GENETIC DIVERSITY AMONG BARLEY (*Hordeum vulgare* L.) LANDRACES FROM SOUTHERN ETHIOPIA

MSc Thesis

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NOVEMBER 2019

JIMMA, ETHIOPIA

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Submitted to Department of Horticulture and Plant Sciences, College of Agriculture and Veterinary Medicine, Jimma University, for the Partial fulfillment of Degree of Master of Science in Plant Breeding.

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November 2019

Jimma, Ethiopia

DEDICATION

This thesis is dedicated to my father Mr. Mengesha W/gebriel and my mother Mrs. Abebech Haile for nursing me with affection and for their committed partnership in the success of my life.

STATEMENT OF THE AUTHOR

First, I declare and affirm that this thesis is my own work and I have followed all ethical and technical principle of research in the preparation, data collection, data analysis and compilation of this thesis. Any scholarly material that is included in the thesis has been given recognition through citation.

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ACRONYMS AND ABBREVIATIONS

ANOVA	Analysis of Variance
CSA	Central Statistical Agency
DAP	Di-ammonium Phosphate
EBI	Ethiopian Biodiversity Institution
EIAR	Ethiopian Institute of Agricultural Research
FAO	Food and Agricultural Organization
GA	Genetic advance
GAM	Genetic advance as percent of mean
GCV	Genotypic coefficients of variation
HARC	Holeta Agricultural Research Center
IPGR	International Plant Genetic Resources Institute
NA	Not available
PC	Principal Component
PCA	Principal Component analysis
PCV	Phenotypic coefficients of variation
SAS	Statistical Analysis System
SNNP	Southern Nations Nationalities and Peoples
SNNPR	Southern Nations Nationalities and People's Region
USAD	United State Department of Agriculture

BIOGRAPHICAL SKETCH

The author, Kochito Mengesha was born in March 11, 1994 from his father Mengesha W/Gebriel and mother Abebech Haile in Kobech Kebele, Gewata Woreda,Kaffa Zone. He attended his primary school at Kobech Primary School from 2002 to 2009. After completion of his primary school, he attended his secondary and preparatory School at Gimbo Secondary and Preparatory School from 2010 to 2013.Then, he joined Mizan Tepi University in 2014 and graduated with BSc degree in plant science in June, 2016. After graduation, he was employed by Mizan Tepi University and served as graduate assistant I. After serving for a year; he joined Jimma University College of Agriculture and Veterinary Medicine to pursue his master of science in plant breeding in October, 2017.

ACKNOWLEDGMENT

I would like to express my deep gratitude to my major advisor Sentayehu Alamerew (Prof) and co- advisor Temesgen Matiwos (Assist.prof) for their follow up, constructive comments, guidance, support and concern from the inception up until the completion of this thesis work. My gratitude also goes to staff members of Bonga Agricultural Research Center for their unreserved effort to cooperate with me from the beginning to the end of the field experiment. I also express my sincere gratitude to Ministry of Education and Mizan Tepi University for sponsoring the study and giving me the opportunity to pursue my graduate studies.

Moreover, I wish to extend my deepest and heartfelt gratitude to my respected and beloved father Mengesha W/gebreiel, my mother Abbebech Haile and my sister Zewditu Mengesha for their unreserved and immeasurable love, encouragement and stringent moral support throughout my study. Finally, it is my pleasure to thank Jimma University for hosting my study and facilitating all the academic processes.

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GENETIC DIVERSITY AMONG BARLEY (*Hordeum vulgare* L.) LANDRACES FROM SOUTHERN ETHIOPIA

ABSTRACT

Barley landraces are the major genetic resources of cultivated barley in Ethiopia. Lack of adequate information on extent of landraces diversity hinders conservation efforts and proper utilization of genetic resource. A field experiment was conducted in order to assess the extent of genetic diversity of barley landraces collection from southern Ethiopia. A total of 105 genotypes were evaluated during 2018 main cropping season using augmented design at Alarigata, substation of Bonga Agricultural Research Center. Data were recorded for twelve quantitative and seven qualitative characters. Analysis of variance indicated highly significant variation ($p<0.01$) among 105 genotypes for all traits except awn length. Genotypic coefficient of variations (GCV) varied from 4.36% for biological yield to 13.22% for number of fertile tillers per plant and phenotypic coefficient of variations (PCV) varied from 6.40% for plant height to 16.27% for spike length. Estimate of broad sense heritability varied from 38.75 % for spike length to 78.13 for grain yield. Estimates of genetic advance as percent of mean ranged from 7.61% for plant height to 23.01% for number of fertile tillers per plant. Phenotypic and genotypic correlation analysis indicated that grain yield had positive and significant phenotypic and genotypic correlation with days to maturity, grain filling period, and plant height, number of fertile tillers per plant, thousand seed weight, harvest index and biological yield. Path analysis revealed that plant height, thousand seed weight and number of fertile tillers per plant showed positive and highest direct effect on grain yield. Cluster analysis grouped 105 genotypes into five groups and one genotype remains ungrouped. Principal component analysis revealed that the variance of 31,15,12,10 and 9 % were extracted for first five PCs respectively, which contributed 78% of total variation among genotypes. Estimate of Shannon -Weaver diversity index H' varied from 0.09 for hoodedness to 0.97 for kernel row number. Pooled over all traits with in each zone, H' value ranged from 0.48 for Sidama to 0.69 for South Omo and individual trait showed different levels of diversity across different zones. In general, the result indicated the existence of wider diversity among the barley collection, showing opportunity to improve important traits of the crop and need to conserve the diversity. As future line work further investigation with inclusion of informative molecular markers and covering different producing area of the region will allow to provide the complete picture of existing diversity.

Key words: Barley, Genetic coefficient of variations, Genetic diversity, Landraces, Phenotypic coefficient of variations.

1. INTRODUCTION

Barley (*Hordeum vulgare*. L) is self-pollinating annual cereal crop which belongs to the grass family *Poaceae* of the tribe *Triticeae* (Von Bothmer, 1992). It is diploid with 2n = 2x = 14 chromosomes (Bennett *et al*., 1976) and one of the first domesticated crops (Zohary and Hopf, 2000).

Barley is the most widely grown crop over wider environmental ranges than any other cereals and has persisted as a major cereal crop through many centuries (Azizi *et al*., 2011). It can be cultivated at altitudes between 1500 and 3600 meters above sea level, but is mainly grown between altitudes of 2000 and 3000 meters above sea level (Birhane *et al*., 1996). It grows best on well-drained fertile loam or light clay soils and can tolerate higher levels of soil salinity than most other crops (Bayeh and Birhane, 2011).

It is one of the most important cereal crops of the world and is a major source of food for large number of people living in the cooler, semi – arid area of the world (Ramjan, 2014). It is produced for human consumption, animal feed, as well as for malting (Harlan, 2008). Nutrition wise, it is a winner crop and called as "nutritional power house. It has health benefit due to the presence of beta-glucan (anti-cholesterol substance), acetylcholine carbohydrate substance which nourishes our nervous system and recovers memory loss, easy digestibility due to low gluten content and high lysine, thiamin and riboflavin render cooling effect in the body (Behall *et al*., 2004). The beta-glucan is effective in lowering serum cholesterol and can reduce the risk of heart disease (Newman and Newman, 2008). In general, the whole barley grain contains about 65-68% starch, 10-17% protein, 4-9% β-glucan, 2-3% free lipids and 1.5-2.5% minerals (Izydorczyk, 2000; Quinde *et al*., 2006).

Globally, barley is the fourth most important crop after maize, wheat and rice both in area coverage and production (FAO, 2019). The global annual production of barley has been estimated as 141.66 million metric tons with area coverage of 47.57 million hectare with per hectare yield of 2.89 metric tons (USDA, 2018). According to USDA (2018), globally, European Union, Russia, Ukraine, Australia and Canada were the top five largest barley producers. In Africa, Morocco, Ethiopia, Algeria, Tunisia and South Africa were the top five

largest barley producers with production of approximately 2.00, 2, 0.97, 0.50 and 0.28 million tons, respectively (USDA, 2018).

Barley has a long history of cultivation in Ethiopia and it is reported to have coincided with the beginning of plow culture (Zemede, 2000). It is a major traditional cereal crop representing about 7.51% of the total national cereal production (CSA, 2018). According to report of CSA (2018) it ranks fifth after maize, sorghum, teff and wheat both in area coverage and production with around 951,993.15 hectare and 2,052996.372 tons, respectively with per yield of 2.11 tons. It is considered as dependable source of food in the highland as it is produced during the main and short rainy seasons as well as under residual moisture (Melle *et al*., 2015).

Landraces are the major genetic resources of cultivated barley in Ethiopia. In contrast to the genetic uniformity of modern cultivars, landraces exhibited variation both between and within populations. This within population diversity might allow them to cope with environmental stresses which are very important for achieving yield stability (Zhu *et al*., 2000).

Moreover, they are a precious source of genes that control important agronomic traits, such as resistance to diseases for example powdery mildew, barley yellow dwarf virus, net blotch, scald and loose smut, to insect attack (Yitbarek *et al*.,1998), high lysine and protein quality and content (Munck *et al*.,1970), and malting and brewing quality (Lance and Nilan, 1980). Consequently, characterization of landraces and knowledge on the extent of diversity is an important prerequisite for the efficient conservation of existing genetic material and selection of parents with diverse genetic background. Owing to these important aspects, tremendous efforts have been done on diversity assessment of barley landraces and variation for important morpho-agronomic traits has been reported by different researchers (Zemede, 1988, 1999; Abebe and Asmud, 1996; Alemayehu, 2003; Tessema *et al*., 2009; Tigist *et al*., 2010; Adugna, 2011, Shegaw *et al*., 2013; Bedasa *et al*., 2014).

However, many studies of diversity assessment in Ethiopia done on random germplasm collection based on samples from various parts of Ethiopia (Birhane and Alemayehu, 2011). These studies on random samples not enable us to capture co-adapted gene in the landraces

for specific geographical regions and micro environments Southern Ethiopia is one of important barley growing region among different barley producing areas in the country. However, barley landraces collection from this area have not been extensively studied (Asfaw, 2000; Shegaw *et al*., 2013). Accordingly, knowledge on pattern of landraces diversity is an important consideration for efficient conservation and utilization of genetic resources. Thus, this research was initiated with the following objectives.

General objective

- To assess the extent of genetic diversity of barley landraces collection from southern Ethiopia.

Specific objectives

- To estimate the variability, heritability and genetic advance of barley genotypes
- To determine association between grain yield and, the different quantitative traits.

2. LITERATURE REVIEW

2.1. Domestication and Dissemination of Barley

Archaeological evidence has suggested that barley is an oldest crop cultivated during ancient times at about 10,000 to 12,000 years ago. It is considered as a founder crop of old world agriculture (Zohary *et al*., 2012). It is thought that barley was first domesticated from its wild relatives, *H.vulgare ssp spontaneum,* in the area of the Middle East known as the Fertile Crescent, most likely from two geographic areas of within Israel/Jordan and the Himalayas as a diversification region of domesticated barley (Badr *et al.,* 2000). Ethiopia was first considered a center of origin for cultivated barley (Vavilov, 1926), later it became regarded as a secondary center of diversity because of the absence of the wild relative.

Migration of people with crop seeds led to a major diversification and adaptation of crops to new areas, and hence barley is now virtually found worldwide (Bothmer *et al*., 2003). According to Bothmer *et al*. (2003), the first route of dissemination of barley was believed to be to Greece, Iran, India, Ethiopia, and North Africa about 8000BP. Then, barley arrived in Spain 7000 BP, and to North Germany and South Scandinavia 6000 BP. Bothmer *et al*. (2003) also pointed out that barley disseminated to Eurasia and China some 4000 and 3000 BP, respectively. Now it is among the top ten crop plants in the world with an area under production of 47.57 million hectare (USDA, 2018).

2.2. Taxonomy of barley

Barley belongs to genus *Hordeum* in the tribe Triticeae of the grass family poaceae also known as gramineae (Von Bothmer, 1992). A triticeae tribe is a temperate plant containing several groups of economically important cereals, forage as well as 350 wild species. There are 32 species with in *Hordeum* genus, all with basic chromosome number of x=7. Cultivated barley, *Hordeum vulgare L. Ssp.vulgare* and its wild progenitor H. *Vulgar L.Ssp. Spontaneum* (C.Koch.) are diploid species with 2n=2x=14 chromosomes (Komatsuda *et al.,* 1999). Other *Hordeum* species are diploid (2n=2x=14), tetraploid (2n=4x=28) or hexaploid (2n=6x=48). Besides, the two species *Hordeum vulgare* and *Hordeum bulbusum* are considered to share

basic common genome, which is not related with other genome in the genus (Von Bothmer, 1992).

2.3. Production and Utilization of Barley in Ethiopia

Barley is an important grain crop grown twice a year from August to December (main season) and from March to July (short season) in altitudes from 1800 to 3400 m. a. s. l (Berhane *et al*., 1996). Barley types are predominantly categorized as food and malting barley based on their uses, while in Ethiopia the highest proportion of barley production area is allocated for food barley. It is a staple food grain, especially in the highlands of Ethiopia and consumed in various form of traditional foods and local beverages.

According to Birhanu *et al*. (2005), it is used in diversity of recipes and deep rooted in the culture of people's diets. Among the traditional recipes prepared from cereals, some recipes such as *besso, zurbegonie,* and *chiko* have a long shelf life and can only be prepared from barley grain. Other barley recipes such as *genfo, kolo,* and *kinche* are the most popular but they can be prepared from other cereals also. Barley after tef is the preferred grain for making the traditional bread, *injera,* which can be made either solely or in combination with tef flour or other cereals (Birhanu *et al*., 2005).

Among local beverages, *tella, borde,* and *areki* are the prominent (Birhane *et al*., 2005). Moreover, it matures early and serves as an emergency crop bridging the critical food shortage occurs in September (Kemelew and Alemayehu, 2011). Besides its grain value, barley straw is an indispensable component of animal feed especially during the dry season in the highlands where feed shortage is prevalent (Girma *et al*., 1996). Due to its wide use for various purposes, farmers in Ethiopia named it as "Gebs Yeihl nigus"literally meaning "King of grains" (USDA, 2015).

2.4. Barley Breeding History and Achievement in Ethiopia.

The onset of Barley research effort date back us more than six decades and within these years several achievement have been recorded. Various evidence shown that barley research was started at Debre Zeit Agricultural Research Centre in the 1950s (Bayeh and Berhane, 2011).

But, more organized research on the crop began in 1966 with the establishment of the Holetta Agricultural Research Centre (HARC) to represent the central highlands of Ethiopia, with barley being a major focus in crop research. However, a comprehensive research plan was set up in 1969, with the bulk of the work being conducted at Holeta, including hybridization; selection from large collections from local and foreign sources; variety trials. Moreover, activities included identification of suitable malting barley production areas, development of suitable malting barley varieties (Bayeh and Berhane, 2011).

The early milestones resulting from the trials conducted in the 1970s include the first advance made in identifying barley varieties of good malting quality and suitable locations (IAR, 1971) and six-row malting barley varieties suitable for Ethiopia were identified (IAR, 1973).

Later in 1980, barley breeding and genetic research focused on developing varieties responsive to high external inputs (Bayeh and Berhane, 2011). However, in the 1990s, the research direction became geared towards a participatory and multidisciplinary approach, with major emphasis on-farm research with the full participation of farmers. In line with this, a research grant was obtained from 1993 to 1998, from the Royal Netherlands Government to strengthen research and transfer of technology for sustained food barley production. It was a collaborative project between the then IAR and the International Center for Agricultural Research in the Dry Areas (ICARDA) (Bayeh and Berhane, 2011).

The general goal of the project was to develop and transfer new technologies to small scale farmers, to increase the productivity of barley and to ensure the sustainability of barley production in the various barley agro-ecologies. In general, the breeding programme has given more emphasis to the evaluation of landraces under low to medium inputs rather than replacing the local germplasm by exotic materials (Bayeh and Berhane, 2011).

In general, since the commencement of barley research, more than 70 varieties (50 food and 20 malt) of barley have been released by federal and regional research institutes. These varieties were developed by hybridization, selection from landraces and introductions from

international research organizations like ICARDA and from other countries such as Germany and Belgium

2.5. Variability Studies in Barley Landraces

Variability is defined as the occurrence of differences among individuals due to differences in their genetic composition or environment in which they are raised (Allard, 1960.). In general, the observed variability in a given germplasm can be partitioned in to phenotypic and genotypic. Phenotypic variability is the observable variation present in a character in a population; it includes both genotypic and environmental variation and, as a result, its magnitude differs under different environmental conditions. In the other words, phenotypic variation is the result of genotypic variation and environmental deviation (Falconer and Mackay, 1996). On the other hand, genotypic variability is the component of variation, which is due to the genotypic differences among individuals within a population, and is the main concern of plant breeders (Singh, 2001).

Progress in plant breeding depends on variability because superior genotypes obviously cannot be selected from homogenous populations, but homogeneity is desirable in the final product of the agricultural variety. Success in improving adaptation requires that the population under selection be genetically variable (Allard and Hansche, 1964). In view of this, in initiating a breeding program with any crop, information on the nature and magnitude of genetic variation within the species for traits of agronomic importance greatly helps in formulating a sound crop breeding program and in efforts to breed better varieties (Baltensperger and Kalton, 1958).

Owing to the importance of information on variability of a given population, great deal of genetic diversity in barley for different agro morphological traits has been investigated in the country. In very early, Birhane *et al*. (1997) reported the presence of wide range of variability for the trait like days to heading, days to maturity, plant height and grain yield. Likely, Shambel (2001) evaluated 47 landraces collection from different region of Ethiopia and reported the existence of highly significant diversity among genotypes for 16 quantitative traits considered. Similarly, Alemayehu (2003) reported high range of variability among

barley landraces for days to heading, days to maturity, plant height, spike length, grain yield and thousand grain weights.

Tigist *et al*. (2010) obtained significant variation among 199 landrace for plant height, thousand seed weight, number of seed per spike, awn length, days to heading and days to maturity. Bedassa *et al*. (2014) reported significant genetic variability for plant height, peduncle extension, Spike length, thousand seed weight, number of seeds per spike, days to 50% flowering and days to maturity of 102 accession collections from various region of Ethiopia. Likely, Shegaw *et al*. (2013) observed wide range of variability for the trait like grain yield, plant height, days to heading and days to maturity among 218 genotypes. Likely, Jimera *et al.* (2015) reported existence of variation among barley genotypes considered in their investigation. They found that considerable wide range of variation for the trait grain yield, effective tillers, days to heading, days to maturity, plant height and thousand seed weight. In general, many sources Indicated that the existence of notable genetic variation for important traits of barley landraces.

Moreover, qualitative traits are considered as important morphological markers in the identification of varieties in any crops, which are less influenced by environmental fluctuations. Accordingly, notable diversity for discrete characters of barley has been reported by number of researchers. For instance, Mulugeta (1985) reported high variation for row number and kernel color. Abebe and Asmund, (1996) obtained diversity for spike row type, lemma and aleurone color, rachilla Hairiness and caryopsis type. Birhane and Alemayehu (2011) reported that the existence of high polymorphism for the trait like kernel row number, spike density and kernel color, however the authors obtained low polymorphism for kernel covering. Likely, Adugna (2011) reported high phenotypic diversity for spike density, spike altitude, awn roughnes and kernel row number.

Kemelew and Alemayehu (2011) reported a high diversity index among 181 barley landraces, using collections from Shewa and Wollo for the eight qualitative characters considered. Bedassa *et al.*(2015) obtained high phenotypic diversity for kernel row number, grain color, and spike attitude and low diversity for lemma color. More recently, Addisu *et al*. (2018)

reported moderate to high diversity index among 36 barley landraces collection from southern high land Ethiopia. In general, Many studies confirm that the existence of substantial diversity in Ethiopian barley.

On top of large diversity in important agronomic traits, many author reported that barley landraces as an important source of resistance genes for different biotic and abiotic stress like, barley yellow dwarf virus, high lysine, drought, resistance to diseases such as powdery mildew, leaf rust, spot blotch, septoria, loose smut (Mulugeta, 1985; Yitbarek *et al*., 1998; Abbebe, 2006). Due to such remarkable diversity, Vavilov (1926) suggested that Ethiopia as a center of origin of barley. However, due to the absence of a wild progenitor *Hordeum spontaneum,* later considered as secondary gene center or secondary center of diversity and not as center of origin (Tolbert *et al*., 1979). Diversity in altitude, soils, climate and topography together with geographical isolation for long periods, are considered as the main factors influencing the large diversity in Ethiopian barley (Bedassa *et al*., 2014). Moreover, the wide cultural diversity in the country also plays an important part in the diversification of the landraces.

2.6. Heritability in Barley Traits

From breeding point of view, usefulness of a character is related to its onward transmission from the parent to the progeny (Raiz and Chowdhry, 2003). A quantitative measure that provides information about the correspondence between genotypic and phenotypic variance is heritability (Dabholkar, 1992). Heritability can be defined, in broad sense, as the proportion of the genotypic variability to the total variance (Allard, 1960). According to Falconer and Mackay (1996) heritability in narrow sense is defined as "the ratio of additive genetic variance to phenotypic variance. Heritability in broad sense estimates the ratio of total genetic variance, including additive, dominance, and epistatic variance to the phenotypic variance whereas heritability in the narrow sense estimates only the additive portion of the total phenotypic variance (Raiz and Chowdhry, 2003) and it expresses the extent to which phenotypes are determined by the genes transmitted from parents.

The most important function of the heritability in the genetic study of metric characters is its predictive role, expressing the reliability of the phenotypic value as a guide to breeding value (Falconer and Mackay, 1996). Therefore, the success in changing the characteristics of the population can be predicted from knowledge of the degree of correspondence between phenotypic value and breeding values (Vimal and Vishwakarma, 1998). Quantitatively inherited characters differ in heritability. Characters not greatly influenced by the environment usually have a high heritability. This may influence the choice of selection procedure used by the plant breeder.

The net gain from selection depends up on the combined effect of the heritability, the amount of genetic variation present, and the selection intensity. Heritability estimates that are consistently high or low when estimated over a series of populations, environments and experiments may be considered to be fairly reliable. Its main use is to determine which selection method would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects which could be transferred from parent to offspring (Poehlman and Sleeper, 1995).

Taking in to account the importance of dealing with heritability, different workers estimated heritability in barley traits. Tesfahun (2000) reported highest heritability estimation for spikelets per spike, thousand-kernel weight, days to heading, kernel number per spike, hectoliter weight, plant height, and tiller per plant and low value of heritability for trait like biological yield and yield per plant. Study of Shambel (2001) revealed high estimate of broad sense heritability for days to heading, days to maturity, number of kernel per spike, number of spikelet per spike, and thousand grain weight. Report of this author also indicated moderate estimate of heritability for grain filling period, node number, yield per spike, plant height and spike length. Sintayehu (2003) reported high estimate of heritability for thousand kernel weights, number of kernels per spike, days to heading, harvest index per plot, days to maturity, number of spikelets per spike, harvest index and plant height. Similarly, Alemayehu (2003) reported higher value of heritability for days to maturity, spike length and number of kernel per spike.

Zerihun *et al.* (2011) also reported high estimates of heritability for days to maturity, spike length, number of kernel per spike, thousand kernel weights and grain yield per plot. Shegaw *.et al* (2013) found that, high heritability for days to heading days to maturity, and lodging susceptibility and spikelet per spike. Other author, Addisu and Shumet (2015) reported high heritability in broad sense for the characters biomass per plant, plant height, maturity date, thousand seed weight, grain filling period, number of grain per spike and grain yield and, moderate heritability in broad sense for harvest index, number of spike per spikelet and number of tiller per plant.

Jimera *et al*. (2015) found that high heritability for grain yield, biological yield, plant height, days to heading, awn length, and number of effective tillers and moderate heritability values for thousand seed weight and harvest index and low heritability values for spike length, days to maturity, number of tillers per plant, and grain yield per spikes. Azeb *et al*.(2016) also reported high heritability for number of days to maturity, number of seeds per spike, days to heading, spike length and harvest index. These authors also reported low estimate of heritability for plant height and biological yield and medium heritability for grain yield. More recently, Tigist (2018) observed highest broad sense heritability for the trait like days to heading, days to maturity, thousand-kernel weight, grain yield, scald diseases, number of kernel per spike, biomass yield, number of fertile tillers per plant, hectolitre weight, spike length, seed harvest index, and plant height.

2.7. Genetic Advance in Barley Traits.

Genetic advance expected from selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at given selection intensity (Singh, 2001). Hence, genetic advance under selection measures the difference between the mean genotypic values of the selected population over the mean genotypic value of the original population (Allard, 1999). According to Burton and DeVane (1953), genetic advance tell us the estimate of the expected gain for a particular character through selection.

The genetic advance that can be expected for a particular trait through selection is the product of heritability, phenotypic standard deviation and selection differential (Sharma, 1998). Genetic advance as percent of mean (GA) is more reliable index for understanding the effectiveness of selection in improving the traits because the estimates are derived by involvement of heritability, phenotypic standard deviation and intensity of selection (Mohammed and Firew,2015).

According to Johnson *et al*. (1955), genetic advance as percent of mean (GAM) can be categorized as high (>20%), moderate (10-20%) and low (0-10). Traits with high genetic advance as percent of mean imply that, they are governed by additive gene. Hence, simple selection based on those traits will result in the improvement of the genotypes. On the other hand, traits with low value of genetic advance as percent of mean indicates they are governed by non-additive gene action and improvement of genotypes through simple selection of these traits may not be effective.

Numerous woks have been reported on genetic advance of important barley traits. Tesfahun (2000) found maximum expected genetic advance as percentage of mean for spikelets per spike, kernel number per spike, tillers per plant, grain weight, kernel weight per spike and spike weight. Report of Shambel (2001) revealed that spike length, tiller number, thousand grain weight, biomass weight, grain yield weight and number of kernel per spike, and number of spikelet per spike showed highest estimate of genetic advance. Zerihun *et al.* (2011) found that high genetic advance for grain yield per plant, and biomass. Shegaw *et al*. (2013) found high genetic advance (as percentage of mean) for the trait likes susceptibility to lodging, flag leaf width, spikelet per spike and grain yield per plant.

Zeynu *et al*. (2015) conducted genetic variability of food barley genotypes across two location at Debark and Holeta and they reported high expected genetic advance as percent of mean for kernel number per spike, biological yield, thousand seed weight and grain yield, moderate genetic advance as percent of mean for the character like days to heading, plant height, spike length and harvest index and low estimate of genetic advance as percent of mean for days to maturity, grain filling period and number of productive tiller per plant at Holeta. And at

Debark, they observed highest estimate of genetic advance as percent of mean for the trait kernel number per spikes, grain yield and harvest index, moderate genetic advance as percent of mean for the trait spike length, grain filling period and biomass yield and low estimate of genetic advance as percent of mean for days to heading, days to maturity, plant height and thousand seed weight.

Meseret (2015) observed high genetic advance as percent of mean for kernel number per spike, harvest index, spike length and days to heading and lowest estimate for grain filling period, biological yield, days to maturity and grain yield at Chencha. They also observed lowest genetic advance as percent of mean for days to maturity, grain filling period, biological yield, and grain yield and hectoliter weight at Angacha. Other author, Kefyalew (2016) detected high genetic advance as percent of mean on number of productive tiller per plant, spike length, harvest index, number of seeds per spike and grain yield. More recently, Work of Temesgen *et al.* (2018) indicated higher values of genetic advance estimates as percentage of mean for number of kernels per spike, grain yield and harvest index and low values of genetic advance estimate as percent of mean for days to maturity, grain filling period, plant height, spike length, peduncle length and awn length.

2.8. Correlation and Path Coefficient Analysis in barley

2.8.1. Correlation coefficient analysis in barley traits

Correlation is the measure of linear association between two traits (Hallauer and Miranda, 1988). It is a useful technique, which provides information about the degree of relationship between plant characters and is also a good index to predict the yield response in relation to the change of a particular trait.

There are two types of correlations; phenotypic and genotypic. Phenotypic correlation measures the extent to which two observed characters are linearly related. Genetic correlation is a measure of the extent to which the same gene or closely linked genes cause simultaneous variation in two different traits. The two possible causes of a genetic correlation are attributed to pleiotropic and/or linkage (Allard, 1960). Pleiotropic occurs when one gene affects simultaneously several physiological pathways, resulting in influence over several observed

traits. Linkage refers to genes that show a tendency to be transmitted together within a population (Hallauer and Miranda, 1988).

Traits of crop plants are generally correlated either positive or negative and correlations between such traits are frequent features in plant breeding. The knowledge of their coefficients provides a measure of genetic association between traits in order to identify the important traits to be considered in a breeding program. When correlation is negative the movements are in opposite directions, that is, high values of one variable are associated with low values of other (Yadav *et al*., 2011). Depending on the sign of genetic correlations between two traits can either facilitate or impede selection progress. Correlation value (r = 1) implies perfect (100%) correlation, where both traits vary hand in hand, (r = -1) means there is 100 % correlation between two characters, but they vary in opposite direction, and (r = 0) carries the implication that there is no correlation at all between the two characters (Falconer and Mackay, 1996).

Yield is an ultimate criterion which a plant breeder has always to keep in view in his/her attempt to evolve improved cultivars of any crop species. However, Yield is a complex quantitative character governed by a large number of genes with small cumulative effect and is highly influenced by environment (Dyulgerova, 2012). Accordingly, selection of superior genotypes based on yield alone is not as such effective. This signifies for successful yield improvement, selection has to be made for the component traits of yield. Hence, knowledge of the association of quantitative characters for yield and its attributes is of immense practical value during selection (Khan *et al.*, 2017***).***

In barley, number of author reported the mutual association of yield and yield related traits. In very early, work of puri *et al*. (1982) shown that yield was highly significantly correlated with harvest index, biomass and thousand grain weight. Fikadu (1982) reported negative and significant association of yield with number of tiller per plant and number of kernel per spike. Correlation analysis undertaken by Sairam and Singh (1989) indicated a positive and significant association of yield with tiller number per plant, Spike length, grain number per spike, thousand-kernel weight, biomass, and harvest index.

Tesfahun (2000) reported positive association of grain yield with spike weight, thousand kernel weight, and grain yield per plant, biomass yield, and harvest index with grain yield at both phenotypic and genotypic levels across two locations. On the other hand, the author observed negative and significant association of plant height and days to heading with yield. Woldeyesus (2002) found that grain yield was positively correlated with plant height, grain-filling period, spikes per square meter and kernels per spike. On the other hand, negative and significant association of grain yield with days to heading and days to maturity was reported by Bhutta *et al*. (2005).

Zerihun *et al*.(2011) observed highly significant phenotypic correlation of grain yield with days to heading, number of spikelets per spike, spike weight, number of kernels per spike, days to maturity, biomass yield per plant, harvest index per plant, harvest index per plot, thousand kernel weight, and grain yield per plant. These authors also observed significant positive genotypic correlation of grain yield with biomass yield per plant, thousand kernel weights, spike weight, grain yield per plant, harvest index per plot, days to maturity, harvest index per plant, days to heading, and number of spikelets per spike.

Study of Jimera *et al.* (2015) revealed that of twelve traits considered in their investigation, grain yield had significant positive correlation coefficient with biological yield and harvest index at both phenotypic and genotypic level and non-significant positive association with days to maturity, plant height, number of tillers, number of effective tillers, grain yield per spike and spike length. Apart from the mutual association of yield and attributer traits, these authors observed association of each trait themselves. They detected that biological yield showed negative and significant phenotypic correlation coefficient with awn length and negative non-significant phenotypic correlation coefficient with spike length and thousand seed weight, while it had positive non-significant phenotypic correlation coefficient with all other traits considered in their study and thousand seed weight had positive significant phenotypic correlation coefficient with awn length but, it had negative significant phenotypic correlation coefficient with spike length .

Kefyalew (2016) reported that high significant positive association of grain yield with number of seed per plant, number of seed per spike and biomass yield both in phenotypic and genotypic level and thousand seed weight and spike length showed non-significant negative association with grain yield at both levels. Azeb *et al*. (2016) found that positive and significant phenotypic and genotypic association of grain yield with biological yield and thousand kernel weights in all environments considered. On the other hand, these authors observed a positive and highly significant phenotypic and genotypic correlation between biological yield with number of productive tillers and 1000 kernel weight in all environments. More recently, Geleta *et al*. (2019) reported positive and significant genotypic correlations of grain yield with weight per spike, spike weight per plant, 1000-seed weight, biological yield, awn length, and plant height. On the other hand, they found negative significant association of yield with days to heading and days to maturity.

2.8.2. Path-coefficient analysis in barley traits

Though correlation coefficient is important to determine characters that directly affect grain yield, it is insufficient to determine indirect effect of these traits on grain yields. Thus, path-coefficient analysis is one of the reliable statistical techniques which allow quantifying the interrelations of different components and their direct and indirect effects on grain yield through correlation estimates (Dyulgerova, 2012). Path coefficient analysis is simply a standardized partial regression coefficient that measures the direct and indirect effects for one variable upon another, and also permits the separation of the correlation coefficient into components of direct and indirect effect (Dewey and Lu, 1959). Path coefficient analysis specifies the cause and measures the relative importance of the characters, while correlation measures only mutual association without considering causation (Dewey Dr and lu, 1959).

In barley, several authors reported direct and indirect effect of different yield attributing traits on yield. Investigation undertaken by Tewari *et al*. (1980) indicated that high positive direct effect of spikelets per spike, thousand grain weight and number of effective tillers per plant on yield. The report also indicated that plant height, length of main spike and number of effective tillers per plant showed negative direct effect on yield. Other Path-coefficient analysis result revealed that biomass and harvest index had maximum effect on grain yield both at genotypic

and phenotypic levels (Sairam and Singh, 1989). Study of Singh *et al*. (1998) also shown that number of tillers per plant thousand grain weights, spikelets per spike, and plant height had direct contribution to grain yield per plant. Tesfahun (2000) found that biological yield and harvest index exerted positive and strong direct effect on yield per plot at phenotypic level. Likewise, Sintayehu (2003) also reported the importance of harvest index per plot and biomass per plot on grain yield.

Ataei (2006) reported number of spike per plant and harvest index showed positive direct effect on grain yield and kernel per spike showed significant indirect positive effect on grain yield. Likely, Zerihun *et al* (2011) observed positive maximum direct effect of spike weight and harvest index on grain yield and negative direct effect of days to maturity on grain yield per plant at phenotypic level. These authors also observed positive and maximum direct effect of spike weight, grain filling period days to heading thousand kernel-weight and number of fertile tillers per plant on gain yield per plant.

Study conducted by Dyulgerova (2012) showed that grain weight per plant and grain number per spike had high direct positive effect on grain yield. Other study conducted by Kefyalew (2016) revealed that the direct effect of biomass yield and harvest index were high and positive. On the other hand, this author reported the direct effect of days to heading, days to maturity, plant height, and number of productive tiller per plant showed positive and very low in magnitude and the direct effect of spike length thousand seed weight and number of seed per spike were negative and non-significant.

Meseret (2015) reported the highest positive direct effect of biological yield on grain yield at phenotypic level. The author also observed direct positive effect of plant height, number of kernel per spike and thousand kernel weights and the respective indirect effect of these characters were negative and negligible. The author also reported the highest positive direct of thousand weight and negative direct of plant height and number of kernel per spike at genotypic level.

Other study conducted by Negash *et al.* (2019) revealed that biological yield showed highest positive direct effect on yield and the indirect effect of the trait through thousand seed weight, total tillers per plant, and grain weight per spike was large at genotypic level. Azeb *et al*. (2016) reported that biological yield exerted maximum positive direct effect on grain yield across locations. Similarly, the highest positive direct effect on grain yield per plant was exerted by biological yield, number of productive tillers per plant, plant height, length of spike, days to maturity, harvest index (Amardeep *et al*., 2017). Mogghhadam *et al*. (2009) and Blanco *et al*. (2010) reported positive direct effect of thousand grain weight on grain yield

2.9. Genetic Divergence (Genetic Distance) Analysis

The pattern and level of genetic diversity in a given crop gene pool can be measured in terms of genetic distances. Genetic distances are measures of the average genetic divergence between cultivars or populations (Souza and Sorrells, 1991). Moll *et al*.(1965) defined genetic divergence of two varieties as a function of their ancestry, geographic separation and adaptation to differing environments. Genetic distance is the extent of gene differences between cultivars as measured by allele frequencies at a sample of loci (Nei, 1987).

It is raw material in plant breeding for developing high yielding varieties and for maintaining the productivity of such varieties by incorporating genes for disease and insect resistance as well as tolerance to abiotic stress as drought, cold and salinity (Allard, 1964). Besides, Conservation of germplasm resources is fundamental to crop improvement programs However, for practical exploitation of the apparent variability, grouping or classification of genetic stocks based on a suitable scale are quite imperative. To that end, D^2 statistic is now most frequently used for these purposes (Sharma, 1998).

The D^2 statistics measures the forces of differentiation at intra- and inter-cluster levels and determines the relative contribution of each component trait to the total divergent (Sharma, 1998). Clusters separated by the largest D^2 (genetic distance) show the maximum divergence, while the genotypes in the same clusters or groups are less divergent (Singh and Chaudhary, 1977). Crossing of genotypes belonging to the same cluster would not be expected to yield desirable recombinants. Consequently, a crossing program might be formulated in such a way

that parents belong to different clusters. The more diverse the parents, within overall limits of fitness, the greater are the chances of obtaining higher among heterotic expression of F1's and broad spectrum of variability in segregating populations (Norden, 1980).

In barley, number of researchers assessed the diversity of barley using this scheme. Using D^2 statistics Shegaw *et al*. (2013) evaluated 225 genotypes 207 landraces collection from southern Ethiopia and 18 released varieties. They found 10 clusters of genotypes and maximum inter cluster between clusters, implying the considerable genetic divergence among genotypes. Report of Shambel (2001) indicated that forty seven genotypes were grouped in to seven district groups for sixteen quantitative traits, implying the existence of genetic dissimilarity for trait considered and the diversity among the genotype used. Similarly, Tigist *et al*., (2010) reported 199 genotype were grouped in to seven clusters indicating the presence of genetic diversity among genotype considered. Likely, Kefyalew (2016) reported highly significant genetic distance between six clusters in which sixty four genotypes grouped. Moreover, he observed the maximum inter cluster distance between 4 clusters of six clusters, this signify how the diverse the genotype the cluster contains.

2.10. Principal Component Analysis.

Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre, 1998). Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). PCA can be used to drive a two dimensional scatter plot of individuals, such that the geometrical distance among individuals in the plot reflect the genetic distances among them with minimal distortion. Aggregates of individuals in such a plot will reveal sets of genetically similar individuals.

The resulting diagram can give the researcher an idea about the correctness and inference of cluster analysis results (Bensmail *et al*., 1997). This will allow visualization of the differences among the individuals and identify possible groups. The first step in PCA is to calculate Eigen values, which define the amount of total variation that is displayed on the PC axes. 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 (Joliffe, 1986). The eigenvectors determine the directions of the new feature space and eigenvalues measure the amount of variation in the total sample accounted for by each factor.

3. MATERIALS AND METHODS

3.1. Description of Experimental Site

The experiment was conducted at Alarigata, substation of Bonga Agricultural Research Center, during main cropping season of 2018. Alarigata is one of major barley growing area which is found in Adiyo Woreda of Kafa Zone, Southern Nations Nationalities and People's Region (SNNPR) and located 491 km southwest of Addis Ababa, which is 21 km away from Bonga town. It lies in altitude of 2476 masl, latitude of 07˚ 17'N, and longitude of 36˚ 21'E. The area experiences long rainy season lasting from March to November and receives mean annual rainfall of 2543mm with mean minimum and mean maximum temperature of 11.77°C and 26.52°C, respectively. It has a soil type of sandy clay loam with a p^H value of 5.6.

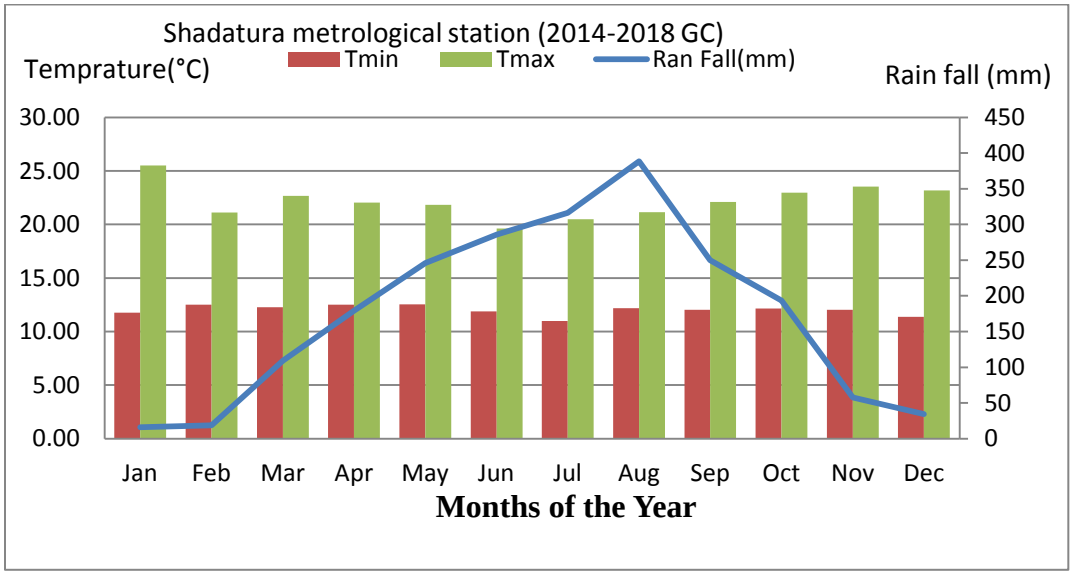

Figure 1: Minimum and maximum temperature as well as monthly rainfall distribution of experimental sites.

3.2. Experimental Materials

A total of 105 barley genotypes were used in this study. One hundred barley landraces were obtained from Ethiopian Biodiversity Institute (EBI) (Appendix Table 1) and five standard checks, Cross 41/98, EH1493, HB 1966, HB 13/07 and Shege were obtained from Holeta Agricultural Research Center.

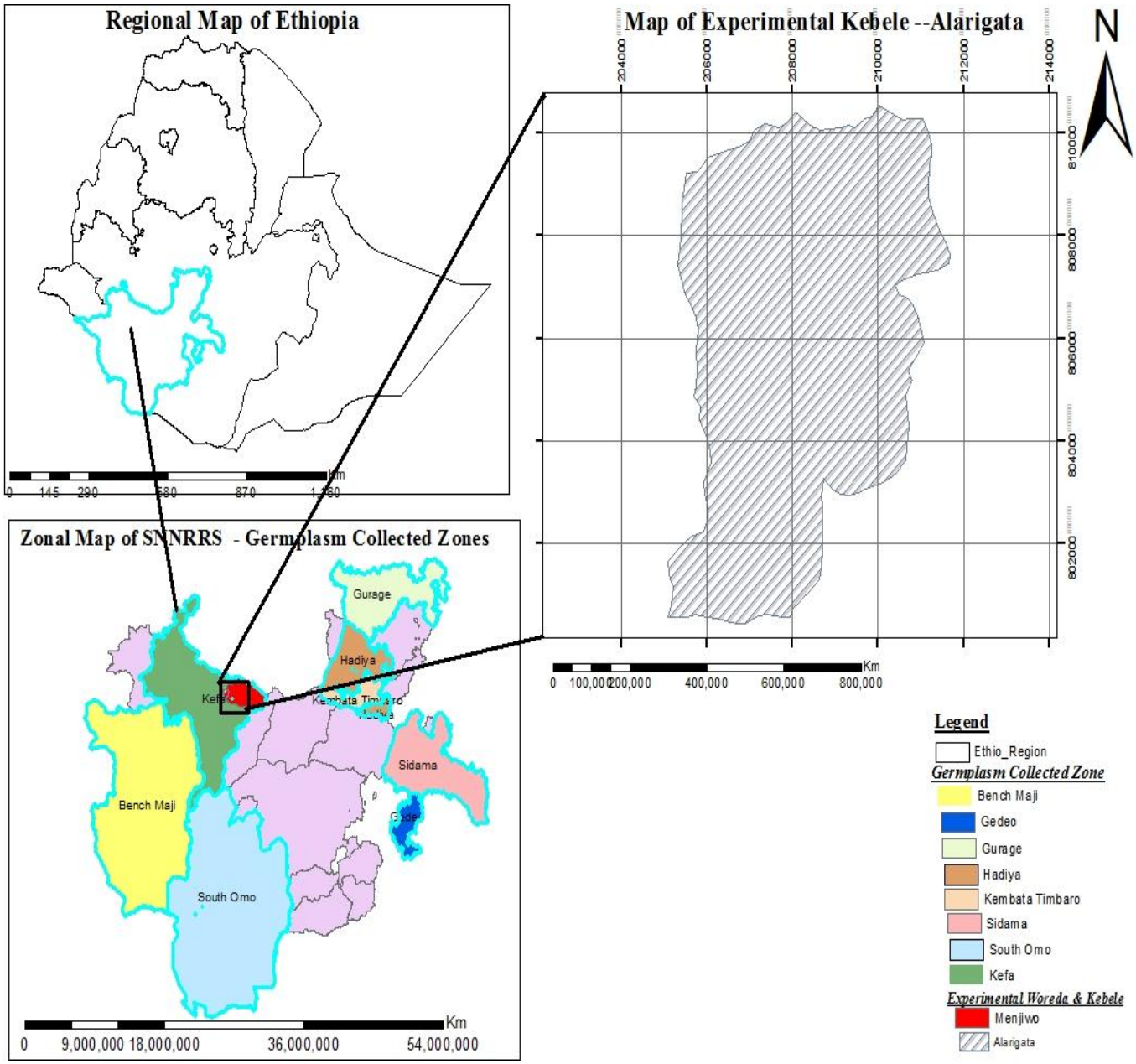

Figure 2**:** Map of landraces collected zones and study area.

3.3. Experimental Design and Trial Management

The experiment was laid out using augmented design consisting of ten blocks in which 100 accession were planted in un-replicated plots and the five checks were replicated ten times to estimates error variance. The plot area was $1m^2$ (0.2m x 2rows x 2.5m) and spacing between plots and blocks was 0.5m and 1m respectively. Seeds were drilled by hand at rate of 100 kg ha^{-1}. DAP fertilizer was applied at the rate of 100 kg ha^{-1} at the time of planting and 100kg

ha¯1 Urea was applied four week after sowing. Other agronomic practices were undertaken uniformly for all experimental units.

3.4. Data Collected

Both Quantitative and qualitative data were recorded according to the International Plant Genetic Resource Institute (IPGR, 1994) descriptor for barley. Accordingly, the following data were taken.

Plant based quantitative data collected

- **Plant Height (cm):** Was measured as the height in centimeter from the soil surface to the tip of spike excluding the awn at maturity and expressed as an average of randomly taken ten plants in each plots
- **Awn Length (cm):** awn length of main plant was measured in centimeter from the tip of the spike to the end of the awn and expressed as the average of randomly taken ten plants.
- **Spike Length (cm):** Spike length of the main plant was measured in centimeter from base to the tip excluding the awns and expressed as the average of randomly taken ten plants.
- **Number of Fertile Tillers per Plant (count):** Fertile numbers of tillers (spike bearing) per plant was counted and expressed as an average of randomly taken ten plants in each plots.
- **Number of Seeds per Spike (count):** Was determined by counting the number of seeds produced on the main tiller of each plant and expressed as an average of randomly taken ten plants in each plot.

Plot based quantitative data collected

- **Days to heading (count):** Number of days from sowing to the day when 50% of the heads fully flower was counted.
- **Days to maturity (count)**: Was recorded as the number of days from sowing to the stage when 75% of a plot reached maturity.
- **Grain filling period:** It was determined by subtracting days to 50% flowering from days to maturity.

- **Biomass yield (t ha^{-1}):** Was determined by weighing the total dried above ground biomass from each plot and expressed as t ha^{-1}.
- **Thousand Seed weight (g**): was recorded by weighing one thousand randomly taken seeds from each plot and by adjusting its moisture to 12.5%.
- **Grain yield (t ha^{-1}):** grain yield was recorded by measuring the grain obtained from each plot and adjusted its moisture content to 12.5% and expressed in t ha^{-1}.
- **Harvest index (%)**: It was calculated as the ratio of dry grain yield to the above ground biomass yield.

Qualitative traits collected

- **Kernel color (KC):** It was recorded on the harvested seeds of each plant and recorded as (1) for white (2) for black (3) for blue and (4) for purple
- **Kernel row number:** The number of spike rows found on the mother plant was recorded as (1) for two-row type, (2) for six row types and (3) for irregular type.
- **Spike density:** was recorded as (1) for lax, (2) for intermediate and (3) for dense.
- **Rachila hair length/type:** It was recorded as (1) for short hair rachilla and (2) long hair rachilla.
- **Hoodedness /awnednes:** It was recorded as (1) for Awnless, (2) for awnleted,(3) for awned (4) sessile hoods.
- **Kernel covering**: It was recorded as (1) - naked grain (grain without glume, (2)-covered grain **(**grain with usually persistent glumes).
- **Susceptible for lodging:** Susceptibility of the crop to resist lodging was recorded as 1, very low or no visible susceptible sign, (3) low (5), intermediate and (7), high

3.5. Data Analysis

3.5.1. Analysis of variance (ANOVA)

All quantitative traits were subjected to analysis of variance using statistical procedure for augmented design. Analysis of variance (ANOVA) was undertaken using Proc GLM procedure of SAS v 9.3 (SAS, 2014).

The model for augmented design is $Y_{ij}=\mu+\beta_i+C_j+\tau_{k(i)}+\varepsilon_{ij}$

Where, Yij =observation of treatment

μ= general mean

$\beta_{i=}$ the effect of j^{th} block

C_j=effect of j^{th} checks

$\tau_{k(i)}$= effect of i^{th} new entries

ε_{ij}=error associated in the observation

3.5.2. Estimation of variance components

The phenotypic and genotypic variances were estimated according to the method suggested by Burton and De vane (1953) as follows:

Genotypic variance (δ^2_g) = $\frac{MSg-MSe}{blocks}$

Where, Msg=mean square of genotypes

Ms_e= mean square of error (environmental variance)

Phenotypic variance (δ^2_p) = δ^2_g +Ms_e

Where, δ^2_g =genotypic variance and

Ms_e= mean square of error (environmental variance)

The coefficients of variations at phenotypic and genotypic levels were estimated using the formula given by Johnson *et al*., (1955).

Genotypic coefficient of variation (GCV) =$\frac{\sqrt{\delta^2 g}}{\bar{x}}$ x 100

Phenotypic coefficient of variation (PCV) =$\frac{\sqrt{\delta^2 P}}{\bar{x}}$X100

Where: δ^2_p =Phenotypic variation;

δ^2_g = Genotypic variation and

$\bar{x}$= Grand mean of the trait

3.5.3. Estimation of heritability in broad sense

Broad sense heritability (H^2) was estimated as the percentage of the ratio of the genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) and was estimated on genotype mean basis as described by Allard (1960) as:

$H^2 = {\delta^2 g}/{\delta^2 p} * 100$

Where: H^2 =heritability in broad sense,

$\delta^2 g$ = Genotypic variance and,

$\delta^2 p$ = Phenotypic variance

3.5.4. Estimation of genetic advance under selection

It was calculated by assuming selection of superior 5% of the genotypes estimated in accordance with the methods illustrated by Johnson *et al* (1955) as:

$GA = K * \sigma p * H^2$

Where, k = the standardized selection differential at 5% selection intensity (K = 2.063)

σp = phenotypic standard deviation

H^2= Heritability

Genetic advance as percent of mean was calculated to compare the extent of predicted advance of different traits under selection, using the following formula.

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

Where, GAM= Genetic advance as percent of the mean

GA= Genetic advance under selection

$\bar{X}$ =Mean of the population in which selection was employed.

3.5.5. Estimation of genotypic and phenotypic coefficient of correlation

Estimate of genotypic and phenotypic association between all possible pair of quantitative character was performed using SAS software version 9.3 (SAS, 2014).

3.5.6. Path coefficient analysis

The direct and indirect effect of yield related traits on yield per plot was computed through path coefficient analysis. The analysis was made following the method suggested by Dewey and Lu (1959), described as follows

$$rij = \Sigma rik\ pkj + Pij$$

Where: rij = Mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient.

Pij = Component of direct effects of the independent trait (i) on the dependent variable (j) as measured by the path coefficient and,

Σrik pkj = Summation of components of indirect effect of a given independent trait (i) on the given dependent trait (j) via all other independent traits (k).

The contribution of the remaining unknown factor was measured as the residual factor (PR), which is calculated as:

$$PR=\sqrt{(1-\sum pijrij)}$$

Where, PR=residual factor

pij=direct effect on yield by i^{th} trait, and

rij =correlation of yield with the i^{th} trait.

3.5.7. Cluster analysis

Clustering was performed using the PROC cluster procedure of SAS version 9.3 (SAS institute, 2014) by employing the method of average linkage clustering strategy of the observation. The values of pseudo F statistic (PSF) and pseudo T^2 statistic were used for defining the appropriate number of clusters.

3.5.8. Genetic divergence analysis

Genetic divergence analysis was performed based on multivariate analysis using Mahalanobis's D^2 statistic (Mahalanobis, 1936) by using the procedure Proc discrim of SAS version 9.3 (SAS Institute, 2014). Significance of the squared distances for each cluster was tested against the tabulated χ^2 values at p degree of freedom both at 1% and 5% probability level, where, p = number of characters used for clustering genotypes (Singh and Chaudhary, 1996).

3.5.9. Principal component analysis

Principal component analysis is a multivariate technique, which is used to identify the traits having a large amount of contribution to the total variation in the studied genotypes. Principal component analysis was performed by using SAS version 9.3 (SAS Institute, 2014). In

principal component analysis, eigenvalues greater than one were considered important to explain the observed variability.

3.5.10. Percentage frequency distribution

The percentage frequency distribution of phenotypic classes for seven qualitative characters were computed using excel computer program (Microsoft excel, 2010) and chi square analysis was performed to test deviations of each characters from the expectation.

3.5.11. Estimation of Shannon-Weaver diversity index

The Shannon-Weaver diversity index (H') which has been widely used in ecological studies of species diversity and in measuring the diversity of germplasm collections were estimated from phenotypic frequency data. It was computed to assess the phenotypic diversity for each character, entire accession and the accession grouped for each zone of collection. The Shannon-Weaver diversity index was calculated as described by Hutchenson (1970), i.e.

$$H' = -\sum_{i=1}^{n} pi(lnpi)$$

Where H' =Shannon weaver diversity index,

Pi = the proportion of the total number of individual accession in the i th class,

ln = natural logarithm and n is the number of phenotypic classes for a given character.

H was standardized by converting to the relative index (H'), where each value of H were divided by its maximum value as follows, in order to keep the value between zero and one

$$H' = H / Hmax$$

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance (ANOVA)

Mean square of 12 traits is presented in Table 1. The result indicated that there were highly significant ($p<0.01$) difference among genotypes for most of the traits except awn length (Table 1), indicating the existence of notable variation among genotypes.

Table 1: Analysis of variance for 12 quantitative traits of 105 barley genotypes evaluated at Alarigata in 2018 cropping season

Traits	MSb (Df=9)	MSg (Df=104)	MSa (Df=99)	MSc (Df=4)	$MSa_{vs}c$ (Df=1)	MSe (Df=36)	CV%
Days to heading	25.86	222.97**	221.00**	247.8**	310.08**	10.96	5.04
Days to maturity	68.89	388.85**	355.73**	405.38**	2598.96**	16.69	3.63
Grain filling period	131.48	249.64**	213.19ns	201.22ns	3447.63**	66.18	11.64
Awn length	0.25	0.35ns	0.36ns	0.11ns	0.05ns	0.30	3.70
Spike length	0.79	6.52**	4.38**	7.06**	0.06ns	0.89	12.74
Number of seeds per spike	39.96	274.98**	203.60**	134.26*	9667.36**	14.91	9.39
Plant height	24.91	198.68**	168.74**	256.26**	631.33**	13.52	4.15
Number of fertile tillers per plant	0.29	3.60**	2.61**	4.77**	0.42**	0.14	8.42
Thousand seed weight	9.85	96.72**	37.27**	70.06**	68.00**	8.34	7.19
Harvest index	24.3	59.45**	56.82**	52.39**	408.31**	2.87	4.12
Biological yield	0.15	1.07**	1.02**	2.31**	7.91**	0.1	4.568
Grain yield	0.1	0.90**	1.54**	1.92**	4.61**	0.02	5.3

Key: *=significant at 0.05 probability level, **= highly significant (p=0.01) and ns=non-significant, MSb=Mean square of block, MSg=Mean square of genotypes (check and accession), MSa=Mean square of accession, MSc=Mean square of checks, $MSa_{vs}c$= mean square of accession versus control, MSe= Mean square of error, Df= Degree freedom and CV=coefficient of variation as percentage.

In support of this finding, Shegaw *et al.* (2013) reported the existence of enormous variability among genotypes for traits like days to heading, days to maturity, plant height, spike length, thousand seed weight and grain yield per hectare. Similarly, Bedassa *et al.* (2014) reported the

presence of highly significant variation for days to heading, days to maturity, number of fertile tillers per plant, plant height and thousand seed weight.

4.2. Estimation of Variability for Quantitative Traits

4.2.1. Mean and range of measured traits

Mean, minimum and maximum value for quantitative traits of 105 genotypes is presented in Appendix Table 2. The mean grain yield ranged from 1.69 t ha^{-1} to 4.12 t ha^{-1} with grand mean yield of 2.96 t ha^{-1} and 33.33% of genotypes gave above grand mean (2.96 t ha^{-1}). The highest yield was obtained from Acc 28062 (4.12 t ha^{-1}) with 11.95% yield advantage over the best standard check cross 41/98 (3.68t ha^{-1}) (Appendix Table 2). Besides, accession 215484, 219301, 29696, 28059,233052 and 27888 gave high yield with notable yield advantage over this check (Appendix Table 2). This showed the presence of high yielding genotypes and opportunity for breeders to further improvement of barley yield through the possible breeding strategy.

Based on their maturity, the genotypes showed wide range of variation. The genotypes varied from 90 to 134 days between early and late maturing genotypes. This the existence of wide spectrum of variation among early and late maturing genotype is a good implication for those breeder who are interested to screen variety for moisture deficit as well as high rain fall areas. In general, wide range of variation was observed for most of traits. This indicated the existence of notable variation among genotypes considered in the investigation. In harmony with this finding, Shegaw *et al.* (2013) reported wide range of variation for grain yield, plant height, days to maturity and days to heading. Likewise, Adisu and Shumet (2015) reported the existence of wide range of variation for the trait like plant height, biomass per plant, number of seed per spike, spike length and number of tiller per plant among 36 barley landraces included in their study, Kefyalew (2016) also reported existence of wide range of variation among barley landraces for trait like biological yield, grain yield and days to maturity.

4.2.2. Estimation of variance components and coefficient of variations

The result of estimated variances component, phenotypic coefficient of variations (PCV) and genotypic coefficient of variations (GCV) of the traits are presented in Table 2. In order to know the actual share of genotypic variance, the phenotypic variance (total variance) was partitioned in to genotypic and environmental variances. The result revealed that the portion of genotypic variance for number of seeds per spike, plant height, number of fertile tiller per plant, thousand seed weight, days to heading days to maturity, harvest index and grain yield were greater than 50% (Table 2) which mean, genotypic effect on the phenotypic expression was greater than the effect of the environment by more than 50%.

On the other hand, the effect of environment on the expression of phenotype for grain filling period, spike length and biological yield were greater than genotypic effect, implying the phenotypic expression is more influenced by environment than the inherent genetic constitute of the characters. In agreement with this finding,Temesgen *et al*.(2018) reported the genotypic variance took much of total variance for days to heading, days to maturity, number of kernel per plant, grain yield,1000-kernel weight and harvest index and environmental variance took relatively much of the total variance for spike length and grain filling period.

Azeb *et al.* (2016) also reported that the genotypic variance took relatively much of the total variance for days to maturity, number of productive tiller and number of kernels per spike. Similarly, Ahmed, *et al.*(2008) reported that high level of genotypic variance for days to heading, maturity, and grains per spike, 1000-seed weight and harvest index than environmental variance.

Estimate of phenotypic coefficient of variations (PCV) ranged from 6.40% for plant height to16.27% for spike length and genotypic coefficient of variations (GCV) ranged from 4.36% for biological yield to13.22% for number of fertile tiller per plant (Table 2). According to Deshmukh *et al*. (1986), PCV and GCV values greater than or equal to 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be medium. Based on this bench mark, medium GCV and PCV (10% up to 20%) were observed for grain filling period, spike length, number of seed per spike, number of fertile tiller per plant, and grain yield (Table 2).

Table 2: Estimation of variance components and coefficient variation for 11 quantitative traits of 105 barley genotypes evaluated at Alarigata in 2018 cropping season.

Traits	δ^2g	δ^2p	δ^2e	Share of %		GCV (%)	PCV (%)
				δ^2g	δ^2e		
DH	21.20	32.17	10.97	65.91		7.01	8.64
DM	37.22	53.91	16.69	69.04	30.96	5.42	6.53
GFP	26.66	56.37	29.71	47.30	52.70	11.03	16.04
SL	0.563	1.45	0.89	38.75	61.25	10.13	16.27
NSPS	24.01	38.92	14.96	63.56	36.44	12.40	15.55
PH	18.52	32.04	13.52	57.80	42.20	4.87	6.40
NFTPP	0.246	0.386	0.14	71.19	28.81	13.22	15.67
TSW	8.83	17.17	8.34	51.43	48.57	7.40	10.34
HI	5.66	8.53	2.87	66.33	33.67	5.79	7.11
BY	0.096	0.202	0.105	48	52	4.36	7.82
GY	0.087	0.112	0.024	77.67	21.42	10.01	11.33

Key: DH= days to heading, DM= days to maturity, GFP = grain filling periods, SL=spike length, NSPS= number of seeds per spike, PH= plant height, NFTPP=number of fertile tillers per plant, TSW = thousand seed weight, HI = harvest index, BY = biological yield GY=grain yield δ^2g = genotypic variance, δ^2p = phenotypic variance GCV(%) = genotypic coefficient of variations and PCV(%) = phenotypic coefficient of variations.

The medium PCV and GCV value indicated that the variation observed among genotypes for these traits were more of due to their genetic difference rather than environmental influences. It directs that simple selection may be effective based on these traits and their phenotypic expression would be a good indication of genetic potential as different genotypes can provide materials for a sound improvement program. In support of this finding, Kefyalew (2016) reported medium estimate of GCV and PCV for number of seed per spike, spike length and grain yield. Low GCV and PCV (< 10%) were observed for days to heading, days to maturity, plant height, thousand seed weight, harvest index and biological yield (Table 5). In agreement with this finding, Shegaw *et al.(*2013*)* reported lower value of GCV for days to heading, days to maturity, thousand seed weight and plant height. Similarly, low GCV and PCV estimate were reported by Jimera *et al*. (2015) for days to heading, days to maturity and harvest index.

The result revealed that for all traits considered in this study, phenotypic coefficient of variability (PCV) were higher than the corresponding genotypic coefficient variation (Table 2). This indicated the observed variation was not totally due to the inherent genetic constitute of the characters, but characters were influenced by environmental factor in some extent. However, the relative narrow gap between phenotypic coefficient of variation and corresponding genotypic coefficient of variation were observed for days to heading ,days to maturity, number of seed per spike, plant height, number of fertile tiller per plant, thousand seed weight, harvest index and grain yield. This suggested that the influence of environmental factors for the phenotype expression of genotypes for these traits was low and possibility of improvement of these traits through selection based on the phenotype of genotypes. In harmony with this finding, Adisu and Shumet (2015) reported that the narrow gap between phenotypic coefficient of variation and corresponding genotypic coefficient of variation for plant height, days to maturity and thousand seed weight.

It is also in agreement with Azeb *et al*. (2016) who reported the existence of small difference between PCV and GCV for days to heading, days to maturity, number of seeds per spike and grain yield. Similarly, Kefyalew (2016) detected the narrow gap for days to heading, days to maturity, plant height, and number of seeds per spike. Likewise, the narrow gap between the phenotypic coefficient of variation and corresponding genotypic coefficient of variation was also reported by Temesgen *et al*.(2018) for days to heading, days to maturity, grain yield, harvest index and 1000-seed weight. On the other hand, larger difference between phenotypic coefficient of variation and corresponding genotypic coefficient of variation were observed for spike length, grain filling period and biological yield. It indicated that high influence of environmental factor for phenotypic expression of these traits and hence improving of these traits through their phenotypic expression may not be effective.

4.3. Estimation of Broad Sense Heritability

In this study, heritability in broad sense ranged from 38.75% for spike length to 78.13%for grain yield (Table 3). According to Singh (2001), heritability values less than 40% are considered as low, heritability values between 40 to 59% are medium, heritability values between 60 to 79% are moderately high and heritability values ≥80% are considered as very high. Based on this

delineation, moderately high heritability value were obtained from grain yield (78.13%), number of fertile tiller per plant (71.19%) days to maturity (69.04%), harvest index (66.33%), days to heading (65.91%) and number of seed per spike (63.56%) (Table 3). These indicated minimum effect of environment on phenotype expression and the effectiveness of selection in these traits for improvement (Singh, 2001).

Medium heritability was observed from, grain filling period (47.30%), biological yield (47.71%), plant height (57.80%) and thousand seed weight (51.19%). However, low estimate of heritability was observed for spike length, suggesting that selection for this trait may be impractical due to superior influence of environment (Singh, 2001). In agreement with this finding, Jimera *et al*.(2015), Adisu and Shumet (2015) and Temesgen *et al*.(2018) reported low value of heritability for spike length. In contrary of this finding, Zerihun *et al*. (2011) and Kefyalew (2016) reported very high value of heritability for spike length.

Genotypic coefficients of variation along with heritability estimate provide reliable estimate of the amount of genetic advance to be expected through phenotypic selection (Wright, 1921). Traits with high genotypic coefficient variations coupled with high heritability indicated that the traits respond effectively to phenotypic selection. Accordingly, traits which had moderately high heritability coupled with medium genotypic coefficient of variation from the present study can be improved through direct selection.

4.4. Estimates of Expected Genetic Advance

Estimate of GA and GAM are presented in Table 3. The result indicated that genetic advance for grain yield was 0.54 t ha^{-1} indicating whenever we select the best 5% high yielding genotypes as parent, the mean grain yield of progenies could be improved by 0.54 t ha^{-1} for first cycle, it mean, the mean grain yield of new population will be improved from 2.96 t ha^{-1} to 3.5t ha^{-1}. Likewise, it will be 49.52 for number of seed per spike, 44.22 for thousand seed weight and 7.66 t ha^{-1} for biological yield.

Table 3: Estimation of broad sense heritability, genetic advance and genetic advance as percentage mean for 11 quantitative traits of 105 barley genotypes evaluated at Alarigata in 2018 cropping season

Traits	**H^2**	**GA**	**GAM (%)**
Days to heading	65.91	7.71	11.74
Days to maturity	69.04	10.46	9.30
Grain filling period	47.30	7.33	15.65
Spike length	38.75	0.96	13.00
Number of seeds per spike	63.56	8.39	20.39
Plant height	57.80	6.73	7.61
Number of fertile tillers per plant	71.19	1.02	23.01
Thousand seed weight	51.19	4.37	10.89
Harvest index	66.33	4.00	9.72
Biological yield	47.71	0.54	7.7
Grain yield	78.13	0.54	18.27

Key: H^2 = heritability in broad sense, GA= genetic advance and GAM (%) = genetic advance as percent of mean

Genetic advance as percentage of mean from the current study ranged from7.61% for plant height to 23.01% for number of fertile tiller per plant. According to Johnson *et al*. (1955), genetic advance as percent of mean (GAM) can be categorized as high (>20%), moderate (10-20%) and low (0-10%). Based on this cut point, high GAM were obtained for number of fertile tillers per plant (23.01%) and number of seeds per spike (20.39%). The result indicated that these traits are governed by additive gene. Hence, simple selection based on these traits will result in the improvement of the genotypes. The finding is in accordance with Tesfahun (2000) and Shambel (2001).

Medium GAM were observed for days to heading (11.74%), grain filling period (15.65), spike length (13.0%) thousand seed weight (10.89), and grain yield (18.27%). However, low GAM was obtained for days to maturity (9.30%), plant height (7.61%) harvest index (9.72%) and

biological yield (7.7%). This indicates that improvement of traits in genotypic value for the produced population compared with the original population under one cycle of selection will be <10% at 5% selection intensity implying traits are governed by non-additive gene action and notable improvement of genotypes through simple selection of these traits may not be effective.

Having high heritability estimate for a character is not the only conclusive factor to make fruitful selection in the advanced generations but should be complemented by a substantial amount of genetic advance. According to Johnson *et al*. (1955), heritability estimate along with genetic advance are more helpful in predicting the gain under selection than heritability alone. According to panse (1957), the effective selection can be done for the characters having high heritability accompanied by high genetic advance which is due to the additive gene effect. If a character is governed by non-additive gene action it may give high heritability but low genetic advance, whereas, if it is governed by additive gene action heritability and genetic advance would be high (pance, 1957).

In this study, moderately high heritability along with relatively high genetic advance as percent of mean was observed from number of fertile tiller per plant and number of seed per spike, implying the dominance of additive gene action over non-additive gene action in expressing of these traits. Hence, selecting superior genotype based on these traits can be effective. In harmony with this finding, Tigist (2018) reported high heritability along with high estimate of genetic advance as percent of mean for number of seed per spike and number of fertile tiller per plant. On the other hand, days to maturity and harvest index shown moderately high heritability but they complemented with low genetic advance as percent of mean, implying the dominance of non-additive gene action for the expression of the traits over additive gene action. Accordingly, direct selection procedure in early segregating generation based on these traits cannot be effective for screening; rather it can be exploited as hetrosis breeding. This finding is in agreement with Zeynu *et al.* (2015) and Kefiyalew, (2016).

4. 5.Association Studies

4.5.1. Genotypic and phenotypic correlation of grain yield with other traits

Estimates of phenotypic and genotypic correlation coefficients for each pair of traits are presented in Table 4. In this study, grain yield showed positive and highly significant ($p<0.01$) genotypic and phenotypic correlation with days to maturity, grain filling period, plant height, number of fertile per plant, thousand seed weight and biological yield (Table 4). This implied that any improvement of these characters would result in a significant increment on barley grain yield. Thus, these traits can be used as selection criterion for barley yield improvement. In agreement with this finding, Tigist (2018) observed positive and highly significant association of grain yield with days to maturity, thousand kernel weights and biomass yield both at phenotypic and genotypic level. Similarly, Azeb *et al.* (2016) reported positive and significant association of grain yield with biological yield and thousand weights. In contradictory to the current finding, Meseret (2015) reported negative and high significant association of grain yield with days to maturity and grain filling period. On the other hand, grain yield showed positive and non-significant genotypic and phenotypic correlation with days to heading, spike length and number of seed per spike (Table 4)

4.5.2. Genotypic and phenotypic correlations among other characters

Days to heading showed positive and highly significant phenotypic correlation with days to maturity and plant height. In addition, it had positive and significant association with grain filling period and biological yield (Table 4). This implied that as days to heading increase there would be a simultaneous increase of days to maturity, plant height, grain filling period and biological yield. This finding is in agreement with finding of Kefyalew (2016) who reported positive and significant genotypic and phenotypic association of days to heading with days to maturity, plant height and biological yield. Likewise, Meseret (2015) reported positive and significant association of days to heading with days to maturity grain filling period and biological yield at phenotypic level.

Table 4: Estimation of correlation coefficients at phenotypic (above diagonal) and genotypic (below diagonal) levels of different characters

Traits	DH	DM	GFP	SL	NSPS	PLH	NFTPP	TSW	HI	BY	GY
DH	**1**	0.69**	0.29*	0.07ns	0.01ns	0.52**	-0.42**	-0.28*	0.05ns	0.27*	0.032ns
DM	0.75**	**1**	0.80**	0.13ns	0.12ns	0.40**	-0.35**	0.22*	0.19*	0.10ns	0.59**
GFP	0.32*	0.86**	**1**	0.02ns	0.01ns	0.52**	0.27*	0.18*	0.26*	0.31**	0.64**
SL	0.09ns	0.13ns	0.04ns	**1**	-0.02ns	0.22*	0.42**	0.02	0.002ns	0.11ns	0.04ns
NSPS	0.02ns	0.15ns	0.01ns	-0.03ns	**1**	-0.02ns	-0.54**	-0.49**	0.17*	0.13ns	0.13ns
PH	0.57**	0.48**	0.57**	0.24*	-0.106ns	**1**	0.31*	0.08ns	0.08ns	0.34**	0.72**
NFTPP	-0.48**	-0.40**	0.32*	0.51**	-0.61**	0.35**	**1**	0.31**	0.11ns	0.48**	0.68**
TSW	-0.34**	0.26*	0.23*	0.05ns	-0.51**	-0.52**	0.42**	**1**	0.10ns	0.29*	0.69**
HI	0.05ns	0.21ns	0.28*	0.001ns	0.19ns	0.12ns	0.112ns	0.10ns	**1**	0.22*	0.21*
BY	0.36*	0.11ns	0.40**	0.15ns	0.15ns	0.38**	0.32*	0.33*	0.24*	**1**	0.61**
GY	0.14ns	0.67**	0.68**	0.04ns	0.14ns	0.74**	0.76**	0.74**	0.4*	0.82**	**1**

***Key*:** *, **, and ns indicates significant at p= 0.05, 0.01 and non-significant respectively, DH =days to heading, DM =days to maturity, GFP=grain filling period, SL=spike length, NSPS=number of seeds per spike, PH=plant height, NFTPP=number of fertile tillers per plant, TSW=thousand seed weight, HI=harvest index, BY =biological yield and GY=grain yield.

On the other hand, it had negative and highly significant association with number of fertile tiller per plant and thousand seed weight both at phenotypic and genotypic level. This indicates, as days to heading increase there would be simultaneous decrease in number of fertile tiller per plant, and thousand seed weight. Besides, this trait exhibited positive and non-significant association with number of seed per spike, spike length and harvest index both at phenotypic and genotypic level.

Days to maturity had positive and highly significant correlation with grain filling period and plant height and had also positive and significant association with thousand seed weight both at genotypic and phenotypic level. This implied a genotype with long maturity day would have long grain filling period, long plant height and heavy thousand seed weight and vice versa. In coincide with this finding, Kefyalew (2016) observed positive and highly significant association of days to maturity with plant height and thousand seed weight.

On the other hand, this trait revealed negative and significant correlation with number of fertile tillers per plant both at genotypic and phenotypic level. The finding is in accordance with Geleta *et al.* (2019) who observed negative and strong association of days to maturity with number of productive tiller per plant. Besides, it had positive and non-significant association with spike length, number of seeds per spike, harvest index and biological yield. In harmony with this finding, Zerihun *et al*.(2011) reported positive and non-significant association of days to maturity with number of seed per spike, harvest index per plant and biological yield per plant.

Grain filling period exhibited positive and highly significant phenotypic association with plant height and biological yield. It had positive and significant association with number of fertile tillers per plant, thousand seed weight and harvest index. This indicated that as grain filling period increase there will be simultaneous increase in plant height, biological yield, number of fertile tiller per plant, thousand seed weight and harvest index. However, it showed positive and non-significant association with spike length and number of seeds per spike, implying the genetic effect of one trait is independent of others.

Spike length had positive and highly significant phenotypic association with number of fertile tiller and plant height. This finding is in line with finding of Geleta *et al*. (2019) who reported positive and highly significant association of spike length with plant height and number of productive tillers. On the other hand, it showed positive and non-significant association with rest of character except number of seed per spike which showed negative and non-significant association. In line with this, Kefyalew (2016) reported negative and non-significant association of spike length with number of seed per spike.

Number of seeds per spike showed negative and highly significant association with number of fertile tiller per plant and thousand seed weight. Indicating improving for number of seed per spike antagonistically decrease number of fertile tillers per plant and thousand seed weight. In coincide with this finding, Bedassa *et al*.(2014) and Kefyalew (2016) observed negative and highly significant association of number of seeds per spike with number of fertile tillers per plant and thousand seed weight. But, it had positive and non-significant correlation with, harvest index and biological yield both at genotypic and phenotypic level.

Plant height showed positive and highly significant phenotypic correlation with number of fertile tillers per plant and biological yield, implying increasing plant height can simultaneously increase number of fertile tillers per plant and biological yield. It had negative and highly significant correlation with thousand seed weight. But, it had positive and non-significant genotypic and phenotypic correlation with harvest index (Table 4).

Number of fertile tillers per plant showed positive and highly significant phenotypic association with thousand seed weight and biological yield. In addition, the association of this trait with harvest index is positive and non-significant. Thousand seed weight showed positive and significant association with biological yield and positive and non-significant association with harvest index. Harvest index showed positive and significant association with biological yield. In general, for most of trait considered in this study the genotypic correlation coefficient were higher than phenotypic correlation coefficient. This indicated that the association of various traits were due to the inherent genetic constitute rather than environment.

4.6. Path Coefficient Analysis

When more characters are involved in correlation study, it becomes difficult to ascertain the characters which really contribute to yield. Therefore, path coefficient analysis provides more effective means of separating direct and indirect factors, permitting a critical examination of the specific forces acting to produce a given correlation and measuring the relative importance of the causal factors. Thus, path coefficient analysis was used to determine direct and indirect associations among different traits. In the current study, only seven out of 11 traits were taken on the basis of genotypic and phenotypic correlations and partitioned into direct and indirect effects using grain yield as a dependent variable.

4.6.1. Phenotypic path analysis

The phenotypic direct and indirect effect of different character on grain yield is presented in (Table 5). The phenotypic path result revealed that thousand seed weight (0.69) and plant height (0.51) exerted the highest positive direct effect on grain yield with positive indicating true relationship with yield and direct selection of these traits for yield improvement can be effective. Indirect effect of thousand seed weight via grain filling period, plant height, harvest index and biological yield was positive and negligible. This indicated that the positive and significant correlation of thousand seed weight with grain yield was due to its large direct effect. But, it had negative indirect effect via days to maturity and number of fertile tiller per plant (Table 5).

Plant height had positive indirect effect via grain filling period, thousand seed weight, harvest index and biological yield. Direct effect of biological yield, number of fertile tiller per plant and harvest index was also positive with positive significant correlation indicating true relationship between yield and these traits. In harmony with this finding, Zerihun *et al.*(2011) reported the positive direct effect of biomass yield per plot, harvest index, thousand seed weight and plant height on grain yield. Likely, Meseret (2015) reported positive direct effect of biological yield, plant height and thousand seed weight with grain yield. However, days to maturity and grain filling period exerted negative direct effect on grain yield, but had positive

and significant correlation. This implies there were no true relationships with grain yield. The indirect effect of days to maturity via grain filling period, plant height and thousand seed weight was positive and high and had positive and negligible indirect effect via rest of characters. Accordingly, it can be suggested that the overall positive and significant association of days to maturity with grain yield was due to the positive and high indirect effect of grain filling period, plant height and thousand seed weight.

Table 5: Phenotypic path coefficient showing direct (bolded and diagonal values) and indirect (out of diagonal and un bolded values) effect of one character on other character and on grain yield of barley genotypes

Traits	DM	GFP	PLH	NFTPP	TSW	HI	BY	rp
DM	**-0.31**	0.55	0.18	0.05	0.1	0.01	0.01	0.59**
GFP	0.46	**-0.2**	0.21	0.04	0.08	0.02	0.03	0.64**
PH	-0.12	0.159	**0.51**	0.05	0.03	0.07	0.03	0.72**
NFTPP	0.11	0.08	0.12	**0.16**	0.15	0.01	0.05	0.68**
TSW	-0.06	0.05	0.03	-0.05	**0.69**	0.009	0.03	0.699**
HI	-0.06	0.07	0.03	-0.01	0.07	**0.09**	0.02	0.21*
BY	-0.03	0.09	0.24	-0.08	0.142	0.04	**0.21**	0.612*
		R=0.44						

Key: DM= days to maturity, GFP=grain filling period, PH= plant height, NFTPP=number of fertile tillers per plant, TSW=thousand seed weight, HI=harvest index, BY=biological yield, rp = phenotypic correlation coefficient and R =residual.

All in all, the result revealed that indirect effect of most of traits considered in this path analysis showed positive and negligible effect via other traits. Thus, their positive correlations with grain yield were due to their direct effect. The results of residual effects (R=0.44) shown that 56% of the yield of barley was contributed by the characters studied in this experiment. The role of other independent variables which had not been included in this experiment were expected to influence grain yield by 44 % (Table 5).

4.6.2. Genotypic path analysis

The genotypic direct and indirect effect of different characters on grain yield are presented in Table 6.The genotypic path analysis revealed that plant height had the highest positive direct effect on grain yield (2.16) followed by thousand seed weight (1.78) and number of fertile tiller per plant (0.63). These traits had also positive and highly significant genotypic correlation with grain yield. The result indicated that the existence of real relationship with the traits and grain yield. Accordingly, these traits can be used for indirect selection criteria in barley yield improvement. The finding is in close agreement with the finding of Sing *et al*. (2014) who found high positive direct of thousand grain weights, number of effective tiller per plant and plant height. In addition, biological yield and harvest index had positive direct effect on grain yield with positive and significant correlation coefficient (rg=0.82), and (rg=0.40) respectively. Number of fertile tillers per plant exerted positive and large indirect effect via plant height (0.75) and thousand seed weight (0.74) and it had negative and large indirect effect on grain yield via grain filling period (-0.84) and days to maturity (-0.61) (Table 6).

Biological yield showed high and positive indirect effect via plant height and thousand seed weight. However, it showed the highest and negative indirect effect on yield via grain filling period (-1.05). On the other hand, grain filling period and days to maturity showed negative and highest direct effect on grain yield, but the traits had positive and significant correlation with grain yield. This implies that there was no true relationship between the traits and grain yield. However, grain filling period had positive and highest indirect effect via days to maturity (1.32), plant height (1.23) and thousand seed weight (0.40). Likely, days to maturity showed positive and highest indirect effect via plant height (1.040) and thousand seed weight (0.36). This indicates the positive correlation of these traits with grain yield could be due to its respective indirect effect via other traits.

The results of residual effects (R=0.18) revealed that 82% of the yield of barley was contributed by the characters studied in this experiment. The role of other independent variables or grain yield characters which had not been included in this experiment were expected to influence grain yield by 18 % (Table 6).

Table 6: Genotypic path coefficient showing direct (bolded and diagonal values) and indirect (out of diagonal and un bolded values) effect of one character on other character and on grain yield of barley genotypes

Traits	DM	GFP	PLH	NFTPP	TSW	HI	BY	rg
DM	**-1.54**	0.92	1.04	-0.17	0.36	0.04	0.02	0.67**
GFP	1.32	**-2.64**	1.23	0.23	0.4	0.05	0.09	0.68**
PLH	0.74	-1.5	**2.16**	0.15	-0.92	0.02	0.09	0.74**
NFTPP	-0.61	-0.84	0.75	**0.63**	0.74	0.02	0.07	0.76**
TSW	0.4	-0.6	-1.12	0.18	**1.78**	0.02	0.08	0.74**
HI	0.32	-0.74	0.26	0.04	0.17	**0.3**	0.05	0.4*
BY	0.16	-1.05	0.62	0.13	0.58	0.04	**0.34**	0.82**
			R=0.18					

Key: DM= Days to maturity, GFP=Grain filling period, NFTPP=Number of fertile tiller per plant, SW=Thousand weight, HI =Harvest index, BY=Biological Yield rg=genotypic correlation coefficient and R=residual

4.7. Cluster Analysis

Cluster analysis grouped 105 genotypes in to 5 distinct groups and one genotype remains ungrouped (Table 7 and Appendix figure 1). Cluster I consisted 56 genotypes which accounts 53.33% of total genotypes. The landraces considered in this cluster scattered over all zone of collection with relatively larger contribution from Keffa and Bench Maji. Landraces grouped in this cluster is characterized by relatively early maturity, short spike length and smaller thousand seed weight.

Cluster II accounts 33.33 % of total genotypes and holds 35 genotypes out of 105 genotypes considered in this study (Table 7). The landraces considered in this cluster came from all zone of collection with the highest share from Sidama (33.33%). Moreover, this cluster is characterized by high number of fertile tillers per plant and the highest thousand seed weight (Table 8). Cluster III consisted seven genotypes which is 6.66 % of total genotypes and characterized by fewer number of seeds per spike and the landraces included in this cluster were collected from South Omo, Gede'o, Hadiya, Kembata and Bench Maji.

Table 7: Clustering pattern of 105 barley genotypes in to five clusters

cluster	Number of genotypes	Proportion	Name of genotypes.
I	56	53.33%	235570,217176,240468,219305,204643,215482,236119,235546,3605,27889,220653240472,219302,240482,3866,233052,240475,3603,64345,235569,27890,27891,212937,208851,240481,215483,212941,240480,219301,27895,27886,235648,236120,28061,236145,235549,215475,235647,27892,220651,27893,235552,3604,233239,235649,220652,3609,208839,244775,235635,215478,240471,240479,215476,217177,212938.
II	35	33.33%	244767,215477,27888,HB13/07,Shege,HB1966,Cross41/98,EH1493,28057,208837,212945,235547,29699,28065,220654,220661,29697,240474,235572,212939,245127,29696,28062,235548,28058,235554,244771,29698,297063,619,235550,215484,212942,28059,1641.
III	7	6.66%	202657, 219300, 236149, 27887,235571,208838,212940.
IV	3	2.86%	236147,235551,235553.
V	3	2.86%	233053,3610,215432.
Solitary			28060

Cluster IV had three genotypes which accounts 2.86 % of total genotypes. The landraces grouped under this cluster were collection of Gede'o and Gurage. Likely, cluster V had also three genotypes and the accessions were collected from Gede'o, Gurage and Bench Maji which are characterized by late heading, early grain filling period, short spike length, less number of fertile tillers per plant and smallest grain yield. In general, landraces grouped in this cluster are characterized by lowest mean performance for most of traits including grain yield (Table 8). The solitary landrace was collected from Sidama Zone and characterized by early heading, late maturing and grain filling period, long spike length, and tallest plant height, higher number of seeds per spike, highest harvest index, highest biological yield and highest gran yield. In general, this landraces is characterized by highest mean performance for most of traits including the breeder interest, grain yield.

Moreover, most of landraces collected from the same province scattered in different clusters, indicating presence of genetic diversity within region of collection. In agreement with this, appearing of landraces from the same or adjacent region in to different cluster were reported by Fassil *et al*., (2001), Tigist *et al*.(2010) and Bedassa *et al*.(2014).

Table 8 : Mean value of 11 traits for five clusters of barley genotypes evaluated at Alarigata in 2018 cropping season

Traits	Clusters					
	I	II	III	IV	V	Solitary genotype
Days to heading	63.02	67.50	65.00	67.00	74**	63*
Days to maturity	102.46*	118.02	126.71	118.33	106	134**
Grain filling period	39.45	50.52	61.71	51.33	32*	71**
Spike length	7.26	7.72	8.17	6.33	6.2*	7.6**
Number of seed per spike	37.89	42.85	31.06*	43.50	38.2	50.6**
Plant height.	85.71	92.22	85.54	67.60	71.4	113**
Number of fertile tiller per plant.	4.44	4.63**	4.31	4.27	3*	4
Thousand seed weight	37.78*	43.52**	39.80	38.69	39.13	40.13
Harvest index	39.34	41.78	40.01	38.47	33.01*	47.48**
Biological yield	6.82	7.04	6.82	7.07	6.67*	7.62**
Grain yield	2.65	2.99	2.76	2.74	2.25*	3.62**

Key:*and **= represents the lowest and highest mean value respectively

4.8. Estimation of Inter-Cluster Square Distances (Genetic Distance)

The average inters cluster distance (D^2) values of 105 genotypes are presented in Table 9. Statistical significance between clusters was detected using chi-Square test. Accordingly, chi-square test indicated that there were statistically significant difference between pair of clusters except cluster I and II, cluster II, and III and cluster IV and V.

The clusters which showed significant and highly significant difference indicated that the presence of genetic diversity between groups of genotypes studied. On the other hand, non-significant genetic distance between clusters indicated that the little genetic divergence between clusters and hence, crossing of genotypes from these clusters might not give higher heterotic value in F1 and narrow range of variability in the segregating F2 population. Maximum genetic recombination is expected from the hybridization of the parents selected from divergent cluster groups (Singh *et al*., 1987).

However, the chance of getting segregants with a high yield level is quite limited when one of the clusters has a very low yield level (Samal *et al*., 1989). Cluster v had the lowest mean performance in grain yield and other important traits. This point out that the chance of getting segregants with high yield is limited between crosses of cluster v with the other clusters. Besides, selection of parents should also consider the special advantages of each cluster and each genotype within a cluster depending on specific objectives of hybridization (Singh, 2001; Chahal and Gosal, 2002).

According to Ghaderi *et al*. (1984), increasing parental distance suggests a great number of distinct alleles at the desired loci and cross of distantly related parents will be produce greater offspring and increases the opportunities for the effective selection for desired traits. Therefore, greatest variation in the subsequent generations is expected up on crossing between parents selected from maximum inter-cluster distances. However, any crossing program depends on the breeder objectives and has to specify his/her objectives in order to get best use of the traits those highly divergent.

Table 9: Average inter cluster divergence (D^2) value among barley genotypes evaluated at Alarigata in 2018 cropping season.

Custers	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V
Cluster-I	0	8.241^{ns}	23.230**	19.793*	19.839*
Cluster-II		0	12.045^{ns}	20.112*	27.660**
Cluster-III			0	19.618*	37.526**
Cluster-IV				0	11.063^{ns}
Cluster-V					0

Key: ns=non- significant,*=significant at 0.05 probablity level (X^2) = 18.31 and **=0.01 probability level (X^2) =23.21

4.9. Principal Component Analysis (PCA).

Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre 1998). It reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998).

Principal component analysis revealed that five principal components PC1 to PC5 with Eigen values greater than one have accounted 78 % of the total variation among genotypes for the eleven quantitative traits (Table 10). The first three principal components PC1, PC2 and PC3 with values of 31 %, 15 % and 12 %, respectively, contributed more to the total variability. According to Chahal and Gosal (2002), traits with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. Thus, in this study, differentiation of the genotypes into different cluster was because of a cumulative effect of the number of traits rather than the contribution of specific few traits.

The first PC which explained 31% of total variation was obtained from variation of all traits. Characters having relatively higher value in the second principal component (PC2) were days to maturity, spike length, grain filling period, days to heading, and number of seed per spike, plant height, grain yield and biological yield had more contribution to the total diversity and

they were the ones that most differentiated the clusters. Traits such as spike length, plant height, days to heading, grain yield, biological yield, harvest index and number of seed per spike had contributed more in PC3. Number of fertile tillers per plant and thousand seed weight were the major contributor in fourth PC and days to heading grain filling period and number of seed per spike was the major contributor in the explaining of fifth PC (Table 10).

Table 10: Principal component analysis for 11 quantitative traits of 105 barley genotypes evaluated at Alarigata in 2018 cropping season

Traits	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
Days to heading	0.40	0.44	0.34	-0.22	0.57
Days to maturity	0.71	0.61	0.11	-0.19	-0.17
Grain filling period	0.60	0.46	-0.09	-0.08	-0.58
Spike length	0.36	-0.49	0.62	-0.07	-0.04
Number of seed per spike	0.49	0.43	-0.30	-0.04	0.41
Plant height	0.58	-0.39	0.43	-0.11	-0.01
Number of fertile tiller per plant	0.53	-0.10	0.25	0.62	0.12
Thousand seed weight	0.35	-0.11	0.29	-0.56	-0.11
Harvest index	0.63	-0.24	-0.32	0.07	-0.26
Biological index	0.68	-0.37	-0.40	-0.01	0.25
Grain yield	0.80	-0.38	-0.43	0.02	0.06
Eagen Value	3.74	1.83	1.49	1.24	1.03
% of total variance	31	15	12	10	9
% of Commutative Variance	31	47	59	69	78

PC=principal component.

4.10. Frequency Distribution for Different Class of Qualitative Traits

The percentage frequency distribution of seven traits with respective chi-square values for entire population is presented in Table 11. Kernel color is one of the most important characters that determine the quality and acceptance of landraces. It has an economic value because it constitutes the basis for farmer's variety identification and commercial

classification of different varieties of crops (Tsehaye and Kebebew, 2002). In this study, the variation in kernel color indicated that white kernel color was found to be the dominant color (53%) followed by black (33%), while blue and purple kernel showed low frequency (8%) and (4%) respectively. This may be due to farmer's preference for white colored seed, or it could be associated with high market value that farmers fetch from white kernel color. In line with this finding, Shegaw *et al*. (2013) reported the predominance of white kernel color among 207 barley landraces considered in their investigation.

The variation in kernel row number in current investigation revealed that, the predominance of two row type (55%). The result for spike density showed that (39%) intermediate type (37%) dense and (24% lax). Likewise, the percentage frequency distribution of rachilla hairs showed 52% long rachilla hair and 48% short rachilla hairs. In the current study, hoodedness showed that except two (2%) landraces which showed awnleted type almost all landraces (98%) were awned.

Variation in kernel covering showed the predominance of covered type (84 %). On the other hand, the proportion of landraces for lodging susceptibility was 40% for low,33% for intermediate (27 %) for very low and (0 %) for high. Chi square result revealed that except spike density and rachilla hairs all traits showed significant deviation from expected distribution of traits, however expected distribution was observed from spike density and rachilla hairs (Table 11).

Table 11: Frequency distribution and chi-square of phenotypic classes for seven qualitative traits

Traits	codes	classes	Frequency distribution	X^2	P-value
Kernel row no	1	Two rowed	55%	24.502**	0.007
	2	Six rowed	15%		
	3	Irregular	30%		
Spike density	3	Lax	24%	3.980ns	0.136
	5	Intermediate	39%		
	7	Dense	37%		
Rachila hairs	1	Short	48%	0.16ns	0.689
	2	Long	52%		
Hoodedness	1	Awnless	0%	284.32**	0.008
	2	Awnleted	2%		
	3	Awned	98%		
	4	Sessile hoods	0%		
Kernel covering	1	Naked	14%	51.84**	0.004
	2	Covered	86%		
Lodging susceptibility	1	Very low	27%	36.72**	0.002
	3	Low	40%		
	5	Intermediate	33%		
	7	High	0		
Table 11 (Continued)					
Kernel color	1	White	53%	63.12**	0.003
	2	Black	33%		
	3	Blue	8%		
	4	Purple	4%		

ns=non-significant, =significant at p≤0.05,**= significant at p ≤0.01.*

4.11. Frequency Distribution of Qualitative Traits with In Respective Zone of Collection

Percentage frequency distribution of seven qualitative traits within zone of collection is presented in Table 12. The result indicated that the predominance of white kernel color in Sidama (100%), Gede'o (100 %), South omo (72.72%) and Bench maji (46.15%), while it was less frequent in keffa (0 %) and kembata (20 %). Likely, black seed color is more concentrated in Keffa, Kembata, and Gurage. The distribution of purple and blue kernel color was low in overall zone of collection (Table 12).

This predominance of white and black kernel color in different zone of collection implies that, both seed colors are important and independently selected for different uses by the farmers. This could be due to farmers preference toward kernel color may differ from one province to other province due to the difference in the socio cultural status of the society. Moreover, both color groups differ in end-use purposes in Ethiopia.

The chi square result also revealed that all zones considered except Bench Maji zones shown significant deviation from the expected distribution of kernel color. However, at Bench Maji expected distribution of trait was observed.

Kernel row number is polymorphic in overall zone of collection. However, two row barley most frequently occurred in Kefa, Hadiya, Bench Maji and Gurage (Table 13). Moreover, result of chi square showed that significant deviation from excepted distribution of kernel row number in these provinces, indicating the concentration of this character in these regions. On the other hand, non-significant deviation was observed from south Omo, Gede'o, Gurage and Kembata (Table, 12).

The variation in spike density across Zone of collection indicated that dense type of spike was predominantly occurred in Sidama and South omo, while it was less frequently occurred in Bench maji, Keffa and Gedeo (Table 12). The distribution of intermediate spike type was more concentrated in Bench Maji and Gedeo, while lax type was more frequent in Keffa zone. The chi-square result indicated that except South Omo, Gurage, Hadiya and Kembata, all Zones demonstrated significant deviation from expected distribution of spike density.

Distribution for rachilla hair indicated that long hair type was most frequent in Kembata, Gurage, Kefa and Gedeo. While short rachilla hair was frequently occurred in bench Maji and Hadiya (Table12).

The variation in hoodedness indicated that the predominance of awned barley type in overall Zone of collection with overall frequency distribution of 98% of entire population. Likely, kernel covering revealed that the predominance of covered kernel type in overall zone of collection. Similarly, the variation in lodging susceptibility of accessions indicate that, the polymorphism of the phenotypic classes in overall Zone of collection, though low lodging susceptibility was predominant in Benchi Maji (69.23%) Gurage (53.84%) and Keffa (50%). However, the genotype with high lodging susceptibility was not seen in overall landraces.

In general, most of the discrete traits studied in this experiment were not unique to any single zone of collection. This could be attributed due to germplasm exchange (gene flow) between adjacent Zones. Besides, human preference for a certain crop type (color, growth habit or the like) also might have played a role. However, the differential frequency representation of the various states of characters studied partly implies either the fitness of the various genotypes in the zone of collection considered or farmer's preference toward the stated characters may differ among zones.

Table 12: Frequency distribution of different phenotypic classes for seven qualitative traits and chi-square values for each zone of collection

zone	KC					KRN				SD				RH		
	1	**2**	**3**	**4**	X^2	**1**	**2**	**3**	X^2	**3**	**5**	**7**	X^2	**1**	**2**	X^2
South omo	72.72	18.18	9.1	0	14090**	45.45	9.1	45.45	2.90ns	9.1	36.36	54.54	3.455ns	54.55	45.45	0.090ns
Gedeo	100	0	0	0	36**	33.34	25	41.66	0.5ns	8.33	66.67	25	6.5*	41.66	58.34	0.333ns
Gurage	46.15	53.85	0	0	13.15**	53.84	30.76	15.38	3.25ns	23.07	30.76	46.15	1.25ns	23	77	4.16*
Hadiya	41.66	50	0	8.34	8.66*	75	0	25	10.5*	33.33	25	41.67	0.5ns	66.66	33.34	1.33ns
Keffa	0	66.67	33.33	0	14.66**	83.33	8.33	8.33	13.5**	66.66	16.66	16.66	6**	41.66	58.34	0.333*
Kembata	20	60	13.33	6.67	10.33**	53.33	26.67	20	2.8ns	13.33	53.34	33.33	3.6ns	40	60	0.6ns
Sidama	100	0	0	0	36**	25	8.34	66.66	6.5*	8.34	16.66	75	9.5**	50	50	0.33ns
Bench maji	46.15	30.76	7.69	15.38	4.53ns	69.23	0	30.76	9.39**	30.76	69.23	0	9.39**	69.24	30.76	1.92ns

Table 12 (Continued)

Zone	H					KK			LS				X^2
	1	**2**	**3**	**4**	X^2	**1**	**2**	X^2	**1**	**3**	**5**	**7**	
South omo	0	18.18	81.82	0	19.909**	9.1	90.9	3.727**	27.27	36.36	36.36	0	3.909ns
Gedeo	0	0	100	0	24**	25	75	3*	41.66	33.33	25	0	4.66ns
Gurage	0	0	100	0	42.33**	0	100	14.16**	23.07	53.84	23.07	0	8.333*
Hadiya	0	0	100	0	36**	33.33	66.67	1.333ns	33.34	33.33	33.33	0	4ns
Keffa	0	0	100	0	36**	8.34	91.66	8.33**	25	50	25	0	6ns
Kembata	0	0	100	0	45**	20	80	5.4*	40	6.66	53.34	0	11.93**
Sidama	0	0	100	0	36**	25	75	3ns	8.33	41.67	50	0	8.66*
Bench maji	0	0	100	0	39**	7.69	92.31	9.30**	15.39	69.23	15.38	0	46.75**

Key:*ns=non-significant,*=significant ,**highly significant, KC=Kernel colour, KRN=Kernel row number,SD=spike density, RH=Rachilla hair=Hoodedness ,KK=kernel covering, LS=lodging susceptibility, X^2=chi- square and 1,2,3,4,5,and 7 are character codes(See Table 11).*

4.12. Estimate of Shannon Weaver Diversity Index within Landraces.

Estimate of Shannon waiver diversity index for seven qualitative trait of entire accession is presented in Table 13. The result indicated H' ranged from 0.09 for hoodedness to 0.97 for kernel row number. According to Firdisa *et al*. (2005), the diversity index was classified as high ($H' \geq 0.60$), intermediate ($0.40 \leq H' \leq 0.60$), or low ($0.10 \leq H' \leq 0.40$). Based on the bench mark of these scholars, highest diversity index were observed for kernel row number (H=0.97), spike density (H=0.96), lodging susceptibility, kernel color (0.74) and rachilla hairs (0.69), implying the existence of wide range of diversity in barley population. Likewise, intermediate diversity was observed for kernel covering (H=0.30) and monomorphisim or low diversity index was observed for Hoodedness (H=0.09). This may be attributed by either genetic drift or loss of genetic integrity caused by selection pressure (Hammer *et al*., 1996).

Table 13: Shannon Weaver diversity index for seven qualitative traits of 100 landraces evaluated at Alarigata in 2018 cropping season

No	Qualitative traits	Diversity index (H')
1	Kernel color	0.74
2	Kernel row no	0.97
3	Spike density	0.96
4	Rachila hairs	0.69
5	Hoodedness	0.09
6	Kernel covering	0.3
7	Lodging susceptibility	0.77
	Mean	0.69

4.14: Estimates of Shannon weaver diversity for each zones

Estimate of diversity index for zone of collection is presented in Table 14. Pooled over all traits with in each zone, H' value ranged from 0.48 for Sidama to 0.69 for South omo. Firdissa *et al*. (2005) described the diversity index as high ($H' \geq 0.60$), intermediate ($0.40 \leq H' \leq 0.60$), or low ($0.10 \leq H' \leq 0.40$). Based on this demarcation, the highest diversity index pooled over all traits were observed for landraces from south omo (H'=0.69) followed by Kembata (H'=0.67) and Hadiya (H'=0.66). Intermediate diversity index were observed landraces from rest of zones. Individual trait showed different level of diversity across different zones. This indicated that pattern of diversity differ between different zones. However, most of trait showed polymorphism across zone of collection (Table 15) implying the existence of notable diversity. But, monomorphisim was observed for hoodedness over all zone of collection. Except from two landraces from south omo zone which had awnleted type; all landraces had awn which is monomorphic (H'=0) (Table 14).

Table 14: Estimate of Shannon weaver diversity index of qualitative trait in each zone

Zones	KC	KRN	SD	RH	H	KK	LS	Mean
South Omo	0.75	0.93	0.91	0.68	0.47	0.3	0.78	0.69
Gede'o	0	0.98	0.82	0.67	0	0.56	0.77	0.54
Gurage	0.69	0.98	0.96	0.53	0	0	0.72	0.55
Hadiya	0.91	0.56	0.98	0.73	0	0.63	0.79	0.66
Keffa	0.63	0.56	0.86	0.67	0	0.28	0.75	0.54
Kembata	0.77	0.91	0.97	0.67	0	0.5	0.88	0.67
Sidama	0	0.82	0.72	0.69	0	0.56	0.57	0.48
Bench maji	0.86	0.61	0.97	0.61	0	0.27	0.83	0.59

Key: KC= kernel color, KRN=kernel row number, SD=spike density, RH= rachilla hair= hoodedness, KK=kernel covering and LS=lodging susceptibility.

5. SUMMARY AND CONCLUSIONS

Knowledge on pattern of landraces diversity is an important consideration for efficient conservation and utilization of genetic resources. Accordingly, 105 barley genotypes, 100 landraces collections from various zones of southern Ethiopia with five standard checks were evaluated at Alarigata, substation of Bonga Agricultural Research Center using augmented design. The result of analysis of variance indicated that except awn length all traits showed highly significant variation among genotype signifying the existence of high genetic diversity among genotypes.

The estimate of phenotypic coefficient of variation (PCV) ranged from 6.40 % for plant height to 16.27 % for spike length, whereas genotypic coefficient of variation (GCV) ranged from 4.36 % for biological yield to 13.22 % for number of fertile tiller per plant. Medium PCV (10 % - 20 %) were observed for grain filling period, spike length, number of seed per spike, number of fertile tiller per plant, thousand seed weight and grain yield, while estimate of PCV for rest of characters were low (<10 %). Medium GCV (10 % - 20 %) were observed for grain filling period, spike length, number of seeds per spike, number of fertile tillers per plant and grain yield, but the remaining traits showed low value of GCV (<10 %).

Heritability in broad sense ranged from 38.75 % for spike length to 78.13% grain yield. Moderately high heritability value (60 %-79 %) were obtained for grain yield, number of fertile tillers per plant, days to maturity, harvest index, days to heading and number of seeds per spike. Low estimate of broad sense heritability was observed for spike length, but remaining trait showed medium value of heritability (40 %-59 %).

Moderately high heritability along with relatively high genetic advance as percent of mean was observed for number of fertile tillers per plant and number of seeds per spike. Thus, these characters can be improved through selection more easily than other characters. Days to maturity and harvest index showed moderately high heritability along with low genetic advance as percent of mean, implying dominance of non-additive gene action and thus, direct selection of these traits cannot be effective.

Correlation analysis revealed that yield had positive and highly significant phenotypic and genotypic association with days to maturity, grain filling period, plant height, number of

fertile tillers per plant, and thousand seed weight and it had positive and significant association with harvest index and biological yield both at phenotypic and genotypic level.

Path analysis revealed that thousand seed weight, plant height and number of fertile tillers per plant had positive and maximum phenotypic and genotypic direct effect on grain yield. In general, traits that showed direct positive effect with significant positive correlation indicate the real association of the traits with the trait of interest, yield. Hence, indirect selection of these traits can be effective in barley grain yield improvement.

Based on eleven quantitative traits considered, 105 genotypes were grouped in to five genetically distinct clusters and one genotype remains ungrouped. The result of inter cluster distance test indicated that there was statistically significant difference between pair of clusters except cluster I and II, cluster II and III and cluster IV and V.

The result of principal component analysis indicated that the first five principal components with Eigen values greater than one, explained 78% of the total variation among genotypes for the eleven quantitative traits. The first three principal components PC1, PC2 and PC3 with values of 31 %, 15 % and 12 % respectively contributed more to the total variability. It was also noted that differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather than the small contribution of each character.

Frequency distribution of qualitative traits of different phenotypic classes indicated the predominance of white kernel color, two row barley type, covered kernel type and awned barley type. Estimate of Shannon-Weaver diversity index indicated high for all characters assessed except hoodedness and kernel covering implying the existence of diversity. Pooled over all traits with in each zone H’ value ranged from 0.48 for Sidama to 0.69 for South Omo and individual trait showed different level of diversity across different zones.

In general, the result indicated wider agro-morphological diversity among barley collection, showing opportunity to improve important traits of the crop and need to conserve the diversity. Moreover, the observed diversity is more or less similar for all zones of collection

pooled over characters. Thus, it can be suggested, future germplasm collection should give equal weight for all zones considered. As future line work further investigation with inclusion of more informative molecular markers and covering different producing area of the region will allow to provide the complete picture of existing diversity.

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APPENDICES

Appendix Table 1: List of 100 barley accessions with detailed passport data

No	Accession No	Region	Zone	Latitude	Longitude	Altitude
1	202657	SNNP	South OMO	NA	NA	NA
2	3605	SNNP	South OMO	05-47-00-N	36-34-00-E	1000
3	3604	SNNP	South OMO	05-47-00-N	36-34-00-E	1000
4	235570	SNNP	South OMO	NA	NA	NA
5	235649	SNNP	South OMO	NA	NA	NA
6	235647	SNNP	South OMO	05-49-00-N	36-27-00-E	1810
7	3603	SNNP	South OMO	05-47-00-N	36-34-00-E	1000
8	235648	SNNP	South OMO	05-49-00-N	36-27-00-E	2000
9	235569	SNNP	South OMO	NA	NA	NA
10	235572	SNNP	South OMO	NA	NA	NA
11	235571	SNNP	South OMO	NA	NA	NA
12	233053	SNNP	GEDEO	06-18-00-N	38-14-00-E	1850
13	233052	SNNP	GEDEO	06-18-00-N	38-14-00-E	1850
14	245127	SNNP	GEDEO	NA	NA	2309
15	219300	SNNP	GEDEO	NA	NA	1750
16	219301	SNNP	GEDEO	NA	NA	1750
17	219302	SNNP	GEDEO	NA	NA	1750

Appendix Table I (Continued)

18	244775	SNNP	GEDEO	NA	NA	2380
19	219305	SNNP	GEDEO	06-03-00-N	38-11-00-E	2220
20	236149	SNNP	GEDEO	NA	NA	2420
21	208851	SNNP	GEDEO	06-00-00-N	38-10-00-E	2600
22	236147	SNNP	GEDEO	NA	NA	2240
23	236145	SNNP	GEDEO	NA	NA	2200
24	235550	SNNP	GURAGE	08-02-00-N	38-02-00-E	2910
25	235547	SNNP	GURAGE	08-05-00-N	38-11-00-E	3050
26	235548	SNNP	GURAGE	08-06-0 –N	37-57-00-E	2890
27	235549	SNNP	GURAGE	08-06-0 –N	37-57-00-E	2890
28	3619	SNNP	GURAGE	08-30-00-N	37-58-00-E	2000
29	235551	SNNP	GURAGE	08-02-00-N	38-02-00-E	2890
30	235552	SNNP	GURAGE	08-01-00-N	38-04-00-E	2900
31	235553	SNNP	GURAGE	08-01-00-N	38-04-00-E	2900
32	235554	SNNP	GURAGE	08-01-00-N	38-04-00-E	2900
33	215432	SNNP	GURAGE	08-07-00-N	38-23-00-E	2090
34	235546	SNNP	GURAGE	08-05-00-N	38-11-00-E	3050
35	204643	SNNP	GURAGE	NA	NA	3120
36	233239	SNNP	GURAGE	NA	NA	NA
37	212941	SNNP	HADIYA	37-53-00-N	07-39-00-E	2640

Appendix Table I(Continued)

38	212940	SNNP	HADIY A	37-53-00-N	07-39-00-E	2640
39	220652	SNNP	HADIYA	07-24-00-N	37-48-00-E	2510
40	212938	SNNP	HADIYA	37-55-00-N	07-36-00-E	2280
41	212937	SNNP	HADIYA	37-53-00-N	07-33-00-E	2300
42	212942	SNNP	HADIYA	37-53-00-N	07-39-00-E	2640
43	212939	SNNP	HADIYA	37-53-00-N	07-33-00-E	2250
44	220661	SNNP	HADIYA	07-42-00-N	37-51-00-E	3030
45	220651	SNNP	HADIYA	07-24-00-N	37-48-00-E	2510
46	212945	SNNP	HADIYA	37-51-00-N	07-35-00-E	2370
47	220653	SNNP	HADIYA	07-24-00-N	37-48-00-E	2510
48	220654	SNNP	HADIYA	07-41-00-N	37-52-00-E	2800
49	64345	SNNP	KEFFA	07-10-00-N	36-21-00-E	2140
50	240479	SNNP	KEFFA	NA	NA	NA
51	240480	SNNP	KEFFA	NA	NA	NA
52	240481	SNNP	KEFFA	NA	NA	NA
53	240482	SNNP	KEFFA	NA	NA	NA
54	217177	SNNP	KEFFA	07-10-00-N	36-21-00-E	2140
55	240468	SNNP	KEFFA	NA	NA	NA
56	240475	SNNP	KEFFA	NA	NA	NA
57	217176	SNNP	KEFFA	07-10-00-N	36-21-00-E	2140

Appendix Table I (Continued)

58	240472	SNNP	KEFFA	NA	NA	NA
59	240471	SNNP	KEFFA	NA	NA	NA
60	240474	SNNP	KEFFA	NA	NA	NA
61	215476	SNNP	KEMBATA	07-28-00-N	37-53-00-E	2180
62	215477	SNNP	KEMBATA	07-20-00-N	37-52-00-E	2210
63	215478	SNNP	KEMBATA	07-20-00-N	37-52-00-E	2230
64	208837	SNNP	KEMBATA	07-22-00-N	37-42-00-E	NA
65	215475	SNNP	KEMBATA	07-25-00-N	37-52-00-E	2190
66	208838	SNNP	KEMBATA	07-25-00-N	36-42-00-E	2650
67	208839	SNNP	KEMBATA	07-21-00-N	37-51-00-E	NA
68	244767	SNNP	KEMBATA	NA	NA	2476
69	215484	SNNP	KEMBATA	07-17-00-N	37-52-00-E	NA
70	215483	SNNP	KEMBATA	07-17-00-N	37-52-00-E	NA
71	236120	SNNP	KEMBATA	NA	NA	2200
72	236119	SNNP	KEMBATA	NA	NA	2200
73	1641	SNNP	KEMBATA	07-17-00-N	37-52-00-E	2540
74	215482	SNNP	KEMBATA	07-22-00-N	37-57-00-E	NA
75	244771	SNNP	KEMBATA	NA	NA	2498
76	29697	SNNP	SIDAMA	06-27-36-N	38-30-04-E	2750
77	29698	SNNP	SIDAMA	06-27-00-N	38-31-07-E	2786

Appendix Table I (Continued)

78	29699	SNNP	SIDAMA	06-27-31-N	38-31-46-E	2748
79	29706	SNNP	SIDAMA	06-30-57-N	38-34-14-E	2565
80	29696	SNNP	SIDAMA	06-28-09-N	38-30-42-E	2773
81	28058	SNNP	SIDAMA	06-27-26-N	38-27-47-E	2752
82	28057	SNNP	SIDAMA	06-27-26-N	38-27-47-E	2752
83	28065	SNNP	SIDAMA	06-28-52-N	38-30-14-E	2776
84	28059	SNNP	SIDAMA	06-27-12-N	38-27-16-E	2791
85	28060	SNNP	SIDAMA	06-27-46-N	38-27-46-E	2658
86	28061	SNNP	SIDAMA	06-27-45-N	38-27-46-E	2670
87	28062	SNNP	SIDAMA	06-27-40-N	38-29-16-E	2707
88	3610	SNNP	BENCH MAJI	05-27-00-N	37-20-00-E	1700.00
89	3866	SNNP	BENCH MAJI	05-39-00-N	37-23-00-E	2020.00
90	27895	SNNP	BENCH MAJI	06-53-34-N	35-44-23-E	2067.00
91	235635	SNNP	BENCH MAJI	05-17-00-N	37-39-00-E	2150.00
92	27893	SNNP	BENCH MAJI	06-53-31-N	35-50-56-E	2014.00
93	27892	SNNP	BENCH MAJI	06-53-30-N	35-50-56-E	2022.00
94	27891	SNNP	BENCH MAJI	06-53-28-N	35-50-55-E	2022.00
95	27890	SNNP	BENCH MAJI	06-52-41-N	35-51-19-E	2044.00
96	27889	SNNP	BENCH MAJI	06-52-40-N	35-51-19-E	2044.00
97	27888	SNNP	BENCH MAJI	06-50-31-N	35-51-57-E	2100.00
98	27887	SNNP	BENCH MAJI	06-50-29-N	35-51-55-E	2100.00

99	27886	SNNP	BENCH MAJI	06-53-49-N	35-33-51-E	2044.00
100	3609	SNNP	BENCH MAJI	05-27-00-N	37-20-00-E	1500.00

NA=not available

Appendix Table 2: Performance of 105 barley genotypes for 11 agronomic traits tested at alarigata during 2018 cropping season

Genotypes	DH	DM	GFP	SL	NSPS	PLH	NFTPP	TSW	HI	BY	GY
235553	58	112	54	7.8	36.8	67.4	3.8	38.72	38.23	6.98	2.67
236149	61	116	55	8.8	26.4	80.6	4.6	46.25	40.37	8.18	3.3
240468	60	97	37	7.4	40.4	88	3.6	32.78	32.49	6.75	2.19
215476	62	90	28	8	39.4	87.8	4.2	48.91	39.36	8.21	3.23
220651	58	109	51	6.8	48.6	85.4	3.6	40.18	43.62	7	3.05
27889	65	95	30	9	39.5	86.4	4.6	45.55	46.91	6.37	2.99
27890	62	92	30	7.8	34.4	81.6	3.4	37.54	35.69	6.96	2.48
27891	62	93	31	7.8	31.5	86	4.8	40.062	39.67	7.96	3.16
27892	56	96	40	6.4	35.6	86	4.8	42.17	31.88	5.8	1.85
27895	61	91	30	7.8	37.2	92.8	4.6	37.44	40.08	7.65	3.06
235572	67	118	51	5.8	41.2	85.8	3.8	52.16	40.93	6.93	2.84
29699	67	118	51	7.8	51.5	102	5	42.36	40.83	6.43	2.62
29697	63	113	50	7.4	41.2	102.6	4.6	48.75	43.01	8.46	3.64
202657	62	129	67	11.2	36.6	95.8	4.4	37.25	38.91	6.27	2.44
204643	65	113	48	5.8	37.8	78.6	4	32.18	33.38	6.29	3.1
208837	66	110	44	8.6	37.8	86.4	3.4	51.75	34.72	5.75	3
208838	69	134	65	7	28.6	84	4.4	44.33	39.16	6.79	2.95
208839	66	106	40	7.8	40.4	88	4.4	43.58	35.52	6.04	2.15
212937	65	102	37	8.4	36.6	85.2	2.6	38.42	43.53	6.69	2.91
219305	60	96	36	5.4	41.8	84	2.6	34.46	34.59	6.47	2.24

Appendix Table II (Continued)

212938	69	92	23	9.4	40.4	93.2	3.4	36.66	34.78	6.91	2.4
27893	57	92	35	6.8	32.4	95	4	33.72	36.34	5.5	2
236119	61	101	40	6.6	35.2	85.8	3.2	37.42	35.73	6.59	2.35
235635	61	104	43	7.4	30.2	81.8	4.2	37.62	43.01	6.47	2.78
235647	63	100	37	7	35.2	96.8	4.2	34	42.86	7.67	3.29
235648	62	104	42	6.4	39.4	71.2	4.4	29.39	42.94	6.33	2.72
235649	67	105	38	6.2	51.5	72	4.4	35.44	36.13	6.17	2.23
28061	66	106	40	7.4	43.4	79.2	4	40.43	31.66	5.96	1.89
3604	66	107	41	6.4	30.6	83.6	4.4	29.88	41.98	7.64	3.21
3866	58	108	50	6	38.5	83.6	4.2	46.19	42.16	7.44	3.14
240475	63	107	44	9.2	32.8	88	5.8	33.28	44.16	6.71	2.96
240471	65	107	42	7.2	35.4	92	5.6	33.02	40.16	6.02	2.42
236120	64	107	43	5.8	39.8	75.6	3.2	33.6	47.7	6.21	2.96
64345	65	108	43	9	32.8	87.4	4	38.43	34.69	6.97	2.42
235547	66	114	48	7.4	51.2	83.2	4.6	42.28	40.7	6.81	2.77
3603	62	110	48	7.2	32.4	84.8	3.2	32.32	45.46	7.2	3.27
233239	61	110	49	4.6	35.4	74.4	4.4	34.46	37.58	6.31	2.37
215484	76	117	41	7.8	41.4	90.2	4.2	54.5	47.63	7.9	3.76
215483	61	101	40	7.6	50	91.8	3.8	32.59	41.22	6.62	2.73
3605	58	99	41	7.2	42	89	4	33.94	36.16	6.41	2.32
219302	67	101	34	7.4	49.2	82	4.4	32.47	38.33	6.82	2.62

Appendix Table II (Continued)

219301	62	102	40	7.2	40.6	83.4	5	35.64	42.49	8.79	3.74
29696	69	118	49	7.8	53.5	109.6	5.8	41.46	43.5	9.4	4.09
219300	67	133	66	8.2	30.6	94.6	4.2	38.77	39.42	6.73	2.65
244771	62	117	55	7.2	54.4	82	3.2	40.36	37.11	6.92	2.57
244767	63	112	49	5.8	39.2	81.2	3.4	37.54	42.56	6.26	2.66
240482	62	99	37	7.2	23.6	91.6	5.6	36.2	42.3	6.67	2.82
240481	65	101	36	7.2	29.4	83.2	4.6	39.77	33	5.23	1.73
240474	59	110	51	7.8	34.4	99.4	5.2	45.45	41.45	7.54	3.13
240479	58	93	35	8	31.8	94	4	45.25	32.39	6.01	1.95
208851	64	98	34	8	35.6	93.2	5.4	45.25	43.06	6.24	2.69
215478	63	104	41	6.4	51.2	95.2	5	45	42.31	6.62	2.8
245127	67	116	49	7.4	42.8	87.6	5.4	30.03	43.3	7.32	3.17
233053	57	91	34	5.6	28.8	70.6	5.6	31.03	32.34	6.11	1.98
235549	63	109	46	8	41.8	89.6	4	46.83	42.66	6.95	2.96
212939	70	114	44	7	41.2	82.8	3	49.67	43.39	6.35	2.76
220654	72	116	44	7.6	33.6	87.8	4.4	48.65	41.64	6.52	2.71
220661	70	116	46	7.8	31.6	96.4	4.6	49.85	43.49	7.11	3.09
235548	69	122	53	5.8	40.2	85.2	5.4	36.37	41.6	6.67	2.77
235550	70	124	54	5.4	54.4	80.2	4.8	36.82	42.74	6.5	2.78
240480	64	93	29	6.8	24.4	86.6	5.2	40.64	35.08	6.1	2.14
235569	62	105	43	6.6	32.8	83.8	4.8	34.77	36.26	6.78	2.46

Appendix Table II (Continued)

236145	62	106	44	5.6	39.8	81.4	3.4	35.56	31.33	5.4	1.69
212945	70	109	39	6.8	40.6	90	4.4	53.18	35.25	6.39	2.25
212942	68	122	54	10.4	37.5	83.8	4.4	43.49	33.99	4.97	1.69
212941	69	110	41	6.4	26.6	86.6	5	40.11	34.73	6.49	2.25
212940	70	122	52	6.6	25.2	81	4	32.59	38.95	6.91	2.69
215432	74	106	32	6.2	38.2	71.4	3	39.13	33.01	6.82	2.25
215475	63	108	45	8.2	37.8	90.6	5.8	40.29	46.74	6.67	3.12
28060	63	134	71	7.6	50.6	113	4	40.13	47.48	7.62	3.62
235570	63	105	42	8.2	46.6	89	5.2	38.33	42.09	8.36	3.52
1641	70	121	51	10	39.2	114.4	5.4	47.01	40.3	6.02	2.42
236147	70	121	51	6.2	46.5	67.8	3.8	34.54	34.63	6.39	2.21
215482	68	113	45	6.4	39.4	76.2	5	31.67	35.38	6.76	2.39
215477	66	112	46	7	42.4	85	3.5	35.6	39.31	5.33	2.09
28065	70	122	52	9	48.8	100.4	5.6	48.21	43.5	6.66	2.9
240472	73	111	38	7.8	38.4	88	4.8	36.16	40.64	5.33	2.17
3619	63	109	46	7	36.38	77.6	3	53.84	41.35	6.07	2.51
3610	62	103	41	5.4	29.2	70	5	30.27	37.1	5.72	2.12
3609	58	102	44	7	41.8	79	4.4	31.35	44.11	6.43	2.83
28057	69	122	53	7.6	42.2	99	5	44.85	40.43	7.27	2.94
28058	76	130	54	8.6	34.6	98.8	5.2	38.47	40.67	6.46	2.63
29698	62	122	60	7.4	46.5	83.2	5.4	41.47	44.25	7.27	3.22

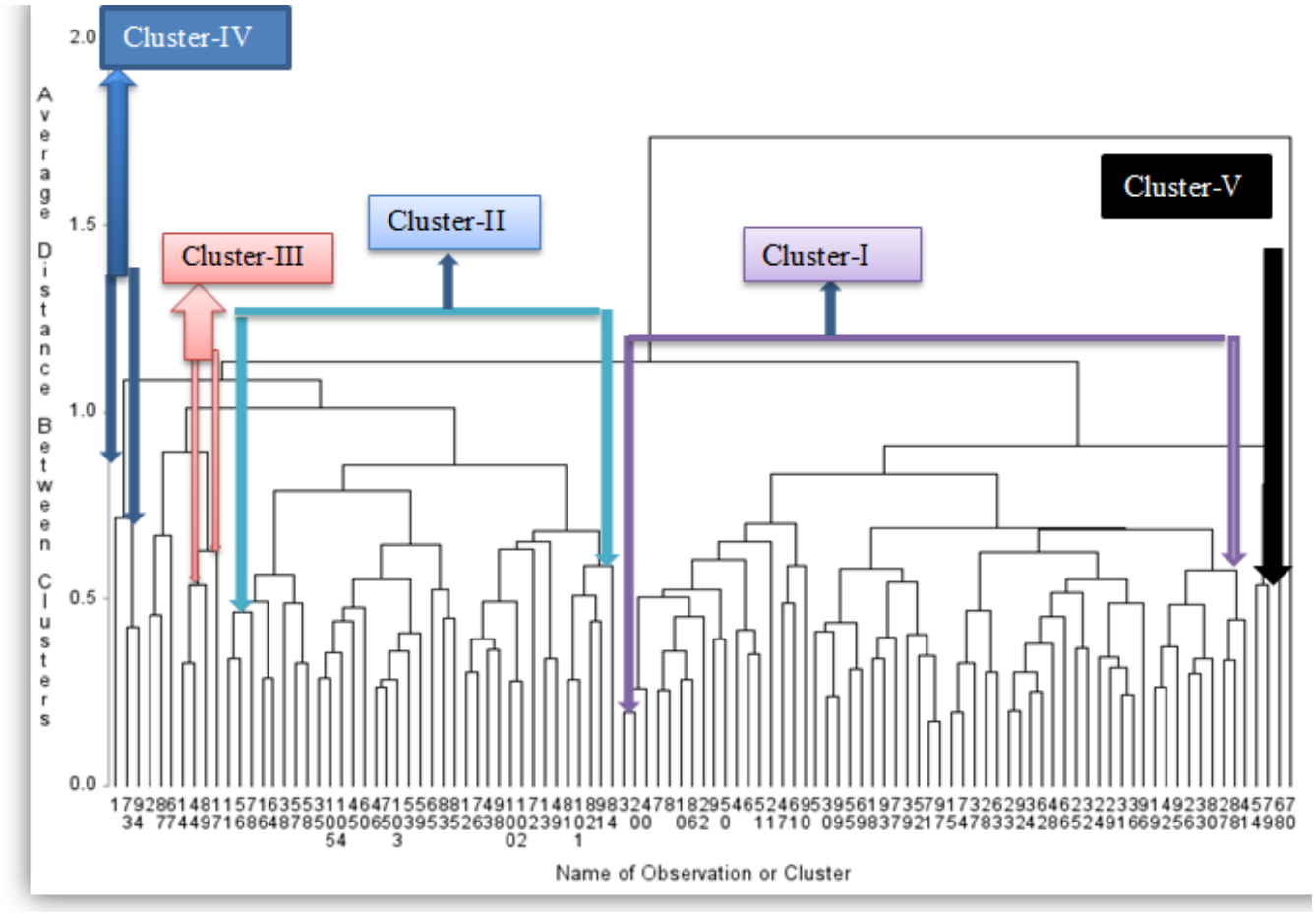
Appendix Table II (Continued)

28059	64	128	64	8.8	45.6	99.4	6	41.37	47.95	7.88	3.78
29706	63	126	63	7.8	37.2	87.8	4.4	45.05	40.08	5.47	2.19
27886	58	90	32	7.4	37.8	86	4.2	35.13	41.25	6.95	2.87
27887	63	124	61	6.6	25.2	74.6	4	47.57	45.1	5.73	2.59
220652	70	107	37	6.6	46.8	74.6	4	39.62	42.11	6.02	2.53
235571	63	129	66	8.8	44.8	88.2	4.6	31.85	38.17	7.1	2.71
235552	71	102	31	9	26.2	100.2	4.9	40.5	38.47	6.94	2.67
235554	67	124	57	9	37.6	102.2	5.3	34.42	40.92	6.45	2.64
235546	60	101	41	7.6	34.4	90.2	5.75	36.32	33.93	6.24	2.12
244775	72	111	39	7.8	44.4	89.6	5.45	43.79	39.48	6.4	2.53
235551	73	122	49	5	47.2	67.6	5.2	42.81	42.56	7.85	3.34
220653	63	98	35	6.8	43.6	78.4	5.2	37.67	45.99	6.15	2.83
217177	58	112	54	7.6	30.6	80.4	4.8	33.49	42.48	6.9	2.93
217176	63	105	42	9.2	44.5	90	5.6	41.89	41.61	6.14	2.56
28062	73	121	48	10	47.2	107.4	5.9	47.42	44.62	9.23	4.12
233052	57	104	47	6.6	42.2	82	5.4	46.33	43.61	8.75	3.82
27888	67	116	49	9.4	46.5	98.6	5.7	34.15	43.81	8.95	3.92
HB13/07	68.2	123.3	55.1	6.42	42.03	91.94	4.61	44.12	43.52	7.63	3.32
Shege	69.8	115.9	46.1	8.4	43.76	99.36	4.27	40.1	45.2	7.77	3.51
HB1966	64.2	115	50.8	7.3	42.17	87.61	4.2	38.7	42.3	7.68	3.25
C 41/98	69.1	118.7	49.6	7.64	50.99	92.17	5.19	44.85	43.48	8.46	3.68

Appendix Table II (Continued)

EH1493	67.2	118.9	51.7	7.34	48.97	86.5	3.75	39.04	42.7	7.59	3.24
Mean	65.67	112.47	46.81	7.41	41.13	88.41	4.45	40.15	41.1	7.12	2.96
Minimum	56	90	23	4.6	23.6	67.4	2.6	29.39	31.33	4.97	1.69
maximum	78	134	71	11.2	56.6	114.4	6	54.5	48.04	9.4	4.12
SE ±	3.31	4.09	5.45	0.94	3.86	3.67	0.37	2.88	1.69	0.33	0.16
CV%	5.04	3.63	11.64	12.74	9.39	4.15	8.42	7.19	4.12	4.568	5.3
LSD (5%)	7.61	9.39	18.69	2.17	8.87	8.45	0.86	6.64	3.89	0.73	0.32

Key: DH= days to heading, DM= days to maturity, GFP= grain filling period, spike length, NSPS=number of seeds per spike, PLH=plant height, NFTPP=number of fertile tillers per plant, TSW=thousand seed weight, HI=harvest index, BY=biological yield and GY=grain yield, LSD=Least significant difference



Appendix figure 1: Dendrogram showing grouping of 105 barley genotypes in to five clusters based on 11 quantitative traits