



### Genetic Variability and Correlation Studies in Yield and Yield Related Characters of Barley (*Hordeum vulgare* L.) Genotypes

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#### ABSTRACT

Twelve genotypes of Barley (*Hordeum vulgare* L.) were evaluated for two years in the field in a randomized complete block design and replicated three times. The results showed year effect to be significant for plant height, grain yield, heading time and greenness of flag leaf, and genotype effect was significant for all the characters. Also, genotype x year interaction was significant for all the characters except for plant height, spike length and kernel weight. The maximum yield among advanced lines studied was obtained from A71-1 (4091.8 kg ha<sup>-1</sup>) and A74-1 (3926.1 kg ha<sup>-1</sup>) which were developed through crossing of *H. vulgare* v. nudum with Bülbül 89 and Karatay 94 cultivars, respectively. Close resemblance between genotypic correlation coefficient (GCV) and phenotypic correlation coefficient (PCV) was observed for grain yield indicating that selection for this character would be effective. Heritability estimates in general were high for all the nine characters studied. Characters studied showed significant positive correlation with grain yield except for plant height and greenness of flag leaf which showed significant positive genotypic correlation only in the second year. Highest heritability couple with high genetic advance was observed for plant height, spike length, number of spikelets per spike, number of kernels per spike, kernel weight per spike, thousand kernel-weight and heading time. Thus, these traits could be used as selection criteria for yield in barley.

#### 1. Introduction

Barley (*Hordeum vulgare* L.) is the world fourth most important cereal after wheat, rice and maize (Bengtsson, 1992). In Turkey, it is the second most important cereal. Increased production per unit area is the primary objective in many barley breeding programmes. Of these, grain yield is the most important and complex characters with which barley breeders work. Grain yield in barley is the product of several interrelated traits; hence, a successful breeding programme depends largely upon the information on the genetic variability and association of desired quantitative traits with yield. Hence, consideration of quantitative approaches for exploitation of the extensive genetic variability available in barley cultivars is of paramount importance. Estimates of genetic parameters serve as a base for selection and hybridization since degree of variability for a given character is a basic prerequisite for its improvement. The study of genotypic correlations of yield and yield related

components is important to enhance selections of genotypes for improvement. Although, several research efforts have been devoted to barley breeding to enhance its improvement, Alemayehu, (2005), Jaradat et al. (2004) and Akgun et al. (2012) reported significant genetic differences for morphological parameters for barley genotypes, Singh and Ceccarelli (1995), Vimal and Vishwakarma (1998) and Akinci and Yildirim (2009) observed considerable genotypic variability among various barley genotypes for grain yield and yield related characters. Although, progress has been made in terms of increased grain yields, the problem of identifying appropriate indicators of grain yield during selection still remains unresolved. The present study was conducted to (i) evaluate the performance of different barley genotypes under field conditions (ii) estimate the nature and magnitude of variability for grain yield and yield related characters among local and improved cultivars of barley (iii) to ascertain the genetic relationship among grain yield and its related components. Information on the

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above objectives will definitely lead to further improvement in the development of adaptable cultivars to Konya state.

## 2. Materials and Methods

The study was carried out at the experimental field of the Department of Field Crops, University of Selcuk, Konya (36°41'-39°16' N and 31°14'-34°26' E, 1016 m of altitude), Turkey during 2008-2009 and 2009-2010 cropping seasons under dry fed conditions. The annual average of the total precipitation is 320 l/m<sup>2</sup> in a year most falling between October and June with peaks in December and May (Figure 1). The temperature ranges from 27.6°C to 0.5°C (Figure 2) with the soil type classified as Clay loam with a pH of 8.00.

Twelve barley genotypes were used for the experiment (Table 1). Eight of the genotypes (A711-1, A74-1, A52, A526, A71-2, A71-1, A78-2 and A72-2) were lines of the F7 generation obtained from the most popular varieties Karatay 94 and Bulbul 89 and local populations of *Hordeum vulgare* L. v. nudum Hook.f. (with naked kernels and early maturity) and *Hordeum spontaneum* Koch. (with hulled kernels and early maturity), which were crossed reciprocally in 4x4 full diallel during 1998-1999 cropping season. The experimental field was manually cleared, tilled to loosen the soil adequately and then laid out in a randomized complete block (RCB) design with three replications. Each genotypes was planted in four rows of 2 m in length and between row spacing of 20 cm.

Table 1

Name, pedigree and maturity group of the barley genotypes (2-rowed) under study

Genotype	Pedigree	Feature
Karatay 94	wide-spread Turkish variety	hulled forage and malting barley with high yielding ability, late maturity and white lemma
Bülbül 89	well-known Turkish variety	hulled malting barley with medium late maturity and white lemma
<i>H. spontaneum</i> Koch <i>H. vulgare</i> L.v. nudum	population, individual bulk population, individual bulk	hulled barley with early maturity and black lemma naked barley with early maturity, weakly colored aleuron and white lemma
A711-1	<i>H.vulgare</i> v.nudum x <i>H.spontaneum</i>	hulled with early maturity, white lemma and pericarp
A74-1	Karatay 94 x <i>H. vulgare</i> v. nudum	hulled with late maturity, white lemma and colored aleuron
A52	Karatay 94 x <i>H. vulgare</i> v. nudum	hulled with late maturity, white lemma and colored aleuron
A526	<i>H. vulgare</i> v. nudum x Karatay 94	hulled with late maturity, white lemma and colored aleuron
A71-2	<i>H. vulgare</i> v. nudum x Bülbül 89	naked with early maturity, white lemma and yellow pericarp
A71-1	<i>H. vulgare</i> v. nudum x Bülbül 89	naked with early maturity, white lemma and yellow pericarp
A78-2	<i>H. vulgare</i> v.nudum x <i>H. spontaneum</i>	hulled with early maturity, white lemma and colored aleuron
A72-2	Karatay 94 x <i>H. vulgare</i> v. nudum	naked with early maturity, white lemma and yellow pericarp

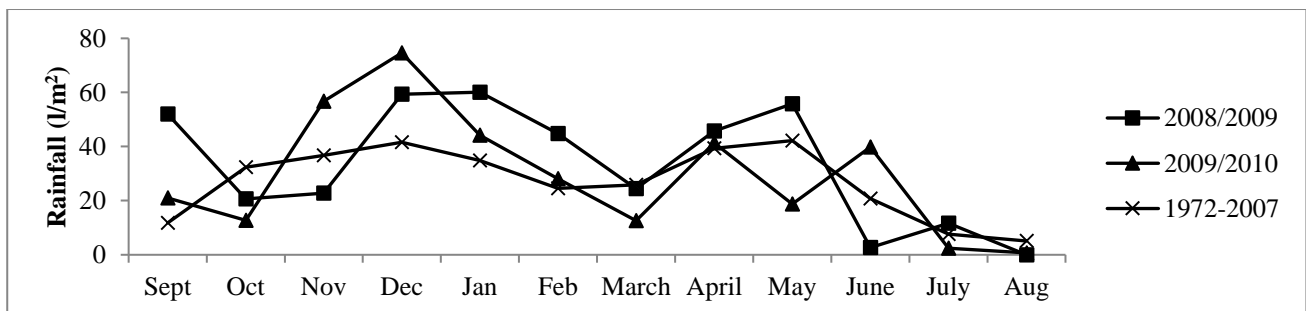


Figure 1

Monthly rainfall data of the experimental field

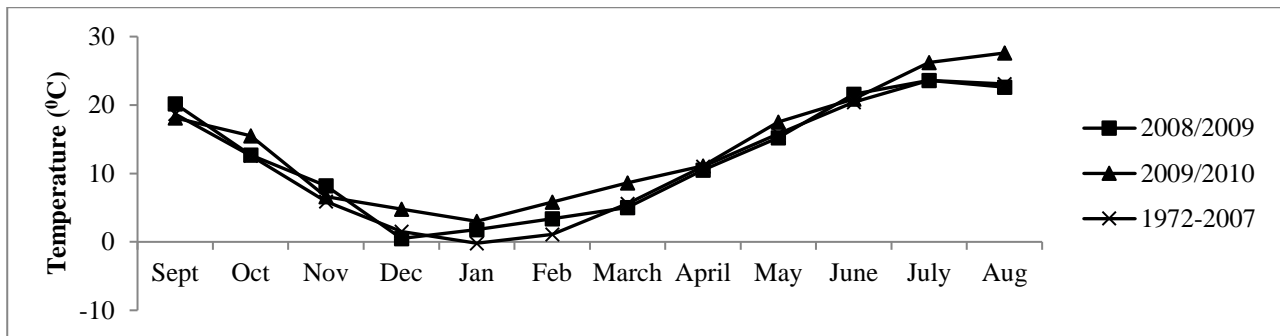


Figure 2

Monthly temperature data of the experimental field

Each year, plots were sown in the beginning of October and received 60 kg ha<sup>-1</sup> N in two applications and 65 kg ha<sup>-1</sup> P<sub>2</sub>O<sub>5</sub>. Days to heading were recorded from the 1<sup>st</sup> of January till the moment when 50% of the spikes had emerged from the boot. At maturity, plant height was measured from the soil surface to the top of the spikes excluding the awns. For each character studied, data were collected from ten randomly selected plants from the two middle rows of each plot. The remaining plants in each plot were harvested by hand.

Greenness was measured with a SPAD-502 meter from the Minolta Camera Co., Ltd, Japan, which is sensitive to photosynthetic pigments of individual leaves. The SPAD-502 measures the amount of chlorophyll in the leaf, which is related to leaf greenness, by transmitting light from light emitting diodes (LED) through a leaf at wavelengths of 650 and 940 nm (Adamsen et al., 1999). A SPAD reading was obtained from randomly selected flag leaves of ten plants in the beginning of flowering and then averaged.

Data was recorded on nine characters such as plant height, spike length, number of spikelets per spike, number of kernels per spike, kernel weight per spike, thousand kernel-weight, grain yield per hectare, days to maturity and greenness of flag leaf for which combined analysis of variance was done (Table 2). Data were recorded on plot basis for days to maturity, grain yield per plot and thousand kernel weight, while, the other characters were taken on plant basis by considering an average of ten randomly sampled plants from each plot. Analysis of variance was done after subjecting mean values of the recorded data to MSTAT-C (Freed et al. 1988).

The phenotypic ( $\delta^2_p$ ) and genotypic ( $\delta^2_g$ ) variances were estimated according to the method suggested by Burton and de Vane (1953) whereas, broad sense heritability ( $H^2$ ) was estimated following Allard (1960) as:

$$H^2 = (\delta^2_g / \delta^2_p) \times 100 \quad (1)$$

and Genetic advance (GA) was calculated in accordance with the methods illustrated by Johnson et al. (1955) as:

$$GA = (K) \sigma_A (H^2) \quad (2)$$

where,  $\sigma_A$  is phenotypic standard deviation, K is the standardized selection differential at 5% selection intensity ( $K = 2.063$ ).

Genetic advance as percent of mean (GAM) was calculated using the formula

$$GAM = (G/X) \times 100 \quad (3)$$

where, G = genetic advance, X = grand mean.

Genotypic and phenotypic coefficients of correlation were also calculated from the genotypic and phenotypic variances and covariances of the characters according to the formula by Miller, et al. (1958).

### 3. Results and Discussion

Table 2 gives the results of combined analysis of variance over two seasons for the nine traits. Significant to highly significant differences were observed between the genotypes for all traits. There were significant differences between the years for plant height, grain yield per hectare, days to maturity and greenness of flag leaf. Significant to highly significant interactions between genotypes and years were observed for all of traits except for plant height, spike length and kernel weight.

The estimates of phenotypic and genotypic variances as well as heritability and genetic advance for the nine characters in barley are presented in Table 3. This result revealed considerable phenotypic and genotypic variations among the genotypes for all traits under consideration. In all of the traits, a large portion of the phenotypic variance was accounted for by genetic components except for grain yield per hectare and greenness of flag leaf in which the contribution of genetic variance to phenotypic variance were 46.57% and 33.20%, respectively. Genotypic variance for the characters ranged from 0.049 for kernel weight per spike to 2726.95 for grain yield per

hectare. Phenotypic variance ranged from 0.055 for kernel weight per spike to 5856.10 for grain yield per hectare.

Table 2

Combined analysis of variance (ANOVA) for grain yield and yield related characters of barley genotypes evaluated in Konya

Source of Variation	Plant DF	Plant height (cm)	Spike length (cm)	Spikelets spike <sup>-1</sup>	Kernels spike <sup>-1</sup>	Kernel weight spike <sup>-1</sup>	1000-kernel Weight (g)	Grain yield (kg ha <sup>-1</sup> )	Heading time (d)	Greenness (SPAD)
Replication	2	0.546	0.347	0.811	4.178	0.040	14.31	20.69	1.260	1.393
Year (A)	1	11173.9**	0.330	0.245	1.668	0.011	6.301	7959.86**	177.35**	623.05**
Genotype (B)	11	537.04**	9.16**	109.48**	95.71**	0.330**	162.95**	35136.6**	400.29**	31.07**
AxB	11	0.371	0.165	2.98*	2.37	0.036**	40.67**	18774.9**	34.92**	20.76**
Error	46	2.42	0.545	1.21	1.19	0.007	4.54	784.43	2.29	1.83
Grand mean		117.30	9.53	29.75	28.19	1.09	38.27	3423.3	115.2	48.66
SE(±)		1.56	0.74	1.10	1.09	0.08	2.13	280.03	1.51	1.35
CV (%)		1.33	7.76	3.70	3.87	7.34	5.57	8.18	1.31	2.77

\*, \*\*: significant at P< 0.05 and P< 0.01, respectively

Table 3

Estimates of variance components, heritability and genetic advance as percent of mean for grain yield and yield related characters of twelve barley genotypes over two seasons

Variance components	Plant height (cm)	Spike length (cm)	Spikelets spike <sup>-1</sup>	Kernels spike <sup>-1</sup>	Kernel weight spike <sup>-1</sup>	1000-kernel weight (g)	Grain yield (kg ha <sup>-1</sup> )	Heading-time (d)	Greenness (SPAD)
Pv	89.51	1.53	18.25	15.95	0.055	27.16	5856.10	66.72	5.18
Gv	89.44	1.50	17.75	15.56	0.049	20.38	2726.95	60.90	1.72
H <sup>2</sup>	99.92	98.04	97.26	97.53	89.09	75.04	46.57	91.28	33.20
GA	19.47	2.50	8.56	8.02	0.43	8.06	73.41	15.36	1.56
GAM (%)	16.60	26.23	28.77	28.45	39.45	21.06	2.14	13.33	3.21

Pv: Phenotypic variance, Gv: Genotypic variance, Ev: Environmental variance, H<sup>2</sup>: Heritability, GA: Genetic advance, GAM: Genetic advance as percent of means.

Table 4

Estimates of phenotypic and genotypic coefficients of variation of yield and yield related characters of twelve barley genotypes over two seasons

Components of coefficient of variations	Plant height (cm)	Spike length (cm)	Spikelets spike <sup>-1</sup>	Kernels spike <sup>-1</sup>	Kernel weight spike <sup>-1</sup>	1000-kernel weight (g)	Grain yield (kg ha <sup>-1</sup> )	Heading time (d)	Greenness (SPAD)	
PCV (%)		8.07	12.98	14.36	14.17	21.52	13.62	2.24	7.09	4.68
GCV (%)		8.06	12.85	14.16	13.99	20.31	11.80	1.53	6.77	2.70

PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation.

Greenness of flag leaf showed lower heritability estimates of 33.20 whereas; moderate to high heritability values of 46.57 was recorded for grain yield per hectare. Very high heritability estimates were obtained for other traits. Also in Table 3, the expected genetic advance val-

ues for nine characters of barley genotypes were presented. These values are expressed as percentage of the genotype mean for each character so that comparison could be made among various characters, which had different units of measurement. Progress that could be expected from selecting the top 5% of the genotypes

ranged from 2.14% for grain yield per hectare to 39.45% for kernel weight per spike. For all characters except for grain yield per hectare and greenness of flag leaf, the genetic advances were considered moderate. Comparatively, the highest genetic advance as percent of mean was recorded for kernel weight per spike (39.45%) followed by number of spikelets per spike (28.77%) and number of kernels per spike (28.45%).

Table 4 presents phenotypic and genotypic coefficients of variation for the nine characters. Phenotypic coefficients of variation were highest for kernel weight per spike (21.52%) and this was followed by number of spikelets per spike (14.36%) and number of kernels per spike (14.17%). These three characters also exhibited highest genotypic coefficients of variation of 20.31%, 14.16% and 13.99%. The PCV and GCV were relatively moderate for plant height (8.07 and 8.06) and heading time (7.09 and 6.77) respectively. Low PCV and GCV estimates of between 1.52 and 4.68 were recorded for grain yield per hectare and greenness of flag leaf.

Table 5 shows genotypic and phenotypic coefficients of correlation ( $r$ ) between grain yield and yield related characters. In the first season, grain yield showed the strongest positive genotypic and phenotypic correlations with spike length, number of spikelets per spike, number of kernels per spike, kernel weight per spike and thousand kernel weight. Meanwhile, greenness of flag leaf was negatively but non-significantly correlated with grain yield at genotypic and phenotypic level ( $r_g = -0.068$ ) ( $r_p = -0.062$ ). In the second season, grain yield showed the strongest positive genotypic correlations with all of traits except thousand kernel weight, and also, positive phenotypic correlations occurred with spike length, number of spikelets per spike, number of kernels per spike, kernel weight per spike and days to maturity. Plant height, thousand kernel-weight and greenness of flag leaf had positive but non-significant phenotypic correlation with grain yield.

Generally, the genotypic correlation coefficients were higher than the phenotypic correlation coefficients for most of the characters.

Table 5

Estimates of phenotypic and genotypic coefficients of correlation between grain yield and yield related characters of twelve barley genotypes (n=36)

Traits		Plant height	Spike length	Spikelets spike <sup>-1</sup>	Kernels spike <sup>-1</sup>	Kernel weight spike <sup>-1</sup>	1000-kernel weight	Heading-time	Greenness (SPAD)
2008-2009	$r_p$	0.164	0.622**	0.697**	0.614**	0.595**	0.511**	-0.062	0.189
	$r_g$	0.174	0.706**	0.710**	0.625**	0.596**	0.521**	-0.068	0.198
2009-2010	$r_p$	0.336	0.364*	0.856**	0.791**	0.513**	0.175	0.812**	0.344
	$r_g$	0.351*	0.471**	0.955**	0.905**	0.559**	0.181	0.859**	0.507**

\*, \*\*: significant at  $P < 0.05$  and  $0.01$ , respectively

$r_p$  : Phenotypic coefficient of correlation,  $r_g$ : Genotypic coefficient of correlation

Table 6 shows the mean grain yield and yield related characters of the twelve genotypes in two seasons. Lines A71-1, A52, A71-2 and A74-1 were among genotypes with the highest spike length. A74-1, A52, A72-2 and Karatay 94 had highest number of kernels per spike, while A711-1, A52, A72-2 and Karatay 94 had higher kernel weight per spike compared to other genotypes. Karatay 94 and A72-2 were among genotypes with highest plant height. Similarly, line A711-1 had the highest 1000-kernel weight (46.52 g). All of lines had higher greenness values compared to *H. vulgare* L.v. nudum, and recorded higher grain yield per hectare compared to *H. spontaneum* and *H. vulgare* L.v. nudum.

Turkish barley landraces are contributing as major sources of genes in barley crop improvement which has many advantages than exotics. In crop genetic improvement, breeding gain requires heritable variation in important agronomic characters of the crop.

Therefore, the available genetic variation, heritability and expected genetic gain in important agronomic characters are useful to design better effective breeding strategies in barley landraces. The presence of significant ( $p < 0.01$ ) variation among barley genotypes for all characters considered implies that there is high variability among genotypes tested. Genotype x environment interaction revealed significant ( $p < 0.01$ ) difference only for kernels weight per spike, thousand kernel weight, grain yield per hectare, heading time and greenness of flag leaf (Table 2) indicating barley genotypes and lines showed inconsistent performances across years for these characters. Similarly, Ceccarelli (1989), Ceccarelli and Grando (1991), Jackson et al. (1993) and van Oosterom et al. (1993) reported genotype-environment interaction in barley for grain yield. The presence of difference in yield performance of the cultivars and lines may be considered during selection. The maximum yield among advanced lines studied was obtained from A71-1 (4091.8

kg ha<sup>-1</sup>) and A74-1 (3926.1 kg ha<sup>-1</sup>) which were developed through crossing of *H. vulgare* v. *nudum* with Bülbül 89 and Karatay 94, respectively. This indicates the

requirement of crossing program with landraces as one option to improve barley yield.

Table 6

Mean and LSD values of grain yield and yield related characters in 2-rowed barley genotypes over two seasons.

Genotypes	Plant height (cm)	Spike length (cm)	Spikelets spike <sup>-1</sup>	Kernels Spike <sup>-1</sup>	Kernel weight spike <sup>-1</sup>	1000-kernel weight (g)	Grain yield (kg ha <sup>-1</sup> )	Heading time (d)	Greenness (SPAD)
Karatay 94	129.73a	9.47b	33.25a	31.08a	1.25b	40.07d	4373.4a	129.5a	50.58ab
Bülbül 89	107.25f	8.05d	29.17e	28.46d	1.05ef	36.83fg	3436.7de	123.8b	48.60e
P-1	120.01d	6.63e	17.50g	16.84g	0.45g	25.92i	1552.9g	108.0fg	50.57ab
P-2	107.77f	9.77b	26.53f	25.67f	1.07de	43.32b	2373.0f	108.0ef	43.08g
A711-1	120.53d	9.39bc	31.07d	28.33d	1.36a	46.52a	3596.6cd	107.7g	48.05e
A74-1	121.57c	10.51a	32.72ab	31.48a	1.05ef	33.37h	3926.1b	120.5c	49.97bc
A52	117.82e	10.79a	32.33bc	30.83a	1.28b	41.48c	3305.9e	123.7b	49.58cd
A526	127.20b	8.99c	31.58d	30.10b	1.16c	39.90d	3662.5c	123.0b	46.47f
A71-2	102.60h	10.60a	29.65e	27.80de	1.00f	35.80g	3609.7cd	109.0e	48.85de
A71-1	120.38d	10.95a	31.75cd	29.25c	1.11cd	37.87ef	4091.8b	109.2e	51.27a
A78-2	104.62g	9.39bc	29.85e	27.33e	1.05ef	38.40e	3408.0e	108.7ef	47.07f
A72-2	128.13b	9.84b	31.58d	31.08a	1.28b	40.78cd	3740.3c	111.2d	49.85bc
LSD	1.00	0.47	0.70	0.69	0.05	1.35	17.74	0.96	0.86

Values within a column with a letter superscript in common are not significantly different at  $P < 0.01$

P-1: *H. spontaneum* ; P-2: *H. vulgare* v. *nudum*

Heritability (broad sense) was high for all important quantitative characters measured. Dabholkar (1992) classified heritability estimates as low (5-10%), medium (10-30%) and high (>30%). Accordingly, all of the agronomic characters considered for analysis showed high heritability constituting high breeding value which has more additive genetic effects which is important for crop improvement. In similar study, Rytger et al. (1967) reported smaller heritability for grain yield than this result. Singh and Ceccarelli (1995) found smaller heritability than this report for grain yield in F<sub>6</sub> barley crosses conducted at Atlas, Tel Hadya, Berda and Bouider in Syria. In another report, Singh et al. (1986) also found heritability estimates for thousand kernel weight and spike length which is relatively lower as compared to this report. While, Vimal and Vishwakarma (1998) and Jalata et al. (2011) reported higher heritability for spike length, grain yield and number of spikelets per spike. Low heritability was reported by Ceccarelli (1994) and Ceccarelli (1996) on barley in low yielding environments. Atlin and Frey (1990) also concluded that heritability in low yielding environment is lower than high yielding environment in Oat (*Avena sativa* L.) and Abdelmula et al. (1999) found similar value in Faba bean (*Vicia faba* L.). Because, the magnitude of heritability is affected by the type of genetic material, character to be measured and environmental conditions to which the individuals are subjected (Dabholkar, 1992; Falconer and Mackay,

1996). In this study, the heritability estimate is relatively high may be due to conducive rainfall and other environmental conditions including the adaptability of barley landraces and crosses used. In characters with highest heritability, phenotypic is a good index of genotypic merit; so that genetic gain can be made easily through selection (Johnson and Frey, 1967).

Phenotypic and Genotypic coefficients of variation across years were relatively high for kernel weight per spike and moderate for spikelets per spike grain, kernels per spike, thousand kernels weight and spike length (Table 4). In addition to this, these characters were accompanied by high heritability (Table 3) expressing the presence of more additive gene effects for possible improvement. Grain yield per hectare, heading time, plant height and greenness of flag leaf showed the least variable traits, but also with high heritability, especially plant height (99.92) and heading time (91.28). Generally, the differences between phenotypic and genotypic coefficients of variability for all the corresponding characters was small indicating that these characters except grain yield and greenness of flag leaf, were less influenced by the environment. Most of the research reports on major crop species indicate that genetic variability of important agronomic traits is predominantly additive genetic variance, while the non-additive genetic variance is generally smaller than the additive genetic variance (Moll and Stuber, 1974, Jalata et al. 2011). Genotypic

coefficient of variability estimate gives good implication for genetic potential in crop improvement through selection (Johnson et al., 1955). For all characters measured, PCV value was greater than GCV. The result of genotypic and phenotypic coefficients of variation obtained suggests that there is a good scope for yield improvement through phenotypic selection for all traits studied. In other reports, Singh et al. (1986) found small PCV for days to maturity. Progress from selection depends on genetic variability existing in the population and selection is more effective when the genetic variation in relation to environmental variation is high (Al-lard, 1960; Poehlman and Sleeper, 1995). The genetic effects are not independent of non-genetic effects (Moll and Stuber, 1974) in crop improvement. In this study, comparably the contribution of non-genetic factors was small for important quantitative traits such as grain yield per hectare, thousand kernel weight and number of kernels per spike.

Estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic traits. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action. Genetic advance (GA), especially genetic advance as percent of means (GAM) was relatively high for kernel weight per spike (39.45%), number of spikelets per spike (28.77%), number of kernels per spike (28.45), spike length (26.23%), thousand kernel weight (21.06%), plant height (16.60%) and heading time (13.33%) and this was coupled with high heritability (Table 2).

According to Johnson et al. (1955), characters with high heritability accompanied with high genetic advance also result in better genetic gain through selection as high heritability will not always be associated with high genetic advance (Amin et al., 1992). Beside this, high heritability coupled with high genetic coefficient of variation estimates also gives a reliable estimate of the amount of genetic advance through phenotypic selection (Burton, 1952) which indicates the effectiveness with which selection of genotypes can be based on phenotypic performance (Johnson et al., 1955).

Genotypic relationship among traits affecting grain yield elucidate true association as they exclude the environmental influences. Grain yield showed significant positive genotypic correlation with spike length, number of spikelets per spike, number of kernels per spike and kernel weight per spike in both seasons. The genes controlling these characters may be linked that is, positioned closely together on the same chromosome or being controlled by pleiotropic gene. Therefore, selection for these traits could be used to indirectly select for grain yield (Jalata et al. 2011).

The phenotypic correlation coefficients were generally lower than genotypic correlation coefficients. The low phenotypic correlation could arise due to the modifying effect of environment on the association character at genetic level. Spike length, number of spikelets per

spike, number of kernels per spike and kernel weight per spike showed significant positive phenotypic correlations with grain yield in both seasons, while heading time showed significant positive correlation coefficient with grain yield only in the second season. Thus suggest that those characters that showed positive phenotypic correlation with grain yield would be of major use in direct selection for grain yield, since selection is usually based on phenotypic expression of traits.

The significant genotypic and phenotypic correlations between grain yield and spike length, number of spikelets per spike, number of kernels per spike and kernel weight per spike in both seasons may be related to proper spike weight provided by greater spike provided by more spikelets, kernels and kernel weight.

Characters that are genotypically correlated but not phenotypically correlated will not be of practical value in selection since selection is often based on the phenotypic performance of the characters (Alake et al. 2012). This is true of the relationship between grain yield and plant height and greenness of flag leaf in the second season. The insignificant association between grain yield and plant height and greenness of flag leaf in first season indicated that yield improvement through direct selection of plant height and greenness of flag leaf as a single character would be impractical. In similar study, Akinci and Yildirim (2009) reported that, despite some significant correlations between grain yield and other traits in the first and second selection years, yield was not significantly correlated with any traits in the last two selection years.

This result demonstrates that there exists variability among barley genotypes tested for important quantitative traits indicating high potential for effective crop improvement. The maximum yield was obtained from the advanced lines A71-1 (4091.8 kg ha<sup>-1</sup>) and A74-1 (3926.1 kg ha<sup>-1</sup>) which were developed through crossing of *H. vulgare* v. nudum with Bülbul 89 and Karatay 94 cultivars, respectively, which is encouraging and showed the possibility of improvement of landraces through crossing. High heritability values obtained for most of quantitative traits in this study indicate the presence of high yielding condition during testing.

In general, the study revealed that direct selection scheme would be more promising and encouraging than indirect selection for improving yield. This could be the nature of landraces because of their better adaptive traits to variable environmental conditions which have important implications for sustainable crop production.

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