31	35.94	23.97	17.24	7.6	29.32	12.46	0.32	3.32
	f-i	c-k	c-k	a-f	b-j	h-p	dce	h-o	b-k	f-o	b-k	i-p	a-f	e-p	g-m	h-n
G30-3	8.5	1.16	26.35	23.2	50.7	0.77	104	33.85	38.53	27.21	17.07	9	24.88	18.42	0.39	4.94
	e-i	a-j	b-i	a-d	abc	c-l	de	b-l	a-e	b-k	b-l	e-k	f-l	a-e	c-i	b-e
G-061/18	8.5	1.05	28.25	21.6	52.7	0.85	104	32.135	35.97	29.94	17.65	8.9	25.35	15.42	0.53	4.05
	e-i	c-k	a-g	a-h	ab	bcd	de	g-o	b-k	ab	b-j	e-k	e-l	b-l	abc	e-k
G-011/18	9.9	1.06	27.135	17.8	48	0.84	112.5	30.205	34.48	22.79	13.53	13.7	27.35	11.16	0.16	3.15
	bcd	b-k	a-h	c-l	a-g	b-e	ab	j-o	c-m	j-o	mn	a	a-j	h-p	op	j-p
G35-1	8.6	1.07	24.88	24.1	47.4	0.67	107	35.825 a-h	35.25	25.16	16.51	8.1	29.17	13.89	0.34	4.13
	d-i	b-j	d-k	abc	a-h	e-p	b-e		b-k	c-n	b-n	h-o	a-g	c-n	e-l	e-j
G39-2	7.8	1.06	24.16	21.9	46.5	0.64	107	34.19	35.69	25.9	16.35	7.8	30.69	13.91	0.35	3.34
	g-i	b-k	g-l	a-g	b-i	i-p	b-e	b-j	b-k	b-l	c-n	h-p	a-d	c-n	e-j	h-m
G10-2	8.6	1.11	24.18	20.7	45.3	0.61	109	33.12	36.05	25.99	16.79	7.8	32.07	14.74	0.36	3.63
	d-i	a-j	g-l	a-i	c-k	l-q	a-d	e-m	b-k	b-l	b-m	h-p	a	b-m	d-j	g-l

G1-1	7.7 g-i	1.02 c-k	24.285 g-k	18.7 c-k	41.5 g-l	0.54 opq	104 de	30.225 j-o	33.59 d-m	23.81 f-o	19.46 bc	5.8 p	30.8 abc	10.19 j-p	0.19 l-p	2.58 m-r
G18-2	9.2 c-f	1.22 a-e	29.235 a-e	23.3 a-d	50 abc	0.81 c-i	104 de	37.66 a-d	38.22 a-g	32.14 a	18.85 bcd	6 op	27.25 b-j	16.49 a-j	0.53 abc	5.38 abc
G14-1	8.5 e-i	1.11 a-j	24.73 d-k	21.9 a-g	44.2 c-k	0.62 k-q	102.5 e	36.31 a-g	38.37 a-f	26.32 b-l	18.43 b-f	6.5 l-p	28.2 a-j	14.48 b-m	0.43 b-g	3.67 g-l
LSD (5%)	1.27	0.26	4.61	6.40	6.68	0.17	6.28	4.53	6.10	4.55	3.41	2.23	4.80	6.50	0.15	0.99

Means followed by the same letter within columns are not significantly different at 5% level of significance; LN = leaf number; LW = leaf width; LL = leaf length; PSH = pseudo stem height; PH = plant height; ND = neck diameter; MD = maturity date; BL = bulb length; BD = bulb diameter; CL= clove length; CD = clove diameter; CN = clove number; TSS = total soluble solid; BW = bulb weight; CW, clove weight; TBY = total bulb yield; CV = coefficient of variation; SE = standard error of the mean and LSD = least significance difference



	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC
Min. To(oc)	16.0	18.6	18.2	17.4	17.8	19.9	20.3	21.0	20.3	20.5	19.9	20.6
Max. To(oc)	27.9	31.3	31.6	31.2	28.7	26.2	24.2	25.6	27.7	28.1	29.2	29.9
RF(mm)	0	0	0.5	33.9	97.8	483.7	471.2	453.8	77.8	84	0.5	0

Appendix figure 1. Rainfall and temperature distribution at FNRRTC on-station for 2020/2021 cropping season

Source: Fogera National Rice Research and Training Center Meteorology data; RF = rainfall in millimeter; Max. T^{o} (^{o}C) = maximum temperature in degree centigrade; Min. T^{o} (^{o}C) = minimum temperature in degree centigrade and FNRRTC = Fogera National Rice Research and Training Center

BIOGRAPHICAL SKETCH

The author was born from his father Ato. Getaneh Melesse and his mother W/ro Tibeyin Belachew in January 1993 in Jabi Tehinan district, West Gojam Zone of Amhara region. He attended his junior and secondary schools at Jiga Tikur Wuha and high school started since 1998 and preparatory schools at Damot, Finote Selam. He earned a BSc. degree in plant sciences in 2013 from Debre Markos University, Ethiopia. Then, he began his work career at Fogera national rice research and training center of Ethiopian Institute of Agricultural Research in October, 2017 as junior researcher. Since then, Mulat has served as researcher in horticultural crops until he joined to Bahr Dar University to pursue his Msc. study in 2021. Currently, Mulat is working on genetic variability and association of traits in Ethiopian garlic genotypes as his Msc. thesis work.