GENETIC VARIABILITY AND ASSOCIATION AMONG AGRONOMIC CHARACTERS IN SOME GENOTYPES OF BARLEY (*Hordeum vulgare* L.) GROWN IN CHENCHA AND ANGACHA, SOUTHERN ETHIOPIA

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This thesis manuscript is dedicated to my father **Ato Zerihun Zeleke** and my mother **W/o Laste Laga** for nursing me with love and affection.

STATEMENT OF THE AUTHOR

By my signature below, I declare and affirm that this thesis is my *own* work. I have followed all ethical and technical principles of scholarship in the preparation, data collection, data analysis and compilation of this Thesis. Any scholarly matter that is included in the Thesis has been recognition through citation.

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BIOGRAPHICAL SKETCH

The author was born on December 19, 1982 at Chencha district, Gamo Gofa Zone of SNNPRS, Ethiopia. He attended his elementary and junior classes at Chencha Elementary and Junior Secondary School and high school education at Chencha Secondary and Arba Minch Comprehensive Secondary School, respectively, and completed his secondary school education in 2000. Then he joined the then Awassa College of Teacher Education but now Hawassa College of Teacher Education in the regular program and graduated in Biology Education (Diploma) in 2002.

After his graduation, he was employed by SNNPRS Education Office as Biology teacher, at Gamo Gofa Zone in Bonke *woreda*. After serving for a while, he joined Dilla University as Summer-In-Service student and graduated with Bachelor of Education in Biology in 2007.Since then, he has been teaching Biology in Chencha Secondary and Preparatory School till present. In July 2010, he joined the School of Graduate Studies at Haramaya University to pursue his study for the degree of Master of Science in Genetics in the summer MSc program of the University.

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ACRONYMS AND ABBREVIATIONS

ANOVA	Analysis of Variance
ARDO	Agriculture and Rural Development Office
DAP	Diammonium Phosphate
HARC	Holetta Agricultural Research Center
masl	Meters above sea level
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis System
SNNPRS	Southern Nations, Nationalities and Peoples' Regional State

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ABSTRACT

Studying genetic variability in crops is important for improving the crops and enhancing the production. Genetic variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised. Fifteen barley (Hordeum Vulgare L.) genotypes were evaluated for 13 traits in RCBD with three replications at two locations, Chencha and Angacha. The overall objective was to study the extent of genetic variation and association among grain yield and the 12 yield-related traits. The PCV values were slightly greater than the GCV values. Relatively higher PCV values were exhibited by number of kernel/spike (15.31%) at Chencha and number of tiller (21.78%), grain yield (20.75%), biological yield (17.05%) and number of kernels/spike (16.95%) at Angacha. Days to heading showed the highest heritability at both locations, that is, (86.70%) at Chencha and (80.00%) at Angacha. Moderate to high heritability was observed for plant height (66.90%), spike length (56.90%), number of kernel/spike (53.20%), days to maturity (51.20%), number of spikelet (48.50%) and thousand kernel weight (24.30%) at Chencha, and spikelet/spike (45.30%) ,days to maturity (43.90%) and hectoliter weight (41.80%) at Angacha. Estimated genetic advance as percent of the mean was generally low for the 13 characters. Among the characters, number of kernel/spike had higher genetic advance as percent of the mean value at both locations and followed by thousand kernel weight. Grain yield showed positive and significant phenotypic correlation with biological yield, harvest index and hectoliter weight at both locations. Path coefficient analysis showed that biological yield, thousand kernel weight and number of kernel/spike exerted positive direct effect at each of the locations and the two combined at both levels. Exception was genotypic path coefficient at Chencha where only biological yield (0.330) showed positive direct effect. Among these characters biological yield showed the highest direct effect except for the combined genotypic path coefficient where thousand kernel weight (8.973) had the highest positive direct effect. While biological yield and thousand kernel weight can be considered for selection, widening the genetic base of the barley germplasm in Ethiopia is a pre-requisite for a successful breeding program.

Key words: *genotype, GCV, heritability, path-coefficient analysis and PCV*

1. INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the most important staple food crops in the highlands of Ethiopia (CSA, 2005). Its grain accounts for over 60% of the food of the people in the high lands of Ethiopia, for whom barley is one of the main sources of calories. It is a cool season crop, the most dependable, early maturing cereal grain with relatively high-yield potential including in marginal areas where other cereal crops are not adapted (Martin and Leonard, 2010; Harlan, 2008). Barely is the world's fourth important cereal crop after wheat, maize, and rice in production (Kling and Hayes, 2004).

Barley can be cultivated at altitudes between 1500 and 3500 masl but, is predominantly grown between altitudes of 2000 to 3000 masl (Berhane *et al.*, 2006). Barley cultivation and use in Ethiopia is unique in that in no other country the crop is grown in environments so diverse in terms of altitude, rainfall, soil and farming systems. About more than 85% of the total production (Chilot *et al.*, 2008) comes from the major barley growing regions, which include Wello, Shewa, Arsi, Gojam, Bale, Gondar and Tigray. This indicates wide ecological and physiological plasticity throughout the country (Asfaw, 2007).It is produced twice annually, i.e. during the main season (*meher)* and the short rainy season (*belg)* (Chilot *et al.*, 2008). The crop is also produced under residual moisture stress in some areas of Gondar, Wellega, and Gojam from September to January (Fekadu *et al.*, 2005).

The major use of barley includes human consumption, in malting processes and feed (Harlan, 2008). In Ethiopia, it is prepared in different forms of indigenous food and homemade beverages (Fekadu *et al*, 2005). Barley grain mainly consists of carbohydrates, proteins, and lipids (Horsley and Hochhalter, 2004). Barley is the 5th most important cereal crop in Ethiopia after maize, *tef*, sorghum and wheat covering about 1.1 million hectares of land with average annual production of over 1.3 million tons (CSA, 2005).

Ethiopian barley breeding program was started in 1955 at Debrezeit research station and breeding focused at selecting and evaluating landraces together with introduced materials. From this, success has been achieved from local landraces (Fekadu *et al.*, 2005). It is reported that over 80% of the barley produced in Ethiopia is derived from landrace varieties (Alemayehu and Gebre, 2010). Landrace improvement has long been recommended as a strategy for crop improvement (Qualset, 2010) but modern agriculture has lagged behind in this regard (Asfaw, 2007).

Barley landraces are reported to have better adaptation and useful traits like vigorous seedling establishment, high tillering capacity, and quick grain filling period, high seed weight and resistance to shoot fly, aphids and frost (Berhane *et al.*, 2006; Hailu *et al.*, 2006). Beside this, the unique feature of Ethiopian barleys have been realized since a long time and has played a prominent role in breeding programs worldwide as source of genes for resistance against diseases and viruses (Harlan, 2008; Arabi *et al*., 1990). In barley production, most of the Ethiopian farmers are relying on local cultivars (Hailu *et al*., 2006) but its productivity is low as compared to some major barley producing countries (Berhane *et al*., 2006). It is constrained by poor yield-potential of varieties, diseases, insects, poor soil-fertility, water logging, drought, soil acidity, and weeds (Berhanu *et al.*, 2006; ICARDA, 2009).

Therefore, one of the ways to improving barley yield could be indirect selection for morpho-agronomic characters including some other genetic variation among the breeding lines. For any planned breeding programs in order to improve grain yield potentials of crops, it is necessary to obtain adequate information on the magnitude and type of genetic variability (Omoigui *et al*., 2006). Correlation studies also help mainly to know or understand about the suitability of various characters for indirect selection since selection for one or more characters result in correlated response for several other traits (Searle, 2005).

Landraces have significant role in the history of civilization and continue to be important genetic resources in plant breeding and the main sustenance for hundreds of millions who live in less favored environments (Frankel *et al*., 2011). They are known for better adaptation to stressful environment and give reasonable yield even under low input. In this regard, the Ethiopian barley landraces are supposed to be important basis in barley improvement (Hailu *et al.*, 2006). Therefore, information on the magnitude of genetic variability and the associations of yield and yield-related traits could help in planning better breeding strategy. Likewise, estimation of genetic progress from a breeding program and periodic evaluation of advancement in the genetic gain of a crop is required to understand changes produced by breeding activities, to assess the efficiency of past improvement works in genetic yield potential and suggest on future selection direction to facilitate further improvement. Even if considerable resources were allocated to barley variety development, there were no studies conducted to determine the progress in genetic gain in grain yield potential and associated agronomic traits, as well as quality attributes in the study areas.

The general objective of the study:

To know the genetic variability and association among agronomic characters in some genotypes of barley grown in Chencha and Angacha.

Hence, this experiment was initiated with the following specific objectives:

1. To estimate the extent of genotypic and phenotypic variability among some barley genotypes grown in Chencha and Angacha.
2. To assess associations among yield and yield-related agro-morphological characters of some barley genotypes in Chencha and Angacha.

2. LITERATURE REVIEW

2.1. Barley Origin, Taxonomy, and World Distribution

Barley *(Hordeum vulgare L.*) belongs to the genus *Hordeum* and in tribe Triticeae of the family Poaceae (Gramineae). The genus, *Hordeum,* has 31 species distributed over wide geographical areas and diverse ecological habitats (Kling and Hayes, 2004). Barley is a diploid species with a chromosome number of 2n=14 (Kling and Hayes, 2009). Barley is recognized as one of the oldest crops, and is believed to have originated in the Fertile Crescent Region some 8,000 to 10,000 years ago (Harlan, 2008). The wild progenitor of the cultivated barley, *Hordeum vulgare* sub sp. *spontaneum*, is still widely distributed along this region (Ceccarelli and Grando, 2008). Barley is also believed to have been cultivated in Ethiopia as early as 3000 B.C (Gamst, 2009). Major production areas of the world include Europe, the Mediterranean fringe of North Africa, Ethiopia, and the Middle East, former USSR, China, India, Canada and USA (Horsley and Hochhalter, 2004).

2.2. Barley Adaptation and Use

Barley fields can be seen as high as 4800 masl. in the Himalayas, in latitudes greater than 60º N in Iceland and Scandinavia and in the rainfed semi-arid regions of West Asia and North Africa with less than 250 mm annual rainfall (Berhanu *et al.*, 2006). Barley is grown in a wide range of environments, but nearly two thirds of the world's production occurs in sub-humid or semi-arid regions. Barley is more tolerant than other cereals to alkaline soils and less tolerant to acid ones (Poehlman and Sleper, 2005). Barley is grown on more than 56 million hectares of land worldwide; close to 15 million is in developing countries. Its average productivity is 2.3 t/ha and 0.8 t/ha, in developed and developing nations, respectively. In developing countries, mostly barley is grown in marginal environments, often on the fringes of deserts and steppes, or at high elevations in the tropics, receiving modest or no inputs (CSA, 2008; Chilot *et al.*, 2008).

It is grown in wide range of environments with altitude range of 1500 to 3500 masl, but predominantly grown between 2000 to 3500 masl (Berhane *et al.*, 2006). It is the fifth most important cereal crop in Ethiopia after tef, maize, sorghum, and wheat in area coverage and production (CSA, 2008). The highlands of the former administrative regions such as Shewa, Arsi, Gojjam, Gonder, Wollo and Bale are major producers of barley where about 85% of the total production comes from. Barley is also an important industrial crop providing raw material for malt and beer production. Its straw is a valuable complement of cattle and small ruminant diet. About 75% of world barley is used for animal feed and 20% for malting, with the remaining 5% used for food. Ethiopia is one of the countries that use the grains as food and the straws are used for animal feed. The average annual national consumption of food barley in 2002 was 12kg/person/year (Faostat, 2005).

2.3. Genetic Variability, Production System and Utilization of Barley

Genetic variability is of immense importance to the breeders, as it is prerequisite for any improvement in crop plants and identification of superior genotype (Welsh, 2008). Barley which has been the world's most ancient crop (Hockett, 2009) is also believed to have been in cultivation in Ethiopia for the past 5000 years (Zemede, 2008) and it exhibits substantial genetic diversity. Combination of agro-climatic and biological process together with diverse socio-cultural conditions have produced suitable environment for genetic variation and existence of different barley landraces in Ethiopia (Melaku, 2010; PGRC/E, 2011; Zemede, 2008). A great deal of genetic variability in barley for different morpho-agronomic traits has been investigated in the country. Dawit and Hailu (2009) indicated presence of abundant genetic variability within Ethiopian barley collection and they noted that more than 14591 accessions were conserved by the gene bank. Berhane *et al*. (2006) evaluated six hundred pure lines extracted from thirty landraces along with original populations and the reported existence of potential genetic diversity within Ethiopian barley germplasm which is source of promising lines for grain yield at low input conditions and disease/ insect resistance.

Other studies also revealed existence of rich genetic variability of various important agronomic traits such as high, seed weight, vigorous seedling establishment, high tillering capacity, and quick grain filling period, tolerance to marginal soil condition and tolerance to frost damage (Hailu *et al*., 2006; Berhane *et al.*, 2006). Study of phenotypic diversity by Abebe and Bjornstad (2009) depicted that pattern of variation was observed in rachilla hair type and row number with range of altitude. The mean diversity index for all characters increases with altitudes between 2,400 and 2,800 masl and decreases below and above that altitude (Engels, 2010). Qualset (2010) indicated that the only known source of resistance to barley yellow dwarf virus was identified from Ethiopian landrace collections. Yitbarek *et al.* (2008) also reported that populations from higher altitudes were more resistant to scald, but susceptible to net blotch, than populations from lower altitudes.

Different production systems have been developed as a result of ingenuity of traditional farming society in different part of the highland in the country that various landraces have been identified to address requirement of each production system. As indicated by Chilot *et al*. (2008) late-barley production is the dominant form of barley production system in *meher* or main rainy season in the high altitude of the country. Likewise, early-barley production system is indispensable in both mid and high altitude areas during main rainy season (Asmare and Alemu, 2010). Significant amount of the *belg* barley and the residual moisture barley production systems are practiced in some regions of Ethiopia depending on topography and rainfall distribution of the area (Chilot *et al*., 2008; Fekadu and Hailu, 2005). The diverse traditional recipes that are prepared from barley along with strong barley consumption habit signify importance of barley crop in Ethiopia (Birhanu *et al.*, 2006). Food barley is mainly used as sources of carbohydrate although the protein content is also significant (Meaza and Lakech, 2007; Ceccarelli *et al.*, 2004).

Furthermore, Ethiopia has enormous potential for malting barley production though its share is very small as compared to food barley. Major locations where malting barley is produced in large quantity in the highland areas are; western side of Galema belt and Shashemene, Kofele and Amigna Seru woredas in Arsi, Genale woreda in Bale areas and also in Gonder (Tadesse, 2006; Muluken, 2007). Besides, it is now realized that popularization of malting barley production beyond these areas is becoming imperative to meet the demand of breweries as import substitute and as potential means of linking agriculture to industry addressing domestic market for malt (Getachew *et. al*., 2006).

2.4. Agronomic and other Requirements of Barley

Climatically, barley requires a shorter growing period and needs an average temperature of 15 to 17 °C during flowering. The annual temperatures required range from 5 to 27 °C (low temperatures and high temperatures during ripening). It tolerates high temperatures and the seasonal water requirement for barley depends on the variety, targeted yield and crop management. Barley is a drought resistant crop and requires 390 to 430 mm of rainfall for optimum yield. Maximum water use will occur for 21 to 28 days. Irrigation scheduling must be done according to evaporation and as per growth stage, because barley is more sensitive to stress during jointing, booting and heading. To optimize yield, soil moisture levels should remain above 50 % of available moisture in the active root zone from seeding to the soft dough stage Rogres *et al*. (2014)

Barley can be grown on a wide range of soil types; ranging from heavy clays to light or sandy loam soils. It grows well on fertile, deep loam soils with a pH of 6 to 7, 5. Soils with a pH lower than 6 may induce aluminum toxicity, leading to poor growth. But it is more sensitive to very wet conditions but more tolerant to alkaline soil than the other small grains Botoro (2009)

The type of fertilizers to be applied depends on soil test results. Rainfall and crop rotation are important factors influencing the nitrogen requirements for barley. Nitrogen increases protein quality of the grain, which is desirable for feeding barley but not for brewing barley. First, nitrogen should be applied prior to or during planting. Split applications of nitrogen fertilizer are more beneficial on lighter sandy soils than on heavier soils. Topdressing is recommended later than 65 days after emergence of the barley to avoid the danger of too much nitrogen levels in the grain. Where topdressing is recommended, lime ammonium nitrate (LAN) is apparently the best source of nitrogen. Accessible nitrogen and adequate phosphorus and potassium are essential for high yields (Abonado *et al*., 2013)

Barley types are planted mainly from early April until early June. Earlier plantings generally have a higher yield potential and barley types are planted over a relatively short period. Late planting results in greater risk in terms of yield and quality (Boeron and Ronald, 2011)

Barley is vulnerable to various pests (oats and wheat aphids; Russian aphids and black sand mites) and diseases (leaf spot, rust; blotch and powdery mildew) that may lead to decrease in yield and poor quality (Ordono *et al*., 2010). Heat together with high humidity encourages the occurrence of diseases such as rust. There is a need for pest and disease control in order to maintain good yield and quality, using different measure ranging from chemical, biological and other cultural practices. Use of resistant cultivars, certified and disease-free seeds as control mechanisms for pests and diseases is encouraged. Barley is very sensitive to competition from weeds and early control measures will therefore enhance the yield potential. Integrating chemical and non- chemical approaches weed controlling approaches should be practiced (Benacho *et al*., 2011).

Barley is ready for harvest in about 4 months after sowing; some varieties in 60 days. It should be harvested as soon as it reaches the moisture content of 13 %. Swath when the heads have lost their green color and with moisture content below 30 %. Barley can be harvested manually under small scale or combine harvesters can be used in large production scales. (Wyand and Rothmann, 2009).

2.5. Genetic Variability

The strategy of crop improvement of any trait comprises the collection or generation of high ranking variant types or populations and the progressive reduction of them by selection (Ashley, 2005). The presence of variation in the germplasm for the trait of interest is, therefore, very important. Variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allard, 2006; Falconer and Mackay, 1996). If the character expression of two individuals could be measured in the environment identical for both, differences in the expression would result from genetic control and hence such variation is called genetic variation (Welsh, 2008; Falconer and Mackay, 1996). Information on the nature and magnitude of genetic variability present in a crop species is thus important for developing effective crop improvement program (Singh, 2006; Welsh, 2008). Genetic variability, which is due to genetic differences among individuals within a population, is the core of plant breeding because proper management of diversity can produce permanent gain in the performance of plant and can buffer against seasonal fluctuations (Welsh, 2008; Sharma, 2004). In addition, estimation of the magnitude of variation within germplasm collections for important plant attributes will enable breeders to exploit genetic diversity more efficiently (Jahufer and Gawler, 2010). The environment of an individual plant species is the sum total of all factors other than the concerned individual plant. Various factors of environment are called biotic and abiotic components depending upon their biological and/or non-biological nature (Welsh, 2008; Singh, 2006; Sharma, 2004). Thus, the environmental deviations, such as differences on fertility level of plots, moisture content of the soil, and seasonal fluctuations contribute to the component of variation. Although some environmental variations can be reduced by proper experimentation, its total elimination is impossible because it includes, by definition, all the non-genetic variance, and much of these are beyond experimental control (Gomez and Gomez, 1984). Phenotypic variation, which is observable variation present in a character of a population, includes both genotypic and environmental components of variation and, as a result, its magnitude differs under different environmental conditions (Singh, 2006). In other words, phenotypic variation is the result of genotypic variation and environmental deviation (Falconer and Mackay, 1996).

Variation is the basis for plant breeding and it is the occurrence of differences between individuals due to variation in their genetic composition and/or the environment in which they are grown (Allard, 2006; Falconer and Mackay, 1996). The genes cannot cause a character to develop unless they have the proper environment, conversely, no amount of manipulation of the environment will cause a characteristic to develop unless the necessary genes are present (Allard, 2006). The main effect of the environment is to mask the differences between different genotypes and produce a continuous variation in the character. As the magnitude of the effect of the environment on the phenotype increases the phenotypic classes progressively overlap each other and form continuous curve (Singh, 2006).

Selection is more effective when the genetic variation in relation to environmental variation is high (Poehlman and Sleeper, 2005). It is essential to divide the observed variability into heritable and non-heritable components. Those characters showing comparatively high genetic coefficient of variation may respond favorably to selection. Phenotypic variability is the observable variation present in a character of a population; it includes both the genotypic and environmental components of variation and as a result, its magnitude differs under different environmental conditions. Genotypic variation, on the other hand, is the component of variation, which is due to the genotypic differences among individuals within a population (Singh, 2006).

Many traits important in plant breeding are not inherited in simple Mendelian terms. Their inheritance is dependent upon several genes at different loci, each contributing a small effect to the phenotypic expression of the character (Poehlman and Sleeper, 2005). Each gene that affects a quantitative trait contributes to an increment that is minimized, maximized, or limited by genetic phenomena such as dominance, epistasis, and linkage and also by environment. Since the contribution from individual genes are difficult to study, statistical estimates help in defining efficient breeding systems that take into account generation of selection, heritability of attribute and amount of available genetic variability (Singh, 2006;Poehlman and Sleeper, 2005).

2.6. Heritability

Heritability can be defined, in broad sense, as the proportion of the genotypic variability to the total variance (Allard, 2006). It refers to the portion of phenotypically expressed variation, within a given environment and it measures the degree to which a trait can be modified by selection (Christianson and Lewis, 2003). According to Falconer and Mackay (1996) heritability in narrow sense is defined as "the ratio of additive genetic variance to phenotypic variance". Since broad sense heritability does not give a clear picture of transmissibility of variation from generation to generation (because the genetic variation includes the fixable and non-fixable dominance and epistatic variation), its utilization is limited in plant improvement program. In contrast, estimate of heritability in a narrow sense can give clearer picture than that of broad sense. In other words; it expresses the magnitude of genotypic variance in the population, which is mainly responsible for changing the genetic composition of a population through selection (Falconer and Mackay, 1996). Heritability is a property not only of a character being studied but also of a population being sampled, of the environmental circumstance to which the individuals are subjected, and the way in which the phenotype is measured (Falconer and Mackay, 1996). It indicates the effectiveness with which selection of genotypes can be based on phenotypic performance (Johnson *et al.*, 2010b).

Estimation of heritability as a ratio of genotypic to phenotypic variance may vary greatly depending upon the unit for which variance is considered (Johnson *et al.*, 2010a). The greater the proportion of the total variability (i.e., due to environment), the more difficult will it be to select for inherited differences. Conversely, if environmental variability is small in relation to genotypic differences, selection will be efficient because the selected character will be transmitted to its progeny. Generally, heritability indicates the effectiveness with which selection of genotypes can be based on phenotypic performance. Heritability value by itself cannot provide the amount of genetic progress that would result from selection of the best individuals (Johnson *et al.*, 2010b).

Thurling (2012) has observed appreciably higher heritability values for flowering time, leaf area and leaf weight than for the yield. However, none of them was suitable criteria for yield selection, as the expected correlated responses to selection for these characters were lower than the direct response to selection for yield. From breeding point of view, usefulness of a character is related to its onward transmission from the parent to the progeny (Raiz and Chowdhry, 2013). A quantitative measure that provides information about the correspondence between genotypic and phenotypic variance is heritability (Dabholkar, 2004). The most important function of the heritability in the genetic study of quantitative 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 value (Dabholkar, 2004; Falconer and Mackay, 1996).

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 upon 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, 2005). If the total variability among the individuals in base population is attributable to non-heritable agencies, selection of phenotypically superior individuals from the population will not lead to improvement (Briggs and Knowles, 2007; Dabholkar, 2004). This makes selection considerably difficult due to the masking effect of the environment on the genotypic effect or inheritance (Briggs and Knowles, 2007; Singh, 2006). Economic characters like grain yield are polygenic in nature and are often influenced by the environment and thus have low heritability (Raiz and Chowdhry, 2013).

Rather if environmental variability is small in relation to genotypic differences, selection will be efficient. This is because the selected trait will be transmitted to its progeny (Briggs and Knowles, 2007). As a result of this, in practice selected phenotypic gain is more nearly maintained in characteristics with high heritability percentages than those with low (Frey and Horner, 2008; Raiz and Chowdhry, 2013).Estimates of heritability also serve as a useful guide to the breeder to appreciate the proportion of the heritable portion of variation that is due to genotypic (broad-sense heritability) or additive (narrow-sense heritability) effects (Singh, 2006). The concept of broad-sense heritability is useful if the interest is in relative importance of genotype and environment in determination of phenotypic value. But, it does not indicate the progress that might be made through selection within a particular population (Dabholkar, 2004).

This is because the genetic variation includes the fixable additive and non-fixable dominance as well as epistatic variation (Welsh, 2008).According to Dabholkar (2004), heritability estimates are classified as low (5-10%), medium (10-30%) and high (30-60%). Even though, estimates of heritability provide the basis for selection on phenotypic performance, Johnson *et al*. (2010a) suggested that the estimates of heritability and genetic advance should be considered simultaneously because high heritability should not always associate with high genetic advance (Amin *et al.*, 2004). Hence, high heritability coupled with genetic advance is more dependable, while for others the intensity of selection should be increased; gives an idea of the possible improvement of new populations through selection and high heritability with low genetic advance indicates the presence of non-additive gene action (Vimal and Vishwakarma, 2009).

2.7. Genetic Advance

Improvement in the mean genetic value of the selected plants over the base population is usually termed as genetic advance under selection. It measures the difference between the genotypic values of the generation obtained from the selected population over the mean value of the population. Genetic advance under selection is a genotypic value which depends on the three things (Allard, 2006).These are genetic variability, heritability and the selection intensity. Genetic progress would increase with increase in the variance. Therefore, the utility of estimates of heritability is increased when they are used in conjunction with the selection differential, the amount that the mean of the selected lines exceeds the mean of the entire group (Johnson *et al.,* 2010a).According to Burton and DeVane (2009) genetic advance tells us the estimate of the expected gain for a particular character through selection.

2.8. Studies on Association of Characters

Correlation coefficient is the measure of the degree for linear association between the two variables (Gomez and Gomez, 1984). A knowledge of correlations that exists between important characters can facilitate the interpretation of results obtained and provide the basis for planning more efficient program for the future (Martintell0 *et al.,* 2005). Correlated characters are important for three basic reasons. First, in connection with the genetic causes of correlation through the pleiotropic action of genes. Second, in connection with the changes brought about by selection. And third, in connection with the effect of natural selection on the relationship of metric characters with its fitness, which is the primary agent, that determines the genetic properties of that character in a natural population (Falconer and Mackay, 1996). Lack of knowledge of interrelationships among various traits and the practice of unilateral selection for agronomic characters frequently ends up with less than optimum result in plant breeding (Bhatt, 2007).

The practical utility of selecting for a given character as a means of improving another depends on the extent to which improvement in major characters is facilitated by selection for the indicators. Such improvement depends not only on the genotypic correlation but also phenotypic correlation (Johnson *et al.,* 2010b). The nature of association between grain yield and its components determine the appropriate traits to be used in the indirect selection for seeking improvement in grain yield. Correlation, measured by a correlation coefficient, is a measure of the degree of association, genetic or non-genetic between two or more traits. If genetic association exists, selection for one trait will cause change in other trait, it is a correlated response. Estimation of phenotypic, genotypic and environmental correlations is based on the components of variances and co-variances from analyses of variance, respectively (Agrawal, 2008).

Genetic association (correlation due to genetic cause) has a wider use in homozygous self-fertilized species and apomictic species. In cross-fertilized species, genetic correlations involving only additive effects (yield) are more appropriate because the formation from the correlations is used in connection with recurrent selection. Additive genetic correlation is important in selection programs because it gives information about the degree of association between two traits by way of additive or breeding values of individuals, which are the effects that can be changed by selection. Thus, selection for one trait will cause a change in the mean value of selected individuals and if another trait is correlated additively to the first, selection will cause an indirect change in the mean of the second trait. This indirect change is known as correlated response can also be predicted in the same way as direct response for one trait. The merit of indirect selection relative to direct selection for the second trait is measured by the ratio of expected correlated response over direct response (Agrawal, 2008). In small cereals, several researches have reported that traits like kernel weight, number of panicle branch per main stem and productive tiller have a strong association with grain yield. These characters are widely accepted as yield components. In a study using early generations of a single cross of tef, Hailu *et al.* (2006) obtained panicle weight per plant (a trait closer to true grain yield) positively associated with panicle weight per primary tiller and harvest index.

2.9. Path- Coefficient Analysis

In plant breeding, path coefficient is used based on the assumption that all the variation is due to additive gene action. Path coefficient analysis is used to further partition the correlation coefficients of the yield attributing traits into direct and indirect effects on grain yield using the general formula of Dewey and Lu (1959). In plant breeding context, the dependent variable (effect) could be the yield and the independent variables could be the yield components and are interrelated among themselves and also correlated to yield and the residual factor is not included in the experiment when the relations are linear that means when the yield is treated as a linear function of a number of others, yield component (Vietmeyer, 2006). Path analysis allows a more precise clarification of the pattern of interaction of other known factors and it permits the identification of direct and indirect causes of association and measures the relative importance of each character. Yield is the result of yield-correlated characters and some other undefined factors. Therefore, the use of this method is important to come up with meaningful results of cause and effect (Ariyo *et al.*, 2007). Path coefficient analysis of yield components allows the separation of the direct influence of each component on yield from indirect influences caused through the mutual relationship among yield components thereby completely determine the impact of independent variables on yield. Hence, yield contributing traits can be ranked and specific characters producing a given correlation can be observed through this technique (Ariyo *et al.*, 2007). According to Solomon (2007), path analysis conducted on RIL_S derived from intra-specific crosses of tef, shoot biomass and harvest index had the highest positive direct effects on grain yield, indicating that the direct effect explain the relationship and the importance of these traits in determine the grain yield.

3. MATERIALS AND METHODS

3.1. Description of the Study Areas

The study was conducted during the 2014 main cropping season at two locations, namely, Chencha and Angacha. Chencha Woreda is one of the 13 woredas in Gamo Gofa Zone, SNNPRS. It is located at an altitudinal range of 1700-3250masl and is found at a distance of 550km southwest of Addis Ababa. Its soil types are primarily clay or clay loams which have evolved from volcanic rocks(basalt) and the dominant soil color is reddish brown to dark brown (Teshome, 2009).The rainfall regime in Chencha is bimodal, that is, the first round season occurs between March to April and the second round takes place from June to August. The mean minimum and maximum annual rainfall are 900mm and 2000mm, respectively, while its minimum temperature varies between 11-13^{0}C and the maximum temperature is in the ranges between 18-23^{0}C. Astronomically, Chencha is located between 37^{0}29'57" to 37^{0}39'36" eastern longitude and 6^{0}8'55" to6^{0}25'30" northern latitude (Chencha woreda ARDO, 2012).

Angacha woreda is one of the six woredas that are found in Kembata Tambaro Zone, SNNPRS. It has an altitudinal range from 1800-3028masl and is located at a distance of about 255km southwest of Addis Ababa. The major soil types of the area include black basaltic (Vertisols) and red basaltic (Nitosols), in addition to this; alluvial and sand soils are also common. The rainfall of the area is characterized by erratic and uneven distribution throughout the year. The highest rainfall occurs from the end of spring season to the beginning of autumn season (May to September) and reaches its peaks in the month of August. The average annual rainfall ranges from 1000-1400mm, while the annual temperature of the area ranges from 12 to 16 ^{0}C.It is situated at latitudinal and longitudinal range of 7^{0}15'N to 7^{0}24'N and 37^{0}47'E to 37^{0}52'E respectively (Angacha woreda ARDO,2012).(Details of meteorological data of the sites are given on Appendix Table 1).

3.2. Experimental Materials

In this study, 15 barley varieties (Table 1) were taken from different sets of barley variety trials conducted by barley breeding section of Holetta Agricultural Research Center, using the purposive sampling procedure.

Table 1: Description of barley varieties

No	Variety Name	Source	Year of Release	Row Number
1	HB-1307	HARC	2006	Six row
2	Cross 41/98	HARC	2012	Six row
3	EH-1493	HARC	2012	Six row
4	Misrach	HARC	1998	Six row
5	Shege	HARC	1996	Six row
6	Ardu-12-60B	HARC	1986	Six row
7	HB-42	HARC	1985	Six row
8	Ahor 880/61	HARC	1980	Six row
9	Balami	HARC	Local	Irregular
10	Bekoji-I	HARC	2010	Two rows
11	Holker	HARC	1979	Two row
12	IBON 174/03	HARC	2012	Two row
13	EH-1847	HARC	2011	Two row
14	HB-1533	HARC	2004	Two row
15	Miscal-21	HARC	2006	Two row

Foot note: HB= Holetta Barley, EH=Ethiopia Holetta, IBON=International Barley Observation Nursery

3.3. Experimental Design and Treatments

The experiment was conducted in a randomized complete block design with three replications .Each treatment was planted on a plot size of 1.2m x 2.5m, consisting of six rows of 2.5m length with 0.2m spacing between rows, 0.4m between plots and 1.5m between blocks. Seed rate was 100kg/ha in both sites. Fertilizer was applied during planting in the form of diammonium phosphate (DAP) only and urea was applied after 40 days from sowing at a rate of 62/69 N/P2O5. Seeds were planted by hand drilling on July 22, 2014 at Angacha and July 29, 2014 at Chencha. For data collection, the middle four rows were used ($2m^2$ area).All experimental factors were applied uniformly to the entire plot.

3.4. Data Collection

Data on agro- morphological traits for barley varieties were collected according to Anderson *et al*. (2012) and descriptors for barley (IPGRI, 2010). The plant basis was on ten randomly selected plants from the central four rows in each plot and the average values were recorded.

The following 13 traits were used to characterize the variability in the barley genotypes.

1. Days to heading (DH): it was recorded as the number of days from sowing to the date on which 75% of the plants in four central rows of a plot have produced heads.
2. Days to maturity (DM): it was recorded as the number of days from sowing to the stage when 75% of plants in four central rows of a plot have reached maturity.
3. Grain filling period (GFP): number of days from heading to physiological maturity.
4. Biological yield (BY): it was determined by weighing the total air dried above ground biomass from the four central rows of each plot and expressed in kilogram per plot.
5. Grain yield (GY): grain yield in kilogram of the four central rows adjusted to 12% moisture content and expressed in kilogram per hectare.

6. Harvest index (HI): It was calculated as the ratio of dry weight of the grain to dry weight of the above ground biomass and expressed as a percentage.
7. Thousand kernel weight (TKW): weight in gram of random sample of thousand seeds per plot.
8. Hectoliter weight (HW): Flour density produced in a hectoliter of the seed and determined using moisture and hectoliter analyzer.
9. Tiller number per plant (TI): Number of tillers per plant excluding the main plant recorded at maturity and expressed as an average of randomly selected ten plants per plot.
10. Plant Height (PH): It was measured as the height in centimeter from the soil surface to the tip of the spike excluding the awns at maturity and expressed as an average of randomly selected ten plants per plot.
11. Spike length (SLN): Spike length of the main plant measured in centimeter from base to tip excluding the awns and expressed as the average of randomly selected ten plants in a plot.
12. Spikelet number per spike (SPL): It was recorded by counting the number of spikelet on each spike on the main tiller of and expressed as the average of randomly selected ten plants in each plot.
13. Kernel number per spike (KN): It was determined by counting the number of kernels produced on the main tiller of each plant and expressed as an average of randomly selected ten plants in each plot.

3.5. Statistical Analysis

All measured agro-morphological traits and quality parameters were subjected to analysis of variance using **SAS** software version 9.00 (Anonymous, 2002). Bartlett's test for homogeneity of variance was carried out to determine the validity of the experiment.

The data were also subjected to analysis of variance (Table 2), phenotypic and genotypic correlation as well as path coefficient analysis using SAS software version 9.00 (Anonymous, 2002)

3.5.1. Analysis of variance

Table 2: RCBD model for individual locations

Source of variation	Degree of freedom	Mean square	Expected mean
Replication	r-l	Msr	$\sigma^2e + g\sigma^2r$
Genotype	g-l	Msg	$\sigma^2e + rg\sigma^2$
Genotype	g-l	Msg	$\sigma^2e + r\ \sigma^2gl + rl\sigma^2g$
Error	(r-l) (g-l)	Mse	σ^2e
Total	gr-le		

Where: σ2g=genotypic variance, σ^2e=error variance, Msr = mean square of replication, Mse = mean square of error, Msg= mean square of genotypes

Table 3: RCBD model for combined analysis over the locations

Source of variation	Degree of freedom	Mean square	Expected mean
Location	l-l		
Rep within location	l(r-l)	Msr	$\sigma^2e + gl\sigma^2r$
Genotype	g-l	Msg	$\sigma^2e + r\,\sigma^2gl + rl\sigma^2g$
Genotype x location	(g-l) (l-l)	Msgl	$\sigma^2e + r\,\sigma^2gl$
Error	r(g-l)(r-l)	Mse	σ^2e
Total	grl-l		

Where: σ^2e =error variance, Msr = mean square of replication, Mse = mean square of error, Msg= mean square of genotypes

3.5.2. Estimation of phenotypic and genotypic parameters

To assess the genotypic variability among the 15 genotypes of barley for the characters under study and to work out the environmental effect on various characters of the phenotypic and genotypic components of variances had estimated from the analysis of variance of simple lattice as suggested by Burton and de Vane (2009):

$\sigma^2p = \sigma^2g + \sigma^2e$, Where: σ^2p = phenotypic variance,σ^2g = genotypic variance, σ^2e = environmental variance (error mean square)

$$\sigma^2g = \frac{\text{(mean square due to lines - mean square due to error)}}{r}$$

Where: r = Number of replications

$$PCV = \frac{\sqrt{\sigma^2 p}}{\overline{X}} x100$$

Where: PCV =Phenotypic coefficient of variation and

$\overline{X}$ =sample mean

$$GCV = \frac{\sqrt{\sigma^2 g}}{\overline{X}} x100$$

Where: GCV= genotypic coefficient of variation and $\overline{X}$ =sample mean

Heritability (H): Heritability in a broad sense for all characters was computed using the formula given by Falconer and Mackay (1996).

$$\text{Heritability (H)} = \frac{\sigma^2 g}{\sigma^2 p} x100$$

Genetic advance under selection (GA): Expected genetic advance for each character at 5% selection intensity was computed using the methodology described by Johnson *et al.* (2010a):

$GA = K * \sigma p * H$

Where: GA = expected genetic advance

K=constant (selection differential where K= 2.056 at 5% selection intensity)

σp =phenotypic standard deviation on mean basis

H = heritability in a broad sense

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

$$GAM = \frac{GA}{\overline{X}} x100$$

Where: GAM = genetic advance as percent of mean, GA = genetic advance under selection

$\overline{X}$ = mean of the population in which selection was employed

3.5.3. Association of characters

Phenotypic correlation (the observable relation between two variables) includes both the genotypic and environmental effects, and the genotypic correlation (the inherited association between two variables) was estimated using the standard procedure suggested by Miller *et al.*, 2008.

Covariance between all pairs of variables followed the same form as the variance. Thus, the estimates of phenotypic and genotypic covariance components between two traits are the same fashion as for the corresponding variance components:

$$rp_{xy} = \frac{covpxy}{\sqrt{\sigma 2px\, \sigma 2py}}$$

Where: rp_{xy} = Phenotypic correlation coefficient between characters x and y

$covp_{xy}$ = Phenotypic covariance between characters x and y

$\sigma^2 p_x$ = Phenotypic variance of character x

$\sigma^2 p_y$ = Phenotypic variance of character y

$$rg_{xy} = \frac{covgxy}{\sqrt{\sigma 2gx\, \sigma 2gy}}$$

Where: rg_{xy} =genotypic correlation coefficient between characters x and y

$covg_{xy}$ =genotypic covariance between characters x and y

$\sigma^2 g_x$ = genotypic variance of character x

$\sigma^2 g_y$ = genotypic variance of character y

3.5.4. Path-coefficient analysis

Path-coefficient analysis was carried out using phenotypic correlation coefficient and genotypic correlation coefficient to know the direct and indirect contribution of all the characters on the seed yield (Dewey and Lu, 1959).

$$r_{ij}=p_{ij}+\Sigma r_{ik}p_{jk}$$

Where: r_{ij} = mutual association between the independent character (i) and dependent character (j) as measured by the genotypic correlation coefficients

p_{ij} = Components of direct effects of the independent character(i) and dependent character (j) as measured by the genotypic path coefficient, and

$\Sigma r_{ik}p_{kj}$ =Summation of components of indirect effects of a given independent character (i) on the given dependent character (j) via all other independent characters.

The residual was estimated as described by Dewey and Lu (1959):

$$l= p^2R + \sum P_{kj}\, r_{ij}$$

4. RESULTS AND DISCUSSION

4.1. Variability Assessment

4.1.1. Analysis of variance

Mean squares of the 13 characters from analysis of variance (ANOVA) at individual locations and combined over the two locations are presented in Tables 4 and 5. At Chencha, significant differences among genotypes ($p \leq 0.01$) were observed for all traits except grain filling period, number of tillers, biological yield, grain yield and hectoliter weight. At Angacha, in addition to those characters significant at Chencha, hectoliter weight was significant ($p \leq 0.01$). Oettler *et al*. (2009) reported significant differences among nine barley genotype for grain yield, spikes/m^2, thousand kernel weight, dry matter, anthesis and plant height.

After pooled analysis, significant location effect for days to heading, days to mature, grain filling period, harvest index and hectoliter weight were observed and indicating that the phenotypic expression of these characters were different at the two locations (Table 5). Genotype effects were significant for all traits except number of kernel/spike, number of tillers, biological yield, grain yield and harvest index. The mean square due to genotype (G) x location (L) interaction was significant only for number of kernels/spike and harvest index indicating the differential response of genotypes for these traits at each location.

Table 4: Analysis of variance (mean squares) for the 13 characters of 15 barley genotypes grown at Chencha and Angacha (2014/15)

Traits	Locations							
	Chencha				Angacha			
	Sources of variation			CV (%)	Sources of variation			CV (%
	Replication (df=2)	Genotype (df=14)	Error (df=28)		Replication (df=2)	Genotype (df=14)	Error (df=28)	
DH	0.04	23.66**	1.56	2.15	15.52	20.11**	2.52	2.47
DM	8.00	19.06**	6.15	2.22	41.80	24.01**	9.36	2.49
GFP	16.33	6.39ns	5.35	4.28	6.38	6.54ns	5.13	3.87
PH	949.24	80.12**	15.90	3.72	144.50	207.07**	100.02	9.63
SLN	1.47	1.55**	0.43	6.98	11.80	1.85*	1.07	10.05
SPL	8.58	1.67**	0.58	5.86	7.44	2.99**	1.13	7.93
KN	112.50	106.97**	32.71	10.47	658.33	103.04**	51.89	13.87
TI	2.61	1.16ns	1.24	21.16	0.37	0.78ns	0.60	20.24
BY	2.09	0.12ns	0.12	10.80	4.98	0.37ns	0.29	14.84
GY	8025093.93	763648.48ns	547921.32	11.75	5869433	1,246,471ns	988878.82	18.52
HI	0.50	21.62*	13.17	9.36	32.00	22.80**	10.96	11.27
HW	2.68	3.35ns	2.75	2.08	3.57	10.51**	4.32	2.82
TKW	18.17	24.24**	3.80	4.54	15.78	34.76**	23.02	11.80

, DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Table 5: Combined analysis of variance (mean squares) for 13 traits of 15 barley genotypes grown at Chencha and Angacha (2014/15)

Characters	Replication within Locations (L) (df=14)	Locations (L) (df=1)	Genotype (G) Location (df=28)	GXL (df=2)		
DH	**7.78**	**1806.25**	**41.44**	**2.33**	**2.04**	**2.34**
DM	**24.89**	**6061.73**	**38.08**	**4.95**	**7.75**	**2.38**
GFP	**11.35**	**974.33**	**7.92**	**5.00**	**5.23**	**4.07**
PH	**949.24**	**80.12**	**15.90**	**3.72**	**4.67**	**5.97**
SLN	**6.63**	**0.02**	**2.76**	**0.65**	**0.75**	**9.26**
SPL	**8.01**	**6.61**	**3.39**	**1.26**	**0.85**	**7.00**	**6.9**
KN	**385.41**	**352.90**	**122.82**	**87.20**	**42.29**	**12.0**
TI	**0.36**	**0.02**	**0.65**	**0.67**	**0.59**	**20.18**
BY	**3.53**	**2.04**	**0.28**	**0.20**	**0.20**	**13.71**
GY	**6947263.50**	**71330620.70**	**991490.90**	**1018628.70**	**68400.00**	**15.39**
HI	**16.25**	**4346.57**	**24.23**	**20.20**	**12.06**	**10.1**
HW	**3.12**	**1718.10**	**9.13**	**4.73**	**3.53**	**2.45**
TKW	**23.02**	**34.76**	**15.78**	**11.80**	**24.63**	**12.71**

CV = Coefficient of variation, df = degree of freedom

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

4.1.2. Variance components and coefficients of variation

Estimates of phenotypic (δ^2p), genotypic (δ^2g) and environmental (δ^2e) variances and phenotypic (PCV) and genotypic (GCV) coefficients of variation are given in Table 6 and 7 for Chencha and Angacha, respectively. The PCV value for days to heading and days to maturity was slightly higher than that of GCV value of these traits at both locations. The relatively larger differences between PCV and GCV values for the rest of the traits suggest that there was high contribution of the environmental variance to the phenotypic variance.

Table 6: Estimates of mean, phenotypic (δ^2p), genotypic (δ^2g) and environmental (δ^2e) components of variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (H), expected genetic advance (GA) and genetic advance as percent of the mean (GA%) for 13 characters at Chencha (2014/15)

Traits	Mean	δ^2p	δ^2g	δ^2e	PCV	GCV
DH	58.10	12.61	11.05	1.56	6.11	5.72
DM	111.55	12.58	6.44	6.14	3.18	2.27
GFP	54.04	5.87	0.52	5.34	4.48	1.34
PH	107.29	48.01	32.11	15.90	6.46	5.28
SLN	9.36	0.99	0.56	0.42	10.64	8.02
SPL	13.01	1.13	0.54	0.58	8.17	5.67
KN	54.60	69.84	37.13	32.70	15.31	11.16
TI	3.16	17.39	4.22	1.23	10.75	5.30
BY	3.16	0.12	0.02	0.11	10.90	1.41
GY	63000.28	655784.89	107863.58	247921.31	12.85	5.21
TKW	38.78	17.39	4.22	13.16	10.75	5.30
HW	79.67	3.05	0.30	2.74	2.19	0.69
HI	42.95	14.02	10.22	3.80	8.72	7.44

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Table 7.Estimate of mean, phenotypic (δ^2p), genotypic (δ^2g) and environmental (δ^2e) components of variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad sense heritability (H), expected genetic advance (GA) and genetic advance as percent of the mean (GA%) for 13 characters at Angacha (2014/15)

Traits	Mean	δ^2p	δ^2g	δ^2e	PCV	GCV
DH	**64.17**	**10.99**	**8.78**	**2.52**	**5.17**	**4.62**
DM	**122.67**	**16.68**	**7.32**	**9.38**	**3.33**	**2.21**
GFP	**58.50**	**5.83**	**0.70**	**5.12**	**4.13**	**1.44**
PH	**103.86**	**153.55**	**53.52**	**100.02**	**11.93**	**7.04**
SPL	**9.34**	**1.46**	**0.39**	**1.06**	**12.94**	**6.73**
SPN	**13.37**	**2.05**	**0.93**	**1.12**	**10.72**	**7.22**
KN	**51.91**	**77.46**	**25.58**	**51.88**	**16.95**	**9.74**
TI	**3.81**	**0.69**	**0.09**	**0.57**	**21.78**	**8.03**
BY	**3.37**	**0.03**	**0.04**	**0.28**	**17.05**	**6.29**
GY	**5093.75**	**111767.40**	**128796.14**	**988878.91**	**20.75**	**7.05**
TKW	**29.36**	**16.88**	**5.92**	**10.95**	**13.99**	**8.29**
HW	**73.75**	**7.41**	**3.09**	**4.32**	**3.69**	**2.39**
HI	**33.67**	**25.27**	**9.48**	**15.78**	**14.93**	**9.15**

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

At Chencha, the highest PCV values were observed for number of kernel/spike (15.31%) followed by grain yield (12.85%), biological yield (10.90%), number of tiller/plant (10.75%) and harvest index (8.72%) and spike length (10.64%). Other workers have reported high PCV and GCV for grain yield, biomass, harvest index, thousand kernel weight and plant height in barley (Amsal *et al.,* 2006; Sharma *et al.,* 2005, Bekele *et al.,* 2008; Desalegn *et al.,* 2007). The highest GCV 11.16% was observed for number of kernel/spike. The lowest PCV and GCV values were observed for days to maturity (3.18%, 2.27%), grain filling period (4.48%, 1.34%) and hectoliter weight (2.19%, 0.69%).

At Angacha, the highest PCV values were obtained for tiller number (21.78%), grain yield (20.75%), and biological yield (17.05%), number of kernel/spike (16.95%), harvest index (14.93%), thousand kernel weight (13.99%), spike length (12.94%) and plant height (11.93%). Relatively higher GCV values were recorded for number of kernel/spike (9.74%) followed by thousand kernel weight (8.29%). The lowest PCV and GCV were recorded for days to heading (5.17%, 4.2%), days to maturity (3.33%, 2.12%), grain filling period (4.13%, 1.44%) and hectoliter weight (3.69%, 2.39%). Among the yield components number of tiller and number of kernel/spike showed considerable variation.

At Chencha, the genotypic variance was found to be relatively greater than its corresponding environmental variance for plant height, spike length, number of kernel/spike, days to heading, days to maturity, number of tiller and harvest index. This implies that in phenotypic expression of these traits, the effect of environmental factors is low. Motzo *et al.,* 2010 in barley reported high genotypic variation for heading date and kernel weight. On the other hand, the magnitude of genotypic variances was smaller than that of environmental variance at the same location for grain filling period, number of spikelet/spike, biological yield, grain yield, thousand kernel weight and hectoliter weight. This signifies the effect of environmental factors on the phenotypic expression of these traits were high. At Chencha, all the 13 characters studied showed a phenotypic variance greater than the genotypic variance (Table 6). At Angacha, the genotypic variance is smaller than that of environmental variance except for days to heading (Table 7).

Table 8: Phenotypic (δ^2p), genotypic (δ^2g), environmental (δ^2e) and genotype × location interaction (δ^2gl) variance for 15 barley genotypes from combined ANOVA over locations, Chencha and Angacha (2014/15)

Traits	δ^2p	δ^2g	δ^2e	δ^2gl
DH	11.95	9.77	2.04	0.14
DM	16.03	8.23	7.75	-0.11
GFP	5.96	0.72	5.23	-0.21
SPL	1.26	0.52	0.75	-0.01
SPN	1.58	0.53	0.85	0.20
KN	65.64	0.90	42.29	22.45
TI	0.63	-0.42	0.59	0.04
BY	0.25	0.02	0.20	0.03
GY	886729.89	-0.03	768400.06	125114.32
HI	17.01	1.00	12.06	4.07
HW	4.63	1.10	3.53	0.60

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, HW= Hectoliter weight, TI= Tiller number per plant, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Combined over the two locations, genotypic variances were larger than their environmental counter parts for days to heading and days to maturity indicating that in the phenotypic variance the contribution of genotypic variances was maximum for these characters. The genotypic variance for the rest of the characters was less than that of the environmental variance. This shows the environmental factors had major contribution to the variability among the genotypes Sharma *et al.,* (2005). After pooled analysis of variance of the characters with homogenous error variance, all except days to heading and days to maturity exhibited genotypic variance less than that of the environmental variance and some had negative genotypic variance (Table 8). These are number of tillers and grain yield. Such negative value was observed for genotype x location interaction variance for number of days to maturity, grain filling period and spike length. These negative numbers suggest the error in the size of sampling. Since the exact estimate of squared numbers cannot be negative, if they appear they are interpreted as being estimate of variance which is zero (Miller *et al.,* 2008). The larger environmental variance than genotypic variance indicates that in the phenotypic expression of that trait with larger environmental variance the contribution of the environment was greater.

4.1.3. Heritability and genetic advance

Heritability estimate for character under study at Chencha and Angacha are indicated in Table 6 and 7 respectively. At Chencha, some characters had relatively high heritability values. Cases in point are days to heading (86.70%), harvest index (72.90%) and plant height (66.90%). Other characters such as days to maturity (51.20%), spike length (56.90%) and number of spikelet/spike (48.50%) had moderately high heritability. At Angacha, days to heading was the only character with high heritability value (80.00%). Other characters such as spikelet/spike (45.30%), days to maturity (43.90%), hectoliter weight (41.80%),harvest index (37.60%),plant height (34.90),number of kernels/spike (33.00%) and harvest index (37.60%) exhibited moderately high heritability values. Mittal and Sethi (2007) reported high heritability for grain yield per plant in barley.

Oettler *et al*., (2009) also reported high heritability in barley for grain yield per plot, thousand kernel weight, plant height and dry matter. Mogghadahm *et al. (*2009) in barley obtained high heritability for thousand kernel weight, tillers/plant, number of kernels/spike and harvest index. Grain yield was found to have low heritability at both of the two locations. This shows the environmental effect constitutes a major portion of the total phenotypic variation Mogghadahm *et al. (*2009).

At Chencha, genetic advance as a percent mean ranged from <1% for hectoliter weight to 16.65% for number of kernels/spike (Table 6).Within this range, a relatively high genetic advance was observed for kernel number per spike (16.65%), harvest index (13.09%), spike length (12.47%) and days to heading (11.03%). The lowest estimate was observed for grain filling period (<1%), biological yield (1.21%), days to maturity (3.39%) and grain yield (4.37%).

At Angacha, the range of genetic advance as percent of mean was from 1.03% for grain filling period to 11.56% for harvest index. At this location, number of kernel/spike showed 11.52%, thousand kernel weight 10.12% and number of spikelet/spike 10.01% genetic advance as percent of mean. The lowest genetic advance as percent of mean observed for days to maturity (3.01%), grain filling period (1.03%), biological yield (4.79%), grain yield (4.92%) and hectoliter weight (3.18%).This low estimate of genetic advance as a percent of mean arises from low estimate of phenotypic variance and heritability.

Selection based on those traits with a relatively high genetic advance as a percent of mean can result in the improvement of the performance of the genotypes for the traits. A case in point is number of kernel/spike. This trait had also moderately high heritability value. Generally, there was no as such appreciable difference between the two locations as far as heritability and genetic advance (as percent of mean) were concerned. Those traits with high heritability and genetic advance at Chencha exhibited high heritability and genetic advance at Angacha. Those having medium to low heritability and genetic advance at Chencha also showed medium to low heritability and genetic advance at Angacha.

4.2. Association Studies

4.2.1. Correlation of grain yield with other traits

Phenotypic (r_p) and genotypic (r_g) correlation estimates among the various characters are presented in Tables 9, 10 and 11 for Chencha, Angacha and the two locations combined, respectively. At phenotypic level, at Chencha grain yield was positively and significantly ($p \leq 0.01$) correlated with biological yield. In the same location, grain yield was negatively and significantly correlated phenotypically with days to heading. This negative correlation between days to heading and grain yield is in harmony with the findings of Blanco *et al. (*2010) in barley. At Angacha, grain yield showed positive and significant phenotypic correlation with days to maturity, grain filling period, plant height, number of kernel/spike, biological yield, and harvest index and hectoliter weight. The result of this study shows days to maturity had positive correlation with grain yield strengthen the similar result reported by Wallace *et al.* (2011), in barley. Vajika (2008) reported lowest coefficient for plant height, spike length and number of spikelet/spike in barley. The significant positive association of grain yield with number of kernels/spike is in agreement with the result of Blanco *et al*. (2010). The result by itself strengthens genotypes producing more number of kernel/spike are high yielder. Combined over the two locations, grain yield had positive and highly significant ($p \leq 0.01$) correlation with plant height, number of kernel, biological yield, harvest index, hectoliter weight and thousand kernel weight. The correlation of grain yield with days to heading and days to maturity were significant and negative at phenotypic level. Genotypically, grain yield was negatively and significantly correlated with days to heading and days to maturity but it had positive and significant correlation with harvest index at Chencha. At Angacha , grain yield had non significant correlation with all the traits under study genotypically. Pooled over the two locations, grain yield was negatively and significantly correlated with days to heading, days to maturity and grain filling period but it had positively and significantly correlated with harvest index and thousand kernel weight.

4.2.2. Correlation among other traits

4.2.2.1. Phenotypic correlation

At Chencha, days to heading had positive and significant association with days to maturity. It was also observed that this character had negative and significant correlation with grain yield. It had non significant correlation with the rest of the characters. Number of spikelet/spike showed significant correlation with days to heading, days to maturity and number of kernel/spike.

Biological yield had positive and significant correlation with plant height. It had non significant correlation with the rest of the characters. Harvest index showed negative and highly significant correlation with days to heading. The correlation harvest index with hectoliter weight and thousand kernel weight was positive and significant. Hectoliter weight had positive and significant correlation with harvest index and thousand kernel weight. Thousand kernel weights had negative and significant correlation with days to heading. It had positive and significant correlation with hectoliter weight.

At Angacha, days to heading had positive and significant correlation with days to maturity, plant height, spikelet/spike, number of kernel/spike and biological yield. This character exhibited negative and significant correlation with hectoliter and thousand kernel weight. Days to maturity had positive and significant association with days to heading, grain filling period, plant height, spikelet/spike, number of kernel/spike and biological yield. The correlation coefficient of days to maturity with hectoliter weight and thousand kernels weight was negative and significant. Grain filling period had positive and significant correlation with days to maturity, plant height and biological yield. Plant height had positive and significant correlation with days to heading, days to maturity, grain filling period, number of kernel per spike and biological yield. Spike length had positive and significant correlation with spikelet/spike, number of kernel per spike and biological yield.

Spikelet/spike had negative and significant correlation with hectoliter weight and thousand kernel weight. Number of kernel/spike had positive and significant correlation with days to heading, days to maturity, plant height, spike length, spikelet/spike and biological yield. Harvest index had positive and significant correlation with hectoliter weight and thousand kernel weight. Hectoliter weight had negative and significant correlation with days to heading spikelet and spikelet/spike. This character exhibited positive and significant correlation with harvest index and thousand kernel weight.

Table 9.Phenotypic (r_p) and genotypic (r_g) correlation coefficient of the 13 character in 15 barley genotypes grown at Chencha (2014/15)

Traits	DM	GFP	PH	SLN	SPL	KR	TI	BY	GY	HI	HW	TKW
DH rg	1.046✶✶	-0.427	-0.026	-0.127	0.874	0.125	-0.009	-0.356	-1.006✶✶	-0.882	-0.693	-0.510
rp	0.725✶✶	-0.185	0.045	-0.097	0.605✶✶	0.089	0.007	-0.056	-0.377✶✶	-0.373✶✶	-0.180	-.40✶
DM rg		-0.503	0.072	-0.176	0.900	-0.035	0.176	-0.954	-1.395✶✶	-1.089✶✶	-1.103✶✶	-0.389
rp		0.166	0.073	-0.072	0.414✶✶	-0.010	0.196	0.008	-0.169	-0.210	-0.051	-0.206
GFP rp				-0.050	-0.356	-0.510	-1.188✶✶	-0.403	-1.228✶✶	-0.588	-0.204	0.211
				-0.413	-0.140	-0.25	10.489	-0.395	-0.030	-0.308	-0.166	0.030
rp					0.095	-0.066	-0.214	-0.212	0.165	0.080	0.014	-0.074
					0.057	0.082	0.007	-0.261	0.586	1.627✶✶	0.175	-0.183
						-0.014	0.017	-2.678	0.368	0.086	0.152	0.030
PH rg-						0.013	0.219	-0.319	0.274	0.043	0.204	-0.604
rp						0.083	0.117	-0.025	0.099	0.363✶	0.232	-0.057
SLN rg							-0.109	-0.102	-0.221	-1.219✶✶	-0.177	0.206
rp							0.099	0.156	-0.025	0.126	0.160	0.075
SPL rg								0.528	-0.534	-1.202✶✶	-0.715	-0.340
								1.052✶✶	-0.573	0.577 0.533✶✶		
rg								0.366✶✶	-0.007	-0.060	-0.255	-0.211
										0.310✶		0.371✶✶
KR rg									-0.180	-1.615✶✶	-0.219	0.190
												-0.485
rg									0.173	0.038	0.056	0.012
TI rg										1.539✶✶	0.707	0.358
rg										-0.046	0.037	0.111
BY rg											0.184	0.291
rp											0.650✶✶	-0.275
GY rg											0.030	0.317
rp												
HI rg												0.030
rp												
HW rg-												0.092
rp												

Table 10.Phenotypic and genotypic correlation coefficient of the 13 characters in 15 barley genotypes at Angacha (2014/15)

Traits	DM	GFP	PH	SLN	SPL	KR	TI	BY	GY	HI	HW	TKW	
DH rg	0.960✶	-0.437	0.593	0.149	0.871	0.538	0.237	0.589	-0.064	-0.487	-0.778	-0.798	
rp	0.807✶✶	-0.029	0.531✶✶	0.227	0.675✶✶	0.430✶✶	0.170	0.410✶✶	0.142	-0.257	-0.470✶✶	- 0.09	
DM rg		-0.168	0.542	0.143	0.804	0.308	0.378	0.469	-0.299	-0.559	0.644	-0.718	
rp		0.568✶✶	0.610✶✶	0.255	0.598✶✶	0.392✶✶	0.111	0.584✶✶	0.362✶	-0.148	-0.292✶	-0.02	
GFP rp			0.346	-0.066	-0.483	-0.904✶	0.382	-0.569	-0.375	-0.083	0.668	0.504	
rp			0.292✶	0.115	0.071	0.063	-0.049	0.416✶✶	0.413✶✶	0.107	0.162	0.033	
PH rg-				-0.139	0.660	0.341	0.293	0.743	0.597	-0.116	-0.528	-0.267	
rp					0.227	0.611	0.591✶✶	0.038	0.630✶✶	0.541✶✶		0.057	
SLN rg					-	0.108	0.440	0.913	0.443	-0.319	-0.567	-0.050	
rp						0.431✶✶	0.327✶	0.180	0.386✶✶	0.146	-0.227	-0.260	
SPL rg							0.670	-0.276	0.637	0.353	-0.213	0.00	
rg							0.628✶✶	0.109	0.432✶✶	0.270	-0.117	-0.380	
KR rg							-0.235	0.447	0.858	0.411	-0.501	-0.057	
rg								-0.114	-0.211	-0.054	0.478✶✶	0.00	
TI rg								0.004	-0.156	0.355	-0.289	-0.501	
								0.472✶✶		0.390✶	0.472✶✶	0.39	
rg										0.053	-0.039	-0.121	
BY rg										0.327	-0.404	-0.729	
rp											0.770✶✶	-0.046	
GY rg											0.006	0.980	
rp											0.760	0.990	
HI rg												0.879	
rp												0.364	
HW rg-													
rp													

Table 11.Phenotypic and genotypic correlation coefficient of the 13 characters in 15 barley genotypes combined over the two locations at Chencha and Angacha (2014/15)

Traits	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI	HW
DH rg	0.958✶	0.841	-0.128	-0.136	0.617	-0.614	0.081	0.574	-0.998✶	-0.392✶	-0.916✶
rp	0.871✶✶	0.398✶✶	0.141	0.055	0.562✶✶	0.043	0.002	0.298✶	-0.397✶✶	-0.661✶✶	-0.687✶✶
DM rg	0.963✶	-0.134	0.002	0.472	-0.692	-0.412	0.766	-0.981✶	-0.974✶	-0.982✶	-0.993✶
rp		0.721✶✶	0.099	0.064	0.410✶✶	-0.071	0.017	0.369✶✶	-0.363✶	-0.692✶✶	-0.728✶✶
GFP rp			-0.158	-0.002	0.208	-0.725	-1.376✶✶	0.831	-0.909✶	-0.937✶	-0.944✶
rp			0.012	0.050	0.089	-0.171	0.050	0.361✶	-0.188	-0.505✶✶	-0.488✶✶
PH rg-				0.254	0.231	0.210	0.831	0.308	0.423	0.287	0.292
rp				0.216	0.457✶✶	0.459✶✶	-0.066	0.538✶✶	0.487✶✶	0.126	0.089
SLN rg					-0.045	-0.125	0.293	0.809	0.289	0.037	-0.075
rp					0.327✶	0.248	0.129	0.338✶	0.165	-0.071	-0.104
SPL rg						0.202	0.171	0.247	-0.251	-0.237	-0.367
rg						0.483✶✶	-0.035	0.353✶	0.035	-0.220	-0.306✶
KN rg							0.278	-0.924✶	0.693	0.792	0.665
rg							-0.125	0.329✶	0.446✶✶	0.243	0.184
TI rg								0.679	0.715	0.142	-0.170
rg								-0.007	-0.025	-0.013	-0.031
BY rg									-0.739	-0.807	-0.917✶
rp									0.520✶✶	-0.243	-0.170
GY rg										0.687✶✶	0.550✶✶ 0.499✶✶ 0.847
rp											0.847
HI rg											
rp											

Phenotypically, combined over the two locations, days to heading had positive and significant correlation with days to maturity, grain filling period, number of spikelet/spike and biological yield. Days to maturity had significant and positive correlation with days to heading, grain filling period, number of spikelet/spike and biological yield but it had negative and significant correlation coefficient with harvest index, hectoliter weight and thousand kernel weight. Plant height had positive and significant correlation with number of spikelet/spike, number kernel/spike and biological yield. It had non significant correlation with the rest of the characters. Spike length had positive and significant correlation with number of spikelet/spike and biological yield. It had non significant correlation with the rest of characters.

Number of spikelet/spike had positive and significant correlation with days to heading, days to maturity, plant height, spike length, number of kernel/spike and biological yield. This character had negative significant correlation with hectoliter weight and thousand kernel weight. Number of kernel per spike had positive and significant correlation with plant height, number of spikelet/spike and biological yield. It had non significant correlation with the rest of the characters.

The correlation of biological yield with days to maturity, grain filling period, plant height, spike length, number of spikelet/spike and number of kernels/spike was positive and significant. Harvest index had negative and significant correlation with days to heading, days to maturity and grain filling period. This character had positive and significant correlation with hectoliter weight and thousand kernel weight. Hectoliter weight had negative and significant association with days to heading, days to maturity, grain filling period and number of spikelet/spike. It had positive and significant correlation with harvest index and thousand kernel weight. Thousand kernel weight had negative and significant correlation with days to heading, days to maturity, grain filling period and number of spikelet/spike. This character had positive and significant correlation with harvest index and hectoliter weight.

4.2.2.2. Genotypic correlation

At Chencha, days to heading showed positive and significant correlation only with days to maturity. It had non significant correlation with the rest of the characters. Days to maturity had negative and significant correlation with harvest index and hectoliter weight but it had positive and significant correlation with days to heading. Grain filling period had negative and significant correlation with number of kernel per spike and biological yield. Grain filling period, spike length, number of kernel and spikelet/spike had negative and significant correlation with biological yield. Number of tillers per plant had positive and significant correlation with biological yield and hectoliter weight.

At Angacha, all characters showed non significant genotypic correlation except days to heading and grain filling period. Days to heading showed positive and significant correlation with days to maturity. Grain filling period on its part showed negative and significant correlation with number of kernels/spike. Genotypically, after pooled analysis, days to heading showed positive and significant correlation with days to maturity but it had negative and significant correlation with hectoliter weight, harvest index and thousand kernel weight. Days to heading had non significant correlation with the rest of the characters. Days to maturity had positive and significant correlation with days to heading and grain filling period, but it had negative and significant correlation with harvest index, hectoliter weight and thousand kernel weight. Grain filling period had negative and significant correlation with number of tillers, harvest index, hectoliter weight and thousand kernel weight but it had positive and significant correlation with days to maturity. Number of kernel per spike had negative and significant correlation with biological yield. Harvest index had negative and significant correlation with days to heading, days to maturity and grain filling period. It had positive and significant correlation with hectoliter weight and thousand kernel weight.

Hectoliter weight had negative and significant correlation with days to heading, days to maturity but it had grain filling period and positive and significant correlation with harvest index and thousand kernel weight. Hectoliter weight had non significant correlation with the rest of the characters. Thousand kernel weight had positive and significant correlation with harvest index and hectoliter weight. This character had negative and significant correlation with days to heading, days to maturity and grain filling period.

4.2.3. Path coefficient analysis

As correlation does not allow the partitioning of both genotypic and phenotypic correlation coefficients into direct and indirect effect, they are further analyzed by path coefficient analysis. In accordance with the work of Dewy and Lu (1959), in the present study, only six out of the 13 characters that are believed to have direct relationship with grain yield were included in path analysis and both genotypic and phenotypic correlations were partitioned into direct and indirect effects using grain yield as a dependant variable. .The phenotypic and genotypic direct and indirect effect of different characters on grain yield for Chencha, Angacha and combined over the two locations are presented in Tables 12 – 17.

4.2.3.1. Phenotypic- path coefficient

At Chencha, biological yield had positive and significant phenotypic correlation coefficient ($r= 0.650^{**}$) with grain yield and it had the highest direct effect (0.602). The magnitude of the direct effect was equivalent to that of the phenotypic correlation coefficient. This justifies that the correlation explains the true relationship and direct selection through this trait will be effective Dewy and Lu (1959).

Table 12: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level of six traits on grain yield of 15 barley genotypes tested at Chencha (2014/15)

Traits	DH	PH	KN	TI	BY	TKW	r_p
DH	**-0.269**	-0.001	0.011	-0.003	-0.034	-0.081	-0.377✶
PH	-0.012	**-0.011**	-0.005	0.014	0.218	0.028	0.232
KN	-0.045	0.001	**0.065**	0.016	0.055	-0.069	0.023
TI	-0.014	0.002	-0.016	**-0.065**	-0.022	-0.001	0.115
BY	0.015	-0.004	0.006	0.002	**0.602**	0.029	0.650✶✶
TKW	0.115	-0.002	-0.024	0.000	0.092	**0.189**	0.371✶

Residual = 0.2311

DH=Days to heading, PH= Plant height, KN= Kernel number per spike, TI= Tiller number per plant, BY= Biological yield, TKW= Thousand kernel weight

Days to heading had negative direct effect. The phenotypic correlation it had with grain yield was negative and significant. The indirect effects via other traits were negligible. Hence, the phenotypic correlation days to heading had with grain yield was largely due to its direct effect. Number of tillers had negative phenotypic correlation coefficient with grain yield. The indirect effects through other traits were negligible. Hence, phenotypic correlation it had with grain yield was as a result of its indirect effect. Number of kernel and thousand kernel weight had positive direct effect. The phenotypic correlations they had with the grain yield were positive. Their indirect effect via other characters was mostly positive and negligible; therefore, their positive correlation coefficient with grain yield was mainly due to direct effect. The phenotypic residual value (0.2311) at Chencha shows that the characters in the path coefficient analysis accounted for 76.89% of the variation in grain yield.

Table 13: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level of six traits on grain yield of 15 barley genotypes tested at Angacha (2014/15)

Traits	DH	PH	KN	TI	BY	TKW	r_p
DH	**-0.201**	0.081	0.094	0.001	0.282	-0.115	0.142
PH	-0.106	**0.153**	0.129	0.000	0.434	-0.069	0.542✶✶
KN	-0.086	0.090	**0.218**	-0.001	0.329	-0.048	0.502✶✶
TI	-0.008	0.004	-0.014	**0.017**	0.058	-0.042	0.015
BY	-0.082	0.096	0.104	0.001	**0.689**	-0.039	0.770✶✶
TKW	0.101	-0.046	-0.046	-0.003	-0.117	**0.229**	0.117

Residual = 0.2787, DH=Days to heading, PH= Plant height, KN= Kernel number per spike, TI= Tiller number per plant, BY= Biological yield, TKW= Thousand kernel weight

At Angacha, like that of Chencha, biological yield had the highest positive phenotypic direct effect (0.689) and it had positive and significant phenotypic correlation with grain yield (0.770✶✶).The existence of low and positive indirect effect of biological yield with most of the other characters ascertains that the correlation of this trait with grain yield was found to be mainly because of the direct effect. Days to heading showed negative direct effect and the correlation coefficient it had with grain yield was positive and the indirect effect via other characters were mostly positive. Therefore, the correlation of days to heading with grain yield was because of indirect effect. Thousand kernel weight had positive direct effect. The phenotypic correlation of thousand kernel weight with grain yield was also positive. The indirect effects were mostly negative and negligible. Therefore, the correlation they had with grain yield was largely due to the direct effect. The phenotypic residual value (0.2787) in this phenotypic path coefficient analysis for grain yield indicates that the characters under study accounted for 72.13% of the variability in grain yield. By comparing the two locations residual value (0.2311) for Chencha and (0.2787) for Angacha, grain yield was better expressed at Chencha than Angacha by the characters in the path analysis. Generally, characters that showed positive direct effect as well as positive and significant correlation coefficient with grain yield were known to affect grain yield to the favorable direction and needs much attention during the process of selection cases in point are biological yield and thousand kernel weight.

Table 14: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level of six traits on grain yield of 15 barley genotypes tested at combined over two locations Chencha and Angacha (2014/15)

Traits	DH	PH	KN	TI	BY	TKW	r_p
DH	**-0.328**	0.020	0.009	0.000	0.161	-0.260	-0.397✶✶
PH	-0.046	**0.144**	0.097	-0.002	0.290	0.004	0.487✶✶
KN	-0.014	0.066	**0.212**	-0.003	0.178	0.008	0.466✶✶
TI	-0.001	-0.009	-0.027	**0.027**	-0.004	-0.012	-0.025
BY	-0.098	0.077	0.070	0.000	**0.539**	-0.068	0.520✶✶
TKW	0.237	0.002	0.005	-0.001	-0.102	**0.359**	0.499✶✶

Residual = 0.2464, DH=Days to heading, PH= Plant height, KN= Kernel number per spike, TI= Tiller number per plant, BY= Biological yield, TKW= Thousand kernel weight

Combined over the two locations, biological yield had positive and significant correlation coefficient and it showed the highest positive direct effect (0.539). The correlation coefficient of this character with grain yield was (0.520**) which is equivalent to its direct effect. This shows the correlation explains the true relationship and the direct selection through this trait will be effective. Plant height, number of kernel and thousand kernel weight had positive and significant correlation with grain yield and they showed positive direct effect. The respective indirect effects of these characters were either negligible or negative. Hence, the correlation coefficient they had grain yield was largely due to their direct effect. Their indirect effects through other traits were mostly positive and negligible. Hence, the correlation they had with grain yield was largely due to direct effect. The correlation coefficient of days to heading with grain yield was negative and significant. Its indirect effects through other traits were mostly positive and negligible. Hence, the correlation of days to heading with grain yield was largely due to direct effect. The phenotypic residual value (0.2464) in this phenotypic path coefficient analysis for grain yield in combined over the two locations indicates that the characters under study accounted for 75.36% of the variability in grain yield.

4.2.3.2. Genotypic path-coefficient

Table 15: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of six traits on grain yield of 15 barley genotypes tested at Chencha (2014/15)

Traits	DH	PH	KN	TI	BY	TKW	r_g
DH	**-0.617**	0.041	-0.292	-0.048	-0.118	0.028	-1.006✶✶
PH	0.016	**-1.580**	0.401	0.812	0.537	-0.012	0.175
KN	-0.212	0.746	**-0.850**	0.263	-1.291	0.054	-1.290✶✶
TI	-0.015	0.660	0.115	**-1.944**	0.186	-0.008	-1.006✶✶
BY	0.219	-2.570	3.321	-1.097	**0.330**	-0.020	0.184
TKW	0.315	-0.346	0.834	-0.292	0.122	**-0.055**	0.577

Residual = 0.2570, DH=Days to heading, PH= Plant height, KN= Kernel number per spike, TI= Tiller number per plant, BY= Biological yield, TKW= Thousand kernel weight

At Chencha, genotypic path analysis showed positive direct effect for biological yield and the direct effects of the rest of characters were negative. The correlation coefficients of plant height, thousand kernel weight and biological yield were positive but their direct effects were negative. Hence, the correlation they had with grain yield was largely due to the indirect effect. The negative direct effect of plant height at Chencha was in harmony with the results of Pathak (2008). The negative direct effect of thousand kernel weight at Chencha contradicts with the findings of Mogghhadam *et al*., (2009) and Blanco *et al*., (2010). Number of kernel, number of tillers and days to heading had negative direct effect and the genotypic correlation coefficient they had with grain yield been significant and negative. The indirect effects they had with other characters were mostly positive. The negative direct effect of the number of tillers per plant was in agreement with the finding of Getachew *et al*., (2007) in Ethiopian barley landraces. Plant height had positive genotypic correlation coefficient but it showed negative direct effect. The genotypic residual value (0.2570) in Chencha indicates that the characters under study accounted for 74.30% of the variability with grain yield.

Table 16: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of six traits on grain yield of 15 barley genotypes tested at Angacha (2014/15)

Traits	DH	PH	KN	TI	BY	TKW	r_g
DH	**-1.188**	0.449	0.593	- 0.008	0.223	-0.134	-0.064
PH	-0.704	**0.758**	0.376	-0.070	0.281	-0.045	0.597
KN	-0.639	0.258	**1.103**	-0.025	0.169	-0.010	0.858
TI	-0.040	0.215	0.111	**-0.246**	0.473	0.067	0.581
BY	-0.700	0.564	0.493	-0.307	**0.378**	-0.101	0.327
TKW	0.947	-0.202	-0.063	-0.098	-0.228	**0.168**	0.524

Residual = 0.2445, DH=Days to heading, PH= Plant height, KN= Kernel number per spike, TI= Tiller number per plant, BY= Biological yield, TKW= Thousand kernel weight

At Angacha, days to heading had negative direct effect and the genotypic correlation coefficient it had with grain yield been also negative (Table 16). The direct effects via other traits were mainly positive and hence the correlation it had with grain yield was largely because of the direct effect. Plant height had positive direct effect and positive correlation effect. Its indirect effects through other traits were mostly negative. Therefore, the genotypic correlation coefficient it had with grain yield was mainly because of the direct effects. Number of kernel had positive genotypic correlation coefficient and showed the highest positive direct effect. The indirect effect through other characters was negligible or negative and hence the correlation it had with grain yield was largely due to the direct effect. Biological yield had a positive direct effect (0.378) which was equivalent to the genotypic correlation coefficient (0.327) it had with grain yield. Number of tillers had negative direct effect but the correlation coefficient it had with grain yield was positive and hence in this case the indirect effects are the cases of the correlation. Generally, the path analysis for grain yield showed the characters included in the path analysis expressed the variability as good at Chencha as at Angacha since the residual value at Chencha (0.2570) was not that much different as that of Angacha (0.2445).

Table 17: Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of six traits on grain yield of 15 barley genotypes tested at combined over two locations Chencha and Angacha (2014/15)

Traits	DH	PH	KN	TI	BY	TKW	r_g
DH	**5.489**	0.406	0.568	0.055	1.202	-8.719	-0.998✶
PH	-0.702	**-3.176**	- 0.194	1.901	0.644	1.949	0.423
KN	-3.373	-0.666	**-0.925**	1.530	-1.937	6.063	0.693
TI	0.446	-8.990	-2.106	**0.672**	5.613	5.081	0.715
BY	3.150	-0.977	0.855	1.799	**2.095**	-7.661	-0.739
TKW	-5.333	-0.690	-0.625	0.380	-1.789	**8.973**	0.917✶

Residual = 0.3001, DH=Days to heading, PH= Plant height, KN= Kernel number per spike, TI= Tiller number per plant, BY= Biological yield, TKW= Thousand kernel weight

Genotypic path coefficient analysis of combined over the two locations showed that thousand kernel weight had the highest direct effect (8.973). It had positive and significant correlation coefficient with grain yield. The indirect effects through other traits were mostly negative. Hence, the genotypic correlation coefficient it had with grain yield was largely due to the direct effect. Plant height and number of kernel had negative direct effect but they had positive correlation coefficient. Hence, the positive correlation coefficient was largely due to their respective indirect effects. This implies restricted simultaneous selection has to be followed; restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect of these traits. The direct effect of number of tillers was positive. The genotypic correlation coefficient it had with grain yield was also positive. Hence, the correlation it had with grain yield was largely due to the direct effect. Combined over the two locations, the path coefficient analysis showed that the residual value (0.3001) which means the characters in path analysis expressed the variability in grain yield by 69.99%.

5. SUMMARY AND CONCLUSIONS

The present study comprises 15 barley genotypes that were evaluated at two locations, namely, Chencha and Angacha with the objectives of assessing the genetic variability and association among agronomic characters for 13 traits. The analysis of variance for each location showed the genotypes were significantly different at for all characters except grain filling period, number of tillers/plant, biological yield and grain yield at each of the locations.

The combined analysis of variance across the two locations showed that genotypes showed significant variation for most of the characters except number of kernel/spike, number of tiller/plant, biological yield, grain yield and harvest index. Phenotypic (PCV) and genotypic (GCV) coefficient of variation were generally low in both of the locations. A relatively higher PCV was observed at Angacha than Chencha. PCV were slightly higher than their corresponding GCV at both locations. A relatively high PCV were recorded for spike length, number of kernel/spike, number of tiller/plant, biological yield, grain yield and harvest index in both locations. The lowest PCV values were observed for days to heading, days to maturity, grain filling period and thousand kernel weight which suggests the limitation of selection for these traits. GCV values were generally low at both locations.

The highest heritability value at both locations was for days to heading. Characters such as days to maturity, plant height, number of spikelet/spike, number of kernel/spike, harvest index and thousand kernel weight were found to have moderately high to medium heritability at both Angacha and Chencha. The lowest heritability value goes for grain filling period. The expected genetic advance as a percent of mean ranged from 0.45% for hectoliter weight to 16.65% for number of kernel/spike at Chencha. The same parameter was ranging from 1.03% for grain filling period to 11.56% for harvest index. Characters with relatively higher genetic advance as a percent of mean allow the improvement of this character through true selection.

At Chencha, grain yield was positively and significantly correlated with harvest index both at phenotypic and genotypic levels. Correlation with biological yield, hectoliter weight and thousand kernel weight were also positive and significant at phenotypic level. Combined over the two locations, grain yield had positive and significant correlation with plant height, biological yield and hectoliter weight phenotypically but it showed positive and significant correlation with harvest index and thousand kernel weight at both phenotypic and genotypic levels. Selecting for harvest index and thousand kernel weight shows positive and significant correlation coefficient for grain yield and there is a possibility to increase grain yield of barley.

Path coefficient analysis based on grain yield as dependent variable shows that biological yield had the highest positive direct effect at phenotypic level at individual locations and even combined over the two locations. The correlation coefficient was also positive and significant at individual locations and when the two are combined. Genotypically, biological yield showed positive direct effect both at Chencha and Angacha and combined over the two locations. Number of kernel also showed positive direct effect at phenotypic level at Chencha and Angacha. Since biological yield and number of kernel had positive correlation with grain yield in process of selection much attention should be given to them as these characters are helpful for indirect selection.

The following conclusions can be made from this study:

There were differences in the performance of the genotypes as there were statistically significant differences among genotypes for most of the 13 characters at both locations. Nevertheless, the level of genetic differences for many traits including grain yield may not be sufficient to expect progress in selection. Biological yield showed positive and significant correlation and positive direct effect at individual locations and combined over the two locations, it will be a useful trait for indirect selection to increase grain yield. Number of kernel/spike as it showed a medium to high heritability, relatively better genetic advance as percent of mean and positive correlation coefficient and direct effect on grain yield, this character may be included as a component of indirect selection.

The recommendations of the study include:

The data generated in one season can be used as a baseline though it may not be comprehensive enough as those data found over many seasons and locations. Hence, it is recommended that other genetic variability and agronomic character experiments need to be conducted in more locations and seasons under both controlled and uncontrolled management conditions. Moreover, gain in relation with some barley physiological parameters and other quality factors should be studied. Since it is one season experiment, the research needs to be conducted for additional two or more years across wide range of environments and planting dates to arrive at concrete recommendations for maximization of barley yields. It is further recommended that future experiments should also include other promising barley varieties in the country. Finally, molecular marker assisted selection in combination with field evaluation of barley traits based on conventional breeding under different environmental conditions could be commendably recommended.

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7. APPENDICES

Appendix Table 1: Average Temperature and Rainfall of Angacha Woreda (2010-2014)

Months	J	F	M	A	M	J	J	A	S	O	N	D
Temperature(^{o}c)	16	15	17	17	16	14	15	15	15	17	17	16
Rainfall (mm)	29	39	94	129	146	130	165	174	158	77	16	23

Source: National Meteorology Agency, South Zone, Hawassa, February 2015

Appendix Table 2: Average Temperature and Rainfall of Chencha Woreda (2010-2014)

Months	J	F	M	A	M	J	J	A	S	O	N	D
Temperature(^{o}c)	14	15	16	15	15	13	14	15	14	17	18	16
Rainfall (mm)	31	40	95	130	150	132	170	175	160	77	17	25

Source: National Meteorology Agency, South Zone, Hawassa, February 2015

Appendix Table 3: Mean values of the 13 traits of 15 barley genotypes grown at Chencha (2014/15)

Variety	DH	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI	HW	TKW
HB-1307	63	111.5	48.5	101.0	8.5	14.0	49.5	2.5	3.30	6341	38.43	77.9	39.85
Cross 41/98	56	109.0	53.0	103.0	9.5	12.0	54.5	2.0	2.90	6328	43.64	81.00	46.90
EH-1493	55	109.0	54.0	105.0	10.0	13.0	70.5	3.0	3.50	6950	39.71	82.15	45.50
Misrach	55	108.5	53.5	110.0	9.5	13.0	49.0	5.0	3.45	7039	40.81	81.35	46.30
Shege	63	114.5	51.0	105.0	9.5	12.0	43.5	3.0	3.15	5745	36.48	80.55	38.80
Ardu-12-60B	57	111.0	54.0	115.0	9.0	14.0	58.5	4.5	2.90	6242	43.05	80.10	41.20
HB-42	56	113.0	57.0	109.5	10.5	12.0	45.0	3.0	3.20	6126	38.29	80.30	46.30
Ahor 880/61	55	111.5	50.5	110.5	10.0	12.0	46.5	3.0	3.45	7146	41.43	79.80	43.95
Balami	62	112.5	50.5	105.5	11.0	14.0	60.0	3.0	2.90	4679	32.27	78.65	38.15
Bekoji-I	57	113.0	56.0	102.5	9.0	13.0	59.5	3.5	2.90	6033	41.61	77.65	41.50

Holker	61	113.0	52.0	110.5	8.5	13.0	54.5	2.0	3.50	6692	38.24	79.70	39.90
IBON 174/03	56	108.5	52.5	99.0	9.0	13.0	63.5	3.5	3.00	6415	42.77	79.30	41.90
EH-1847	57	111.0	54.0	111.0	9.0	12.0	55.0	4.0	3.50	5107	34.90	80.15	43.10
HB-1533	61	115.5	54.5	110.0	9.0	15.0	58.5	2.5	3.15	6058	38.46	78.30	43.75
Miscal-21	57	112.5	55.3	112.0	8.5	13.0	51.5	3.0	3.60	6603	36.68	78.45	45.55

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Appendix Table 4: Mean values of the 13 traits of 15 barley genotypes grown at Angacha (2014/15)

Variety	DH	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI	HW
HB-1307	69	126.5	57.5	100.0	9.5	14.0	55.5	3.5	3.30	5528	33.50	72.05
Cross 41/98	63	121.0	58.0	95.0	9.0	13.0	46.0	4.0	3.40	4689	27.58	73.50
EH-1493	61	119.0	58.0	100.0	8.5	12.0	52.0	3.5	3.20	4977	31.11	78.75
Misrach	64	117.5	53.5	97.5	8.0	12.0	39.0	4.5	2.70	3900	28.89	75.45
Shege	70	128.5	58.5	110.0	10	13.5	51.5	3.5	3.55	5735	32.31	74.35
Ardu-12-60B	67	124.5	57.5	123.0	9.0	14.5	50.5	4.0	3.85	5454	28.33	70.55
HB-42	61	123.5	62.5	102.5	9.5	12.0	42.0	3.5	3.80	5020	26.42	77.20
Ahor 880/61	63	124.5	61.5	120.0	10	13.5	57.0	4.5	4.40	6871	31.23	72.75
Balami	67	126.0	59.0	112.5	11.1	14.0	60.5	4.0	3.55	5251	29.58	72.85
Bekoji-I	68	126.5	58.5	97.5	8.5	13.5	54.5	3.0	3.30	4987	30.22	74.60
Holker	68	120.5	52.5	102.5	10.0	14.5	60.3	3.5	3.05	4242	27.82	71.40
IBON 174/03	63	118.5	55.5	105.0	9.5	14.0	46.0	3.5	3.15	4594	29.17	72.05
EH-1847	62	120.0	58.0	85.0	9.0	13.0	49.0	4.0	2.65	4648	35.08	74.05
HB-1533	66	121.5	55.5	87.5	9.0	13.0	55.0	4.0	2.95	4382	29.71	72.55
Miscal-21	66	122.0	56.5	120.0	9.5	14.0	60.0	4.1	3.70	6128	33.12	74.20

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per sp

Appendix Table 5: Mean values of the 13 traits of 15 barley genotypes combined over the two locations (2014/15

Variety	DH	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI	HW	TKW
HB-1307	66	119.0	53.0	100.5	9.0	14.0	52.5	3.0	3.30	5935	35.97	74.98	36.60
Cross 41/98	60	115.0	55.5	99.0	9.3	12.5	50.3	3.0	3.15	5509	35.61	77.25	39.53
EH-1493	58	114.0	56.0	102.5	9.3	12.5	61.3	6.3	3.35	5964	35.41	80.45	39.68
Misrach	60	113.0	53.5	103.8	8.8	12.5	44.0	4.8	3.08	5470	34.85	78.40	4o.43
Shege	67	121.3	54.8	107.5	9.8	12.8	47.5	3.3	3.35	5740	34.40	77.45	35.30
Ardu-12-60B	62	117.8	55.8	119.0	9.0	14.3	54.5	4.3	3.38	5848	35.69	75.33	36.60
HB-42	59	118.3	59.8	106.0	10.0	12.0	43.5	3.3	3.50	5573	32.36	78.75	40.65
Ahor 880/61	59	118.0	59.0	115.3	10.0	12.8	51.8	3.8	3.93	7009	36.33	76.28	38.15

Balami	65	119.3	54.8	109.5	11.1	14.0	60.3	3.5	3.23	4965	30.93	75.75	35.25
Bekoji-I	63	119.8	57.3	100.0	8.8	13.3	57.0	3.0	3.10	5510	35.92	76.13	38.48
Holker	65	116.8	52.3	106.5	9.3	13.8	57.4	2.8	3.28	5467	33.03	75.55	36.08
IBON 174/03	60	113.5	54.0	102.0	9.3	13.5	54.8	3.8	3.08	5505	35.97	75.68	37.48
EH-1847	60	115.5	56.0	98.0	9.0	12.5	52.0	4.0	3.08	5378	34.99	77.10	40.45
HB-1533	64	118.5	55.0	98.8	9.0	14.0	56.8	3.3	3.05	5220	34.09	75.43	38.23
Miscal-21	61	117.2	55.9	116.0	9.0	13.5	55.8	3.6	3.65	6366	34.90	76.33	41.25

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Appendix Table 6: Minimum values of the 13 traits of 15 barley genotypes grown in Chencha (2014/15)

Varieties	DH	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI
HB-1307	58	105	45	95	6.5	12	45	2.0	2.5	6250	35
Cross 41/98	53	104	47	97	7.0	10	50	2.0	2.2	6200	40
EH-1493	52	104	50	95	7.0	10	65	2.0	2.5	6500	35
Misrach	50	105	50	90	8.0	10	45	3.0	2.5	6700	35
Shege	55	110	47	95	7.0	11	40	2.0	2.5	5500	35
Ardu-12-60B	54	105	50	110	8.0	10	55	3.0	2.0	6000	40
HB-42	50	108	50	105	8.0	10	41	2.0	2.4	5900	35
Ahor 880/61	49	105	50	105	7.0	11	43	2.0	2.5	6512	37
Balami	55	105	45	100	8.0	10	57	2.0	2.1	4500	30
Bekoji-I	50	110	50	98	7.0	10	55	2.1	2.0	5500	37
Holker	55	108	47	105	6.0	9	50	1.2	2.1	6500	35
IBON 174/03	50	100	47	87	7.0	10	58	2.0	2.2	6351	38
EH-1847	52	107	50	107	7.0	9	52	2.1	2.0	5800	33
HB-1533	53	108	51	108	7.0	12	55	2.0	2.0	5810	35
Miscal-21	52	105	51	108	7.0	9	46	2.1	2.1	6250	35

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Appendix Table 7: Minimum values of the 13 traits of 15 barley genotypes grown in Angacha (2014/15)

Varieties	DH	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI
HB-1307	60	115	50	87	7	11	50	2.0	3.1	5850	33
Cross 41/98	55	111	52	95	8	11	47	2.1	2.5	5450	32
EH-1493	56	110	54	100	8	10	58	5.7	3.0	5761	30
Misrach	56	108	50	100	7	10	42	3.0	2.1	5450	31
Shege	62	115	50	105	7	10	45	2.1	2.5	5700	30
Ardu-12-60B	60	114	53	115	6	11	50	2.1	3.0	5840	31
HB-42	55	115	55	102	8	10	40	2.5	2.7	5500	30
Ahor 880/61	54	116	54	110	7	11	49	3.1	3.0	6950	32
Balami	60	115	51	103	9	12	56	2.1	2.5	4960	28
Bekoji-I	59	116	55	95	7	11	55	2.5	2.8	5450	30
Holker	60	112	49	103	8	11	54	2.4	2.8	5450	30
IBON 174/03	55	110	51	100	8	11	52	2.5	2.5	5480	30
EH-1847	54	110	53	95	7	10	48	3.0	2.4	5370	32
HB-1533	60	115	52	97	8	12	55	2.0	2.0	5200	31
Miscal-21	59	116	54	113	8	10	53	2.0	2.1	6350	30

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Appendix Table 8: Minimum values of the 13 traits of 15 barley genotypes combined over the two locations (2014/15)

Varieties	DH	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI
HB-1307	59	110.0	47.5	91	6.8	11.5	47.5	2.0	2.8	6050	34.0
Cross 41/98	54	107.5	74.5	96	7.3	10.5	48.5	2.1	2.4	5825	36.0
EH-1493	54	57.0	52.0	97.5	7.5	10.0	61.5	3.9	2.8	6131	32.5
Misrach	53	106.5	50.0	95.0	7.5	10.0	43.5	3.0	2.3	6075	33.0
Shege	58.5	112.5	48.5	100	7.0	10.5	42.5	2.1	2.5	5600	32.5
Ardu-12-60B	57	109.5	50.0	112.5	7.0	10.5	52.5	2.1	2.5	5920	35.5
HB-42	52.5	111.5	48.5	103.5	8.0	10.0	40.5	2.3	2.6	5700	32.5
Ahor 880/61	51.5	110.5	51.5	107.5	7.0	11.0	46.0	2.6	2.8	6731	34.5
Balami	57.5	110.0	52.5	101.5	8.5	11.0	56.5	2.1	2.3	4730	29.0
Bekoji-I	54.5	113.0	52.0	96.5	7.0	10.5	55.0	2.3	2.5	5475	33.5
Holker	57.5	110.0	48.0	104	7.0	10.0	52.0	2.3	1.5	5975	32.5
IBON 174/03	52.5	105.0	48.0	93.5	7.5	10.5	55.0	2.3	2.4	5916	31.5
EH-1847	53	108.5	49.0	101	7.0	9.5	50.0	2.6	2.2	5585	32.5
HB-1533	56	111.5	51.5	102.5	7.5	12.0	55.0	2.0	2.3	5505	33.0
Miscal-21	55.5	110.5	52.5	110.5	7.5	9.5	49.5	2.1	2.4	6300	32.5

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Appendix Table 9: Maximum values of the 13 traits of 15 barley genotypes grown in Chencha (2014/15)

Varieties	DH	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI
HB-1307	68	120	52	105	9	15	52	3.0	4.0	6420	40
Cross 41/98	60	120	56	106	10	14	56	5.0	3.5	6350	45
EH-1493	59	112	57	110	11	15	72	5.0	4.0	7200	41
Misrach	60	110	55	115	10	15	51	6.0	4.0	7200	45
Shege	65	119	53	110	12	14	45	3.5	3.5	5850	40
Ardu-12-60B	60	113	56	120	11	15	60	5.0	3.3	6300	45
HB-42	59	115	58	112	12	14	48	3.5	3.8	6200	41
Ahor 880/61	61	115	60	115	11	13	50	3.8	4.0	7210	43
Balami	65	114	57	110	13	15	63	3.6	3.3	4800	35
Bekoji-I	60	119	60	110	10	14	65	4.2	3.2	6200	44
Holker	63	116	54	115	10	14	60	2.4	3.7	6800	40
IBON 174/03	60	120	55	112	11	15	65	4.0	3.5	6500	45
EH-1847	59	115	56	115	12	14	60	4.3	3.7	6200	40
HB-1533	63	118	56	113	10	17	61	3.0	3.8	6100	40
Miscal-21	60	115	60	115	11	15	54	3.5	4.0	6700	41

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Appendix Table 10: Maximum values of the 13 traits of 15 barley genotypes grown in Angacha (2014/15)

Varieties	DH	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI
HB-1307	70	121	55	103	10	16	55	3.5	4.8	6100	38
Cross 41/98	63	117	58	112	10	15	52	3.3	3.3	5600	39
EH-1493	62	117	60	105	11	14	63	6.5	3.7	6000	38
Misrach	63	115	56	106	9	15	48	5.0	3.5	5700	36
Shege	69	125	56	110	10	14	51	3.5	3.6	5800	38
Ardu-12-60B	65	120	60	124	11	16	60	4.5	4.0	5920	39
HB-42	61	122	61	110	12	13	46	4.0	4.1	5610	35
Ahor 880/61	62	121	62	118	12	14	53	4.0	4.0	7100	39
Balami	68	122	57	112	14	15	63	4.1	3.5	5100	33
Bekoji-I	64	121	61	105	10	15	60	4.0	3.5	5500	38
Holker	67	120	54	110	11	14	61	3.0	3.6	5500	35
IBON 174/03	61	115	57	107	12	15	57	4.1	4.0	5600	40
EH-1847	63	119	58	100	11	14	54	4.5	3.2	5400	37
HB-1533	65	121	59	103	11	15	61	4.2	4.2	5350	38
Miscal-21	63	122	60	120	12	15	58	4.0	3.9	6380	37

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike

Appendix Table 11: Maximum values of the 13 traits of 15 barley genotypes combined over the two locations (2014/15)

Varieties	DH	DM	GFP	PH	SLN	SPL	KN	TI	BY	GY	HI
HB-1307	69	120.5	53.5	104.5	9.5	15.5	53.5	3.3	4.4	6260	39.0
Cross 41/98	61.5	118.5	57.0	109.0	10.0	14.5	54.0	4.2	3.4	5975	42.0
EH-1493	60.5	59.5	58.5	107.5	14.5	14.5	67.5	5.8	3.9	6600	39.5
Misrach	61.5	112.5	55.5	110.5	9.5	15.0	49.5	5.5	3.8	6450	40.5
Shege	67.0	112.0	54.5	110.0	11.0	14.0	48.0	3.5	3.6	5825	39.0
Ardu-12-60B	62.5	116.5	58.0	122.0	13.0	15.5	60.0	3.9	3.7	6110	42.0
HB-42	60.0	118.5	59.5	111.0	12.0	13.5	47.0	3.8	4.0	5905	38.0
Ahor 880/61	61.5	118.0	61.0	116.5	11.5	13.5	51.5	3.9	4.0	5950	41.0
Balami	66.5	118.0	57.0	111.0	13.5	15.0	63.0	3.9	3.4	4950	34.0
Bekoji-I	62.0	120.0	60.5	107.5	10.0	14.5	62.5	4.1	3.9	5850	41.0
Holker	65.0	118.0	54.0	112.5	10.5	14.0	60.5	2.7	3.7	6150	37.5
IBON 174/03	60.5	117.5	56.0	109.5	11.5	15.0	61.0	4.1	3.8	6050	40.0
EH-1847	61.0	117.0	57.0	109.0	11.5	14.0	57.0	4.4	3.5	5800	38.5
HB-1533	64.0	119.5	57.5	108.0	10.5	16.0	61.0	3.6	3.9	5725	39.0
Miscal-21	61.5	118.5	60.0	117.5	11.5	13.0	56.0	4.0	4.0	6540	39.0

DH=Days to heading, DM= Days to maturity, GFP= Grain filling period, BY= Biological yield, GY =Grain yield, HI=Harvest index, TKW= Thousand kernel weight, HW= Hectoliter weight, TI= Tiller number per plant, PH= Plant height, SLN= Spike length, SPL= Spikelet number per spike, KN= Kernel number per spike