

## Genetic Variability, Heritability and Genetic Advance for Yield and Yield Related Traits in Barley (*Hordeum vulgare* L.) Germplasm

<sup>1</sup>Azeb Hailu, <sup>2</sup>Sentayehu Alamerew, <sup>3</sup>Mandefro Nigussie, <sup>4</sup>Ermias Assefa and <sup>5</sup>Abdul Kabir Khan Achakzai

<sup>1</sup>Tigray Agricultural Research Institute, Mekelle Agricultural Research Center, Mekelle, Ethiopia

<sup>2</sup>Colleges of Agriculture and Veterinary Medicine, Jimma University, Ethiopia

<sup>3</sup>Oxfam America, Horn of Africa Regional Office

<sup>4</sup>Southern Agricultural Research Institute, Bonga Agricultural Research Center,  
P.O. Box: 101, Bonga, Ethiopia

<sup>5</sup>Department of Botany, University of Balochistan, Quetta, Pakistan

**Abstract:** Sixty four barley genotypes were tested in 8x8 simple lattice design at Atsbi, Ofla and Quiha environments in Tigray region, in 2009/10. The overall objective was to study the extent of genetic variability, heritability and genetic advance among the said genotypes. Analysis of variance (ANOVA) study revealed that there was a significant difference ( $p < 0.001$ ) among the genotypes for all the characters studied except for 1000-kernel weight at Quiha which was significant ( $p < 0.05$ ) and plant height was non-significant at Atsbi and Ofla. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for number of productive tillers/m<sup>2</sup> and number of kernels/spike across locations. High GCV along with high heritability and genetic advance was obtained from number of productive tillers/m<sup>2</sup> and number of kernels/spike across locations.

**Key words:** PCV · GCV · Heritability in the broad sense · Genetic advance

### INTRODUCTION

Barley (*Hordeum vulgare* L.) belongs to the family Poaceae, tribe Triticeae and genus *Hordeum*. The genus *Hordeum* consists of 32 species and 45 taxa including diploid ( $2n = 2x = 14$ ), tetraploid ( $2n = 4x = 28$ ) and hexaploid ( $2n = 6x = 42$ ) cytotypes with a basic chromosome number  $x = 7$  [1]. Globally, barley ranks fourth among cereal crops after wheat, maize and rice and is among the top ten crop plants in the world [2]. In the year 2008/09, the area planted to barley was estimated at about 55.27 million hectare (ha) with global production of around 153.96 Million Metric Tons [3].

Barley is a main food crop in the highlands and marginal areas where other cereals cannot grow, as well as animal feed and forage around the world. It is an important industrial crop providing raw material for malt, which is used for beer and whisky production. Barley grain contains 3 to 7%  $\beta$ -glucan, an important dietary fiber [4, 5, 6] that has significant blood cholesterol lowering

effects [7]. Barley plays an important role in ensuring food security, as it requires relatively low input. Its yield stability is far better than other cereals, making it a dependable source of food in bad seasons [8].

The most important factors that reduce yield of barley in Ethiopia are low-yield capacity of farmers' varieties (landraces) and an inadequate number of improved varieties adapted to the different production systems and varied agro-ecological zones [9], poor agronomic practices, poor soil fertility, low soil pH, drought, water logging and frost. The major biotic constraints are diseases such as scald (*Rhynchosporium secalis* Oud.), net blotch (*Helminthosporium teres* Sacc.), spot blotch (*Helminthosporium sativum* Pum.) and leaf rust (*Puccinia hordei* Oth.); insect pests including Russian wheat aphid (*Diuraphis noxius*), barley shoot fly (*Delia arambourgi*) and chaffer grub (*Melolontha* sp.) and both broad leaved and grass weeds that contribute to reduced barley yields. In studies conducted at Holetta, scald and net blotch may reduce grain yield by 21-67% and 25-34%, respectively

[10]. Barley shoot fly may reduce yield by more than 56% and aphids may cause 4% to 79% [11] loss or even total crop failure.

Genetic variability is defined as the occurrence of differences among individuals due to differences in their genetic composition and of the environment in which they are raised [12]. The knowledge of nature and magnitude of variation existing in available plant breeding materials are very important for further improvement of the crop. Therefore, the objective of this study was to estimate the extent of phenotypic and genotypic variability, heritability (in the broad sense) and the genetic advance expected under selection of the introduced materials.

## MATERIALS AND METHODS

**Description of the Study Sites:** The experiment was conducted at three locations of Tigray region, namely Atsbi, Ofla and Quiha where barley grows most with an erratic rainfall where heavy rain alternate with dry periods resulting in alternating floods and dry periods. The region receives the least rainfall compared to other parts of Ethiopia. The average annual rainfall for the period from 1961 to 1987 was 571 mm, which was 38% less than the national average (921mm) for the same period [13]. The mean annual rainfall ranges from 980 mm on the Central plateau to 450 mm on the Northeastern escarpments of the region [14]. The annual rainfall shows a high degree of variation ranging from 20% in the Western to 49% in the Eastern parts of Tigray [15]. The different characteristics of each location are presented in Table 1.

**Experimental Materials:** A total of 64 barley genotypes from ICARDA and one local check (Saesea) were considered in this study. List of barley genotypes, code, pedigree and origin are given in Table 2.

**Experimental Design, Management and Season:** The experiments were conducted in 2009/10 main cropping season. The trials were laid out in 8x8 Lattice design with two replications at three locations. Each plot was 2m long and 0.8m wide, which consisted of four rows with a spacing of 20 cm between rows. The middle two rows were used for data collection. Planting was done by hand drilling using a seed rate of 80kg ha<sup>-1</sup> for each treatment. All other management practices such as weeding and fertilization (urea 50kg ha<sup>-1</sup> and DAP 100kg ha<sup>-1</sup>) were uniformly applied to all plots.

**Data Collected:** Data were collected for both qualitative and quantitative parameters. Quantitative characters like

plant height, spike length and number of kernels per spike were recorded on plant basis by randomly selecting 10 plants from each plot. Number of productive tillers/m<sup>2</sup> was recorded by counting the whole second row and then converted into 1m<sup>2</sup> area, whereas days for heading, days for maturity, 1000-kernel weight, biological yield, grain yield and germination test were estimated on plot basis. The germination test was done by soaking 100 seeds of each genotype in water for 12 hours. Then the seeds were planted using top-dressing method on filter paper and two batches of fifty seeds of each genotype were germinated per germination box, which were kept under its plastic cover to reduce evaporation. The germination boxes were placed on the laboratory bench at room temperature of 20°C (± 0.5) and were watered every other day. Finally, evaluation for the germination test was done on seventh day from the day of sowing. A seed was considered to have germinated if the radicle exceeded 2mm in length [16].

**Statistical Analysis:** The data collected for each quantitative trait were subjected to analysis of variance (ANOVA) using Proc lattice and Proc GLM procedures of SAS version 9.2, [17] after testing the ANOVA assumptions. Before pooling the data across environments, test of heterogeneity for error of variance was done. The difference between treatment means was compared using DMRT at 5% probability levels.

The phenotypic and genotypic variances and coefficients of variation were estimated according to the method suggested by [18] as follows:

Environmental variance ( $\sigma^2_e$ ):

$$\sigma^2_e = MSe$$

Genotypic variance ( $\sigma^2_g$ ):

$$\sigma^2_g = \frac{MSg - MSe}{r}$$

where, r = number replication, MSg = mean square due to accessions and MSe = mean square of error (Environmental variance).

Phenotypic variance ( $\sigma^2_p$ ):

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

where,  $\sigma^2_g$  = genotypic variance and  $\sigma^2_e$  = mean square of error (Environmental variance).

Table 1: Different characteristics of locations.

| Testing location | AEZ           | Altitude (m.a.s.l) | Location |           | Annual Rainfall (mm) | Annual Temperature |        | Soil Type  | Soil pH |
|------------------|---------------|--------------------|----------|-----------|----------------------|--------------------|--------|------------|---------|
|                  |               |                    | Latitude | Longitude |                      | Min.               | Max.   |            |         |
| Atsbi            | SM2e          | 2630               | 13°52'N  | 39°44'E   | 500 - 600            | 15°C               | 35°C   | Sandy loam | 6.1     |
| Quiha            | Not available | 2247               | 13°30'N  | 39°29'E   | 812.4                | 15.4°C             | 20.4°C | Clay loam  | 6.7     |
| Ofla             | SM2a          | 2539               | 12°30'N  | 39°31'E   | 450 - 800            | 6°C                | 32°C   | Clay loam  | 5.2     |

Source: [1, 2]

Phenotypic coefficient of variation (PCV):

$$PCV = \frac{\sqrt{\sigma^2 P}}{\bar{X}} * 100$$

where,  $\sigma^2 P$  = phenotypic variance and  $\bar{X}$  = mean of the character being evaluated.

Genotypic coefficient of variation (GCV):

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} * 100$$

where,  $\sigma^2 g$  = genotypic variance and  $\bar{X}$  = mean of the character.

**Heritability (In the Broad Sense):** Heritability in the broad sense for quantitative characters was computed using the formula suggested by [19] as:

$$H = \frac{\sigma^2 g}{\sigma^2 P} * 100$$

where, H= heritability in the broad sense,  $\sigma^2 g$  = genotypic variance and  $\sigma^2 P$  = phenotypic variance.

**Genetic Advance Expected (GA):** The genetic advance expected under selection assuming selection intensity of the superior 5% of the plants was estimated in accordance with the methods illustrated by [19]:

$$GA = K * \sigma_p * H$$

where, GA = expected genetic advance, H = heritability in the broad sense, K = the selection differential and  $\sigma_p$  = phenotypic standard deviation on mean basis.

The Genetic advance as % of mean (GAM) was computed as:

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

where, GAM = genetic advance as percent of mean, GA = genetic advance under selection and  $\bar{X}$  = mean of the population in which selection was employed.

## RESULT AND DISCUSSION

**Analysis of Variance (ANOVA):** The analysis of variance for different characters at Atsbi, Ofla and Quiha locations are presented in Appendices 1, 2 and 3, respectively. There was very highly significant differences ( $P < 0.001$ ) among genotypes for all characters considered in all environments except for 1000-kernel weight at Quiha which was significant ( $p < 0.05$ ) and plant height was found non-significant at both Atsbi and Ofla locations.

The relative efficiency of the two designs showed that for most characters simple lattice design is not more efficient than complete randomized block design (RCBD) (Appendices 1, 2 and 3). Results obtained from test of homogeneity for error of variance showed the computed Chi-square test ( $\chi^2$ ) value exceeds the corresponding tabular ( $\chi^2$ ) value at 5% and 1% level of significance for all traits. Therefore, the hypothesis of homogeneous variance is rejected [20]. Therefore, the analysis of variance and other statistical analysis were run for the three locations separately.

**Range and Mean of Different Characteristics:** Estimated range, mean and standard error of the mean for the 11 characters are presented in Tables 2, 3 and 4. There is a wide range of variability obtained from the characters tested in different locations. The 2009/10 main season was known by its early halted rainfall across Ethiopia as well as Tigray. Therefore, it is an ideal season to test the introduced drought tolerant barley genotypes.

**Phenotypic and Genotypic Variations:** According to [21] PCV and GCV values  $> 20\%$  regarded as high, PCV and GCV values between 10 and 20% medium, PCV and GCV values  $< 10\%$  low. Estimated variance components, phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) for the characters studied are presented in Tables 2, 3 and 4, respectively.

Table 2: Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variations and genetic advance as percent of mean for characters of barley genotypes studied at Atsbi

|                                   | Range          | Mean ± S.E Mean | $\delta^2_g$ | $\delta^2_e$ | $\delta^2_p$ | GCV (%) | PCV (%) | H <sup>2</sup> (%) | GA    | GAM   |
|-----------------------------------|----------------|-----------------|--------------|--------------|--------------|---------|---------|--------------------|-------|-------|
| Plant height                      | 40.3 - 84.9    | 62.21 ± 0.44    | 7.92         | 32.15        | 40.07        | 6.26    | 14.08   | 19.76              | 2.57  | 5.73  |
| Days to maturity                  | 69 - 94        | 79.17 ± 0.13    | 16.22        | 2.87         | 19.09        | 5.37    | 5.83    | 84.96              | 7.63  | 10.20 |
| Days to heading                   | 38 - 65        | 48.54 ± 0.08    | 15.75        | 1.49         | 17.24        | 8.79    | 9.20    | 91.27              | 7.79  | 17.29 |
| 1000-kernel weight                | 15.2 - 54.4    | 40.84 ± 0.20    | 16.78        | 7.65         | 24.43        | 12.79   | 15.43   | 68.68              | 6.98  | 21.83 |
| Productive tillers/m <sup>2</sup> | 26.25 - 481.25 | 253.16 ± 3.16   | 578.11       | 249.15       | 827.26       | 29.48   | 35.26   | 69.90              | 41.34 | 50.78 |
| Spike length                      | 3.8 - 8.8      | 5.81 ± 0.03     | 0.72         | 0.19         | 0.91         | 15.55   | 17.48   | 79.19              | 1.55  | 28.51 |
| Kernels per spike                 | 15.3 - 48.1    | 25.85 ± 0.12    | 62.01        | 5.53         | 67.54        | 31.88   | 33.27   | 91.77              | 15.51 | 62.90 |
| Biological yield                  | 24.70 - 131.84 | 77.33 ± 85.61   | 36.99        | 45.83        | 82.82        | 19.24   | 28.79   | 44.68              | 20.49 | 26.50 |
| Grain yield                       | 8.51 - 66.65   | 36.02 ± 45.83   | 6.59         | 4.78         | 11.37        | 27.03   | 35.51   | 57.95              | 13.59 | 42.39 |
| Harvest index                     | 0.278 - 0.565  | 0.46 ± 0.0015   | 0.0015       | 0.0005       | 0.002        | 12.82   | 13.95   | 84.45              | 0.07  | 24.26 |
| Germination test                  | 66 - 100       | 92.95 ± 0.17    | 32.27        | 5.56         | 37.83        | 6.11    | 6.62    | 85.34              | 10.79 | 11.63 |

S.E Mean= Standard error of the mean,  $\delta^2_g$ = Genotypic variance,  $\delta^2_e$  = Environmental variance,  $\delta^2_p$ = Phenotypic variance, H<sup>2</sup> (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation, (%) GA= Genetic advance, GAM= Genetic advance as percent of mean.

Table 3: Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variation and genetic advance as percent of mean for characters of barley genotypes studied at Ofla

| Characters                        | Range        | Mean ±S.E Mean | $\delta^2_g$ | $\Delta^2_e$ | $\delta^2_p$ | GCV (%) | PCV (%) | H <sup>2</sup> (%) | GA    | GAM   |
|-----------------------------------|--------------|----------------|--------------|--------------|--------------|---------|---------|--------------------|-------|-------|
| Plant height                      | 40.8-91.6    | 71.51 ± 0.528  | 22.95        | 85.7         | 108.65       | 6.70    | 14.58   | 21.12              | 2.06  | 6.34  |
| Days to maturity                  | 86-104       | 95.70 ± 0.112  | 10.84        | 4.94         | 15.78        | 3.44    | 4.15    | 68.67              | 4.11  | 5.87  |
| Days to heading                   | 51-68        | 62.05 ± 0.133  | 6.95         | 6.55         | 13.50        | 4.25    | 5.92    | 51.48              | 6.17  | 6.28  |
| 1000-kernel weight                | 13.6-24.8    | 19.95 ± 0.066  | 4.22         | 1.47         | 5.69         | 10.30   | 11.95   | 74.22              | 8.22  | 18.27 |
| Productive tillers/m <sup>2</sup> | 16.25-407.5  | 163.23 ± 2.380 | 5224.80      | 1657.86      | 6882.66      | 44.28   | 50.83   | 75.91              | 10.28 | 79.48 |
| Spike length                      | 3.1-8.5      | 5.82 ± 0.017   | 0.88         | 0.09         | 0.97         | 16.15   | 16.93   | 90.97              | 12.34 | 31.73 |
| Kernels per spike                 | 15.3-51      | 26.30 ± 0.134  | 100.61       | 4.82         | 105.43       | 38.14   | 39.04   | 95.43              | 14.39 | 76.75 |
| Biological yield                  | 19.76-122.36 | 78.60 ± 84.681 | 182.57       | 278.54       | 461.11       | 17.19   | 27.32   | 39.59              | 16.45 | 22.28 |
| Grain yield                       | 5.44 -56.09  | 35.87 ± 41.414 | 40.04        | 58.67        | 98.71        | 17.64   | 27.70   | 40.56              | 18.50 | 23.14 |
| Harvest index                     | 0.28-0.57    | 0.46 ± 0.001   | 0.002        | 0.001        | 0.003        | 10.71   | 11.64   | 84.60              | 20.56 | 20.29 |
| Germination test                  | 66-100       | 88.70 ± 0.152  | 73.52        | 7.92         | 81.44        | 9.67    | 10.17   | 90.28              | 22.62 | 18.92 |

S.E Mean= Standard error of the mean,  $\delta^2_g$ = Genotypic variance,  $\delta^2_e$  = Environmental variance,  $\delta^2_p$ = Phenotypic variance, H<sup>2</sup> (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation, (%) GA= Genetic advance, GAM= Genetic advance as percent of mean.

Table 4: Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variation and genetic advance as percent of mean for the characters of barley genotypes studied at Quiha

| Characters                        | Range       | Mean ± S.E Mean | $\Delta^2_g$ | $\delta^2_e$ | $\delta^2_p$ | GCV (%) | PCV (%) | H <sup>2</sup> (%) | GA    | GAM   |
|-----------------------------------|-------------|-----------------|--------------|--------------|--------------|---------|---------|--------------------|-------|-------|
| Plant height                      | 29.3-61.6   | 44.96 ± 0.221   | 37.37        | 21.85        | 59.22        | 13.60   | 17.12   | 63.10              | 2.06  | 22.25 |
| Days to maturity                  | 68-82       | 74.99 ± 0.055   | 15.52        | 1.04         | 16.56        | 5.25    | 5.43    | 93.72              | 4.11  | 10.48 |
| Days to heading                   | 38-53       | 45.15 ± 0.067   | 13.33        | 2.74         | 16.07        | 8.09    | 8.88    | 82.96              | 6.17  | 15.17 |
| 1000-kernel weight                | 14.8-54.8   | 32.03 ± 0.328   | 13.31        | 32.86        | 46.17        | 11.39   | 21.21   | 28.83              | 8.22  | 15.17 |
| Productive tillers/m <sup>2</sup> | 16.25-212.5 | 81.56 ± 1.195   | 1503.64      | 501.17       | 2004.81      | 47.54   | 54.90   | 75.00              | 10.28 | 84.82 |
| Spike length                      | 2.5-8.3     | 5.45 ± 0.036    | 0.92         | 0.38         | 1.30         | 17.64   | 20.89   | 71.29              | 12.34 | 30.67 |
| Kernels per spike                 | 13.9-43.4   | 24.70 ± 0.149   | 53.17        | 7.45         | 60.62        | 29.52   | 31.52   | 87.71              | 14.39 | 56.95 |
| Biological yield                  | 10.14-67.83 | 32.05 ± 28.640  | 57.60        | 56.51        | 114.11       | 23.68   | 33.33   | 50.48              | 16.45 | 34.66 |
| Grain yield                       | 1.63-29.75  | 9.58 ± 10.894   | 0.889        | 0.680        | 0.957        | 9.84    | 10.21   | 84.56              | 18.50 | 19.54 |
| Harvest index                     | 0.081-0.514 | 0.29 ± 0.002    | 0.007        | 0.003        | 0.01         | 29.84   | 34.88   | 73.16              | 20.56 | 52.57 |
| Germination test                  | 64-100      | 92.97 ± 0.129   | 1961.59      | 358.28       | 2319.87      | 47.64   | 51.81   | 92.89              | 22.62 | 90.24 |

S.E Mean= Standard error of the mean,  $\delta^2_g$ = Genotypic variance,  $\delta^2_e$  = Environmental variance,  $\delta^2_p$ = Phenotypic variance, H<sup>2</sup> (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation, (%) GA= Genetic advance, GAM= Genetic advance as percent of mean

The genotypic variance took relatively much of the total variances for days to maturity, number of productive tillers/m<sup>2</sup>, spike length, number of kernels/spike and germination test across locations. In addition to this, higher genotypic variance was recorded for grain yield and days to heading at Atsbi and Quiha, 1000-kernel weight at Atsbi and Ofla and biological yield only at Quiha environments. These traits could be utilized efficiently for developing a new plant variety according to the need of different regions of the country. Similarly, [22] reported that, high level of genotypic variance was observed for days taken to heading and maturity, grain-filling period, flag leaf area, spikelets per spike, grains per spike, 1000-grain weight and harvest index. On the other hand, relatively lower variances share of the total variance were observed for plant height and biological yield at Atsbi and Ofla and 1000-kernel weight at Quiha respectively, indicating the greater share of environmental variance in the total variability.

In general, PCV values were greater than GCV values across environments although the differences were small. The small differences indicated that the environmental effect was small for the expression of most characters. Among all characters, high PCV and GCV values (> 20%) were observed for number of productive tillers/m<sup>2</sup> and number of kernels/spike across locations. Besides, at Atsbi location grain yield and at Quiha biological yield, harvest index and germination test had high PCV and GCV values. This indicates that selection may be effective based on these characters and their phenotypic expression would be a good indication of genotypic potential. The estimates are consistent with the findings of [22] where, high level of genetic variation was observed for days taken to heading and maturity, grain filling period, flag leaf area, plant height, spikelets per spike, grains per spike, biomass, 1000 grain weight and harvest index.

On the other hand, low GCV and PCV values (< 10%) were observed for days to heading and maturity in all environments. This traits offered less scope of selection, as they under the influence of environment [23]. This agrees with the findings of [24], where days to maturity showed considerable low variability, which indicates little opportunity for improvement through selection.

Spike length and 1000-kernel weight across locations, as well biological yield and harvest index at Atsbi and Ofla and plant height only at Quiha showed medium GCV and PCV values (>10% and <20%). This is in harmony with the findings of [25] reported similar variation in

barley for plant height and spike length. From the present finding, one can conclude that the test genotypes contained a wealth of genetic variability, which could be used for future breeding program.

**Heritability Estimates:** The concept of heritability explains whether differences observed among individuals arose as a result of differences in genetic makeup or due to environmental forces. According to [26] heritability, estimates can be placed in the following categories: low heritability < 40%, medium heritability 40-59%, moderately high 60-79% and very high heritability 80% or more. If heritability of a character is very high, say 80% or more, selection for such characters could be easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype [26]. The estimated broad sense heritability for the studied characters is presented in Tables 2, 3 and 4.

Based on the above classification, number of kernels/spike with a value of 91.77, 95.93, 87.7% and germination test 85.34, 90.28 and 92.89% resulted in very high heritability estimates in the broad sense for Atsbi, Ofla and Quiha environments, respectively. Likewise, days to heading (91.27%), days to maturity (84.96%) and harvest index (84.45%) at Atsbi, spike length (90.97 %) and harvest index (84.60%) at Ofla and days to heading (82.96%), days to maturity (93.82%) grain yield (84.56 %) at Quiha showed very high heritability estimates in the broad sense. Traits that exhibited a very high heritability estimates indicating the minimum effect of environment on the phenotypic expression of these characters and the effectiveness of selection in the improvement of these traits [26]. In agreement with the current study, [24] reported high estimates of heritability in broad sense for number of grains per spike followed by biological yield and grain yield per plant.

Moderately high heritability estimates were obtained from traits like number of productive tillers/m<sup>2</sup> 69.90% at Atsbi, 75.91% at Ofla and 75% at Quiha locations, while 1000-kernel weight was 68.68% at Atsbi and 74.22% at Ofla. Similarly, spike length at Atsbi had moderately high heritability estimates with a value of 79.19% and 71.29% at Quiha environments. In addition, at Ofla location days to maturity (68.67%) and at Quiha plant height (63.10%) and harvest index (73.16%) resulted in moderately high heritability estimates. Medium heritability estimates was observed for traits like biological yield at Atsbi (44.68%) and at Quiha (50.48%) and grain yield at Atsbi (57.95%) environments.

On the other hand, broad sense heritability in these barley genotypes gave low value for plant height at Atsbi (19.76%), plant height (21.12%) at Ofla and biological yield (39.49%) and 1000-kernel weight (28.83%) at Quiha, respectively. Characters with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment. Contradictory to the current findings [27], reported that heritability estimates for plant height, number of filled grains per panicle, panicle length and 1000-grain weight in rice.

**Estimates of Expected Genetic Advance:** Genetic advance under selection (GA) refers to improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity [26]. Generally, large heritability values showed relative ease with which selection can be made based on phenotype, but their practical utility in plant breeding is further enhanced if accompanied by concomitantly high GA estimates [28]. The estimated genetic advance and expected genetic advance as percent of the mean for the characters considered at Atsbi, Ofla and Quiha are presented in Tables 2, 3 and 4, respectively. Genetic advance expressed as percent of mean showed a wide range of variations across the environments. It ranged from 5.73% for plant height to 62.90% for kernels/spike, from 5.87% for days to maturity to 79.48% for number of productive tillers/m<sup>2</sup> and from 10.48% for days to maturity to 90.24% for germination test at Atsbi, Ofla and Quiha environments, respectively.

The effectiveness of selection depends upon genetic advance of the character selected along with heritability [29]. High heritability coupled with relatively high genetic advance as percent of the mean was observed for number of productive tillers/m<sup>2</sup>, spike length, number of kernels/spike and harvest index across locations. Likewise, estimates of genetic advance (as percent of the mean) with together high heritability for biological yield and germination test were also considerably high at Quiha and 1000-kernel weight at Atsbi. This reflected the involvement of additive gene action for the inheritance of these traits and selection will be effective. This is in close agreement with the findings of [24], where high heritability estimates in barley were associated with high genetic advance for number of grains per spike, biological yield per plant and grain yield per plant.

As opposite to the above, the traits days to maturity and days to heading in all environments and germination test at Atsbi and Ofla locations each, depicted high heritability estimates with lower genetic advance as

compared to other traits. The traits possessing low genetic advance with high heritability indicates the presence of non-additive gene action, thus simple selection procedure in early segregating generations will not be effective for screening of the desirable traits. Further explanation by [30] suggested that high heritability might not necessarily lead to increased genetic gain, unless sufficient genetic variability existed in the germplasm. In agreement with the current finding, [24] reported that, the high estimates of heritability with low genetic advance were detected for days to ear emergence in barley.

Low heritability coupled with low genetic advance values observed for plant height at Atsbi and Ofla sites. The reason for the low heritability is a result of some variances constituting the environmental variance. This low estimate of genetic advance as a percent mean arises from low estimate of phenotypic variance and heritability. This is consistent with [31], where low heritability with low genetic advance values was found for plant height and number of grains, indicating slow progress through selection for thesis traits in wheat.

Generally, high GCV along with high heritability and genetic advance was obtained from number of productive tillers/m<sup>2</sup> and number of kernels/spike across locations, while grain yield at Atsbi and germination test, harvest index and biological yield at Quiha. Wide range of variability coupled with high heritability and high genetic advance for these traits indicated that selection is effective. High GCV along with high heritability and genetic advance provide better information than other parameters alone [29].

## CONCLUSIONS

This study generally indicates that there was a genetic variability among genotypes. Thus, there is enormous opportunity in the improvement program of the ICARDA barley genotypes. Therefore, the information generated from this study needs to be used by breeders who are interested in early maturing barley genotypes. Besides, these barley materials need to be tested in similar agro-ecologies for their stability.

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Appendix 1: Analysis of variance (ANOVA) for the 11 characters of barley genotypes tested at Atsbi, using Simple Lattice Design

| Source of variance                 | Replications | Treatments |            | Blocks within Reps (adj) | Error      |         | R <sup>2</sup> (%) | Efficiency Relative to RCBD (%) |
|------------------------------------|--------------|------------|------------|--------------------------|------------|---------|--------------------|---------------------------------|
|                                    |              | Unadj.     | Adj.       |                          | Intrablock | RCBD    |                    |                                 |
| Degrees of freedom                 | 1            | 63         | 63         | 14                       | 49         | 63      |                    |                                 |
| Plant Height                       | 50.63        | 91.38      | 83.12      | 50.71                    | 65.07      | 61.88   | 67.15              | 95.10                           |
| Days to maturity                   | 5.28         | 37.71      | 33.86**    | 4.65                     | 5.32       | 5.17    | 90.37              | 97.19                           |
| Days to heading                    | 8.51         | 38.29      | 32.58**    | 2.15                     | 2.26       | 2.24    | 95.67              | 98.90                           |
| 1000-Kernel Weight                 | 29.07        | 73.54      | 68.60**    | 24.68                    | 13.78      | 16.20   | 88.12              | 107.07                          |
| Productive tillers /m <sup>2</sup> | 7225.52      | 13792.00   | 11549.63** | 3706.4                   | 3310.38    | 3398.38 | 85.12              | 100.28                          |
| Spike Length                       | 0.02         | 1.85       | 1.53**     | 0.20                     | 0.24       | 0.23    | 90.94              | 95.63                           |
| Kernels per Spike                  | 2.65         | 142.75     | 117.68**   | 4.01                     | 4.98       | 4.76    | 97.38              | 95.65                           |
| Biological Yield                   | 214.92       | 721.55     | 575.48**   | 385.70                   | 243.14     | 274.82  | 81.09              | 104.45                          |
| Grain Yield                        | 69.40        | 265.33     | 203.50**   | 90.95                    | 69.67      | 77.40   | 84.10              | 101.51                          |
| Harvest Index                      | 0.002        | 0.009      | 0.0064**   | 0.0008                   | 0.0012     | 0.001   | 90.33              | 91.59                           |
| Germination Test                   | 6.13         | 61.93      | 51.18**    | 6.27                     | 10.00      | 9.17    | 89.07              | 91.70                           |

\*, \*\* Indicates significance at 0.05 and 0.01 probability levels, respectively.

Appendix 2: Analysis of variance for the 11 characters of barley genotypes tested at Ofla, using Simple Lattice Design

| Source of variance                 | Replications | Treatments |           | Blocks within Reps (adj) | Error      |         | R <sup>2</sup> (%) | Efficiency Relative to RCBD (%) |
|------------------------------------|--------------|------------|-----------|--------------------------|------------|---------|--------------------|---------------------------------|
|                                    |              | Unadj.     | Adj.      |                          | Intrablock | RCBD    |                    |                                 |
| Degrees of freedom                 | 1            | 63         | 63        | 14                       | 49         | 63      |                    |                                 |
| Plant Height                       | 25.56        | 124.14     | 110.61    | 89.39                    | 92.57      | 91.87   | 66.73              | 99.24                           |
| Days to maturity                   | 13.13        | 26.61      | 25.86**   | 7.72                     | 4.15       | 4.94    | 89.84              | 108.04                          |
| Days to heading                    | 10.70        | 20.78      | 20.23**   | 8.01                     | 5.89       | 6.36    | 83.22              | 101.99                          |
| 1000-Kernel Weight                 | 3.65         | 9.74       | 8.24**    | 1.18                     | 1.42       | 1.37    | 90.08              | 96.16                           |
| Productive tillers /m <sup>2</sup> | 101.09       | 11582.00   | 9671.34** | 2162.09                  | 1878.65    | 1941.64 | 89.20              | 100.43                          |
| Spike Length                       | 0.55*        | 1.82       | 1.55**    | 0.06                     | 0.092      | 0.086   | 96.24              | 92.95                           |
| Kernels per Spike                  | 23.38        | 201.84     | 173.61**  | 5.21                     | 5.97       | 5.80    | 97.77              | 97.16                           |
| Biological Yield                   | 1.59         | 644.96     | 569.94**  | 250.73                   | 237.92     | 240.76  | 79.11              | 100.06                          |
| Grain Yield                        | 17.94        | 148.37     | 137.14**  | 65.43                    | 56.89      | 58.79   | 78.67              | 100.42                          |
| Harvest Index                      | 0.0024*      | 0.0052     | 0.0044**  | 0.0004                   | 0.0005     | 0.0004  | 93.79              | 96.17                           |
| Germination Test                   | 1.13         | 154.96     | 132.73**  | 8.66                     | 7.71       | 7.91    | 96.32              | 100.30                          |

\*, \*\* Indicates significance at 0.05 and 0.01 probability levels, respectively.



Appendix 3: Analysis of variance of the 11 characters of barley genotypes tested at Quiha, using Simple Lattice Design

Mean square

| Source of variance                 | Replications | Treatments |           | Blocks within Reps (adj) | Error      |         | R <sup>2</sup> (%) | Efficiency Relative to RCBD (%) |
|------------------------------------|--------------|------------|-----------|--------------------------|------------|---------|--------------------|---------------------------------|
|                                    |              | Unadj.     | Adj.      |                          | Intrablock | RCBD    |                    |                                 |
| Degrees of freedom                 | 1            | 63         | 63        | 14                       | 49         | 63      |                    |                                 |
| Plant Height                       | 157.53*      | 90.87      | 74.89**   | 16.52                    | 16.25      | 16.3133 | 88.47              | 100.01                          |
| Days to maturity                   | 0.01         | 32.09      | 24.80**   | 1.12                     | 1.02       | 1.0396  | 97.62              | 100.22                          |
| Days to heading                    | 0.01         | 26.41      | 21.27**   | 1.02                     | 1.47       | 1.3729  | 95.87              | 93.0996                         |
| 1000-Kernel Weight                 | 2.08         | 59.46      | 59.79*    | 22.79                    | 35.74      | 32.8652 | 69.90              | 91.9488                         |
| Productive tillers /m <sup>2</sup> | 775.20       | 3659.18    | 3244.83** | 542.29                   | 473.37     | 488.69  | 91.15              | 100.4                           |
| Spike Length                       | 2.05*        | 2.22       | 1.74**    | 0.17                     | 0.43       | 0.3722  | 87.29              | 86.7616                         |
| Kernels per Spike                  | 66.85*       | 113.82     | 101.57**  | 7.92                     | 7.32       | 7.4506  | 95.35              | 100.14                          |
| Biological Yield                   | 72.50        | 164.78     | 153.67**  | 11.21                    | 27.21      | 23.65   | 88.84              | 86.91                           |
| Grain Yield                        | 3.65         | 34.99      | 33.16**   | 2.43                     | 3.94       | 3.60    | 92.08              | 91.49                           |
| Harvest Index                      | 0.001        | 0.015      | 0.014**   | 0.001                    | 0.0012     | 0.0011  | 94.28              | 96.29                           |
| Germination Test                   | 1.13         | 170.86     | 162.45**  | 7.16                     | 5.52       | 5.90    | 97.57              | 101.43                          |

\*, \*\* Indicates significance at 0.05 and 0.01 probability levels, respectively