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Variability, Heritability and Genetic Advance for Some Yield and Yield Related Traits in Ethiopian Barley (*Hordeum vulgare* L.) Landraces and Crosses

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ABSTRACT

The aim of this study was to find out variability, heritability and genetic advance for some yield and yield related traits in Ethiopian Barley. Thirty six barley landraces and crosses were tested at three locations in Bale highlands of Southeast of Ethiopia in 6×6 simple lattice design with two replications during 2006 Bona (July-December) cropping season. Variances component method was used to estimate variability, broad sense heritability and genetic advance of yield and some yield related characters. Statistically, significant ($p < 0.01$) variation was observed among materials tested for important quantitative traits across locations indicating the presence of variability. In addition, Genotypic Coefficient of Variability (GCV) and Phenotypic Coefficient of Variability (PCV) was relatively higher for grain yield per plot (20.13, 23.27%), number of kernels per spike (18.30, 20.70%) and spike weight (11.80, 15.20%), respectively, across locations. And relatively high heritability was obtained for spike length (0.868) followed by thousand kernel weight (0.856), number of kernels per spike (0.785), grain yield per plot (0.714) across locations showing better condition for effective selection in these characters. This implies the presence of more additive gene effects for potential crop improvement. Beside this, high genetic advance was observed for spike length, number of kernels per spike and thousand-kernel weight. These indicate that there is good scope for crop improvement through selection. This study revealed that greater yield response could be obtained through direct selection scheme in barley landraces and crosses tested. This may be the nature of landraces with better adaptive traits to variable environmental factors which has paramount importance for the local farmers to reduce risk.

Key words: Barley (*Hordeum vulgare* L.) landraces, variability, heritability, selection, quantitative characters

INTRODUCTION

Barley (*Hordeum vulgare* L.) belongs to the genus *Hordeum*, in tribe Triticeae of the family Poaceae (Gramineae) (Von Bothmer *et al.*, 1995; Kling and Hayes, 2004). Ethiopia is considered as center of diversity for food barley crop (Firdissa *et al.*, 2010). It is one of the major cereal crop produced on about 1.1 million hectares producing annual production of 1.3 million tons (CSA, 2005). Lack of improved varieties, disease, insect, pest problem, weed competition and poor

soil fertility has been indicated as major constraints in barley improvement (Birhane *et al.*, 1996). The presence of long history of cultivation of barley crop, wide ecological and cultural diversity in Ethiopia has resulted in a large number of landraces which can adapt to various environmental conditions (Asfaw, 2000).

Creation of genetic variability and selection for important traits is crucial activities that any plant breeder should apply to achieve better yield and other desirable agronomic traits. However, to carry out effective selection, the information on available genetic variation among barley genotypes, the nature of component traits on which selection would be effective and the influence of environmental factors on each trait need to be known. There is no literature available in this regard in the study area where barley is the second major food crop and farmers commonly use their landraces. Thus, effective selection not only depends on estimation of genetic variation among genotypes but also on the proportion of heritable variation and the expected genetic gain that would be obtained. 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 (Falconer and Mackay, 1996; Singh, 2000). Heritable variation is useful for permanent genetic improvement (Singh, 2000). A major factor limiting the rate of progress in plant breeding has been low heritability of quantitative traits such as yield. Heritability in broad sense estimates the ratio of total genetic variance, including additive, dominance and epistatic variance to the phenotypic variance (Falconer and Mackay, 1996; Raiz and Chowdhry, 2003). The most important function of the heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Falconer and Mackay, 1996; Dabholkar, 1992). 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 to decide 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 (Poehlman and Sleper, 1995). The magnitude of components of variances has been obtained from analysis of variance to estimate the different genetic parameters as described by Burton and de vane (1953), Dabholkar (1992), Falconer and Mackay (1996) and Singh (2000). Variability studies have been reported by Alemayehu, (2005) on Ethiopian landraces and Jaradat *et al.* (2004) for thousand kernel weight (0.769) and spike length (0.782) in barley population. On the other hand, heritability estimates were also reported in barley by Singh and Ceccarelli (1995) and Vimal and Vishwakarma (1998).

Landraces represent over 90% of the barley cultivated in Ethiopia (Tanto *et al.*, 2010). Ethiopian barley landraces are reported to have better adaptation and useful traits like vigorous seedling establishment, high tillering capacity, quick grain filling period, high seed weight and resistance to shoot fly, aphids and frost (Birhane *et al.*, 1996; Hailu *et al.*, 1996). As grain yield is a complex product of many yield components and has low heritability, direct selection for yield may not be sufficiently effective (Singh, 2000; Raiz and Chowdhry, 2003). However, to design an effective selection strategy for the utilization of the existing breeding materials, the knowledge on the extent of variation, heritability of the trait and genetic gain is important. Therefore, this study was conducted with the following objectives:

- To estimate the extent of genetic variability, heritability and expected genetic advance existing in this barley landraces and crosses
- To suggest an effective or better selection scheme that could be useful in barley landrace improvement program

MATERIALS AND METHODS

Breeding materials and testing sites: Thirty six advanced barley landraces and crosses were planted in Bale highlands at Agarfa, Robe and Sinana locations in the southeast of Ethiopia during 2006 Bona (August-December) cropping season. Seven of these barley lines were developed from local crossing, whereas, the other materials were landraces developed in barley landrace enhancement programs (Table 1). These evaluation sites are characterized by bimodal rainfall with two cropping seasons; the *Bona* season extends from August to December; and the Ganna season extends from March to July. The average rainfall of Bona ranges from 270-560 mm and that of

Table 1: Description of breeding materials used in the experiment

Genotype/cross name	Row type	Collection site	Altitude (m.a.s.l)
Acc. 3852-1 (Sn01B)	Two	Semen Omo	2200
Acc.1796-1 (Sn01B)	Two	Jimma	2010
Acc.3840-1 (Sn01B)	Two	North Omo	2180
Acc.3842-1 (Sn01B)	Two	North Omo	2000
Acc.3836-1 (Sn01B)	Two	North Omo	2235
Acc.1695-1 (Sn01B)	Irregular	Arsi	2400
Aruso/HB42 SNR FBC 99B 0003-9	Irregular	*	
Aruso/HB42 SNR FBC 99B 0003-10	Irregular	*	
Acc.1718-15	Irregular	Arsi	2600
Acc.1742-16	Irregular	West Shoa	2670
Acc.3283-16	Irregular	Bale	2410
Acc.3285-12	Irregular	Bale	2480
Acc.1694-5	Irregular	Arsi	2430
Acc.1775-13	Irregular	West Shoa	2460
Acc.1721-4	Irregular	Arsi	2550
Acc.3694-7	Irregular	North Gondar	2370
Acc.3936-3	Irregular	NA	
Acc.1611-16	Irregular	East Welega	2500
Acc.3234-19	Irregular	North Gondar	2510
Acc.1775-22	Irregular	West Shoa	2460
Acc.3554-6	Irregular	Metekel	2310
PGRC/E 230591-23	Irregular	Bale	2400
Acc.3296-11	Irregular	Bale	2450
Shasho # 22 Go-1 (sn98B)	Six	Bale	2000
Aruso /EH/956 F2 8H-6-4 SNR FBC 99G 0003-10	Six	*	
Acc.3260-18	Six	Bale	2430
Aruso EH/956 F2 8H-6-4 SNR FBC 99G 0003-12	Six	*	
Aruso EH/956 F2 8H-6-4 SNR FBC 99G 0003-13	Six	*	
Acc.3260-3	Six	Bale	2430
Acc.3261-10	Six	Bale	2385
Aruso EH/956 F2 8H-6-4 SNR FBC 99G 0003-19	Six	*	
Aruso EH/956 F2 8H-6-4 SNR FBC 99G 0003-21	Six	*	
PGRC/E 235647-20	Six	South Omo	1810
PGRC/E 235648-23	Six	South Omo	2000
Acc.3947-1	Six	West Hararghe	2310
Acc.3709-9	Six	NA	

NA: Not available, m.a.s.l: Meter above sea level, *: Line obtained from crossing in barley breeding program at sinana agricultural research center

Ganna ranges from 250-560 mm. Agarfa is located at 460 km in the south east of Addis Ababa which is 38° 40' to 46° 3' E longitude and 4° to 8° 11' N latitude with the altitude of 2350 meters above sea level (m.a.s.l). The annual temperature ranges from a minimum of 5.5 to 8.7°C to a maximum of 17.5 to 32°C. In addition, the mean annual rainfall varies from 800 to 1000 mm and the soil type is Cambisol. On the other hand, Sinana is located at 07° 07'N latitude and 40° 10'E latitude (Geremew *et al.*, 1998) with 2400 m.a.s.l and 463 km from Addis Ababa. Average annual minimum and maximum temperature of Sinana is 9 and 21°C, respectively and the soil is with light clay type. Robe site is situated nearest to Robe (main town) which have somewhat similar climatic, topographic and edaphic conditions with Sinana.

Experimental design and agronomic practices: Barley seeds were planted in 3 m² plot area of six rows with 20 cm spacing between rows and of 2.5 m length in 6×6 simple lattice design with two replications at each location during 2006 Bona season. Recommended rate of 125 kg ha⁻¹ barley seeds and 50 kg ha⁻¹ DAP (Di-Ammonium Phosphate) fertilizer was used. Planting was conducted in mid August 2006 during Bona rainy season. Data was collected from the central four rows. The normal crop management and cultural practices were carried out uniformly at all locations.

Data collection and statistical analysis: Data was recorded on eighteen characters on plot and plant basis, however, test of homogeneity of error variance showed that the error mean squares were homogeneous only for the following eight characters such as number of spikelets per spike, spike length, spike weight, number of kernels per spike, biomass yield per plant, days to maturity, thousand kernel-weight and grain yield per plot 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 MSTATC (Freed *et al.*, 1988). Since the relative efficiency of lattice design was very similar with randomized complete block (RCB) design so that for the flexibility of lattice design (Cochran and Cox, 1957) data were analyzed as per RCB design.

The phenotypic (δ^2_p) and genotypic (δ^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:

Table 2: Combined analysis of variance, heritability and genetic advance (GA) for number of spikelets per spike (NSPK), spike length (SPL), spike weight (SPW), number of kernels per spike (NK), biomass yield per plant (BM/pl), days to maturity (DM), thousand kernel weight (TKW) and grain yield per plot (GY/P) studied in barley landraces and crosses across locations (Sinana, Robe and Agarfa) in Bale during 2006 Bona cropping season

Sources of variation	Mean squares							
	NSPK	SPL	SPW	NK	BM/pl	DM	TKW	GY/P
Genotype	1.67**	7.32**	2.23**	4.10**	4.66 **	1.86**	6.96**	3.74**
Genotype x environment	10.12*	0.63ns	0.13ns	62.67**	6.75ns	6.19ns	9.06**	0.21**
Error	6.48	0.49	0.1	28.28	7.44	5.02	3.42	3.73
CV (%)	12.94	9.74	21.25	15.83	16.98	2.07	6.21	19.00
SE(+)	2.55	0.35	0.07	5.32	5.26	3.55	1.85	1.93
Heritability	0.401	0.868	0.6	0.785	0.413	0.461	0.856	0.714
GA	1.4	15.59	0.27	11.27	3.03	1.32	5.71	0.54

*,**Significance test at 0.05 and 0.01 level, respectively, ns: Non significant, CV: Coefficient of variation, SE: Standard error

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

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

$$GA = K * \sigma_p^2 * h^2$$

where, K is the standardized selection differential at 5% selection intensity (K = 2.063).

RESULTS

Combined analysis of variance across locations showed that there was significant ($p < 0.01$) variation among barley landraces and crosses tested for all characters considered. On the other hand, genotype x environment interaction revealed significant ($p < 0.01$) difference only for grain yield per plot, thousand kernel weight and number of kernels per spike (Table 2). Overall mean grain yield for genotypes ranged from 1.1 to 2.6 t ha⁻¹ (data not shown). Aruso/EH/956 F₂ 8H-6-4 SNR FBC 99G 0003-21 advanced line which was obtained from crossing gave the highest mean grain yield (2.6 t ha⁻¹), whereas, Aruso/HB42 SNR FBC 99B 0003-9 and Acc.1718-15 barley lines gave the lowest mean grain yield per (1.1 t ha⁻¹). When the different rowed types were compared, the six and two rowed types showed different response for some characters such that six rowed barleys tended to produce higher mean grain yield per plot, grain yield per plant, number of kernels per plant and spike weight. As opposed to this, lowest mean values were recorded for thousand kernel weight and spike length in six rowed barleys. Whereas, two rowed barleys tended to give highest values for thousand kernel weight and spike length but low values were obtained for number of kernels per plant and spike weight (data not shown).

Phenotypic Coefficient of Variability (PCV) and Genotypic Coefficient of Variation (GCV) across locations was relatively high for grain yield per plot (23.27, 19.50%), number of kernels per spike (20.70, 18.30%), biomass yield per plant (22.10, 14.20%) and spike weight (15.20, 11.80%) (Table 3), respectively. On the other hand, days to maturity showed very minimum GCV (0.90%) and PCV (1.30%) values across locations.

Table 3: Estimates of genotypic, phenotypic, and environmental coefficient of variability for number of spikelets per spike (NSPK), spike length (SPL), spike weight (SPW), number of kernels per spike (NK), biomass yield per plant (BM/pl), days to maturity (DM), thousand kernel weight (TKW) and grain yield per plot (GY/P) studied in barley landraces and crosses at Sinana, Robe, Agarfa and across locations in 2006 Bona cropping season

Characters	Sinana			Robe			Agarfa			Across location	
	GCV	PCV	ECV	GCV	PCV	ECV	GCV	PCV	ECV	GCV	PCV
NSPK	10.36	15.28	11.24	10.27	15.74	11.93	6.89	14.55	12.81	5.40	8.5
SPL	11.61	16.47	11.69	11.64	14.25	8.23	17.60	19.71	8.86	11.30	12.1
SPW	19.8	44.28	39.60	20.47	25.31	15.12	12.63	17.87	12.63	11.80	15.2
NK	20.17	29.79	21.92	20.34	23.82	12.38	21.22	25.70	14.50	18.30	20.7
BM/pl	15.6	23.30	17.40	15.5	22.60	16.40	8.90	15.20	12.40	14.20	22.1
DM	1.06	3.16	2.97	1.06	1.87	1.54	1.22	1.82	1.35	0.90	1.3
TKW	12.86	14.76	7.23	12.29	13.37	5.26	10.80	12.70	6.80	10.00	10.8
GY/P	31.31	38.35	21.78	30.93	56.47	20.62	15.20	20.96	14.42	20.13	23.27

GCV: Genotypic coefficient of variability (%), PCV: Phenotypic coefficient of variability (%) and ECV: environmental coefficient of variability

Broad sense heritability and expected genetic advance (at 5% selection intensity) was estimated across locations for all agronomic traits considered (Table 2). Therefore, for pooled analysis, heritability ranged from 0.401 to 0.868. It was high for spike length (0.868) which was followed by thousand kernel weight (0.856), number of kernels per spike (0.785), grain yield per plot (0.714), spike weight (0.600), days to maturity (0.461), biomass yield per plant (0.413) and number of spikelets per spike (0.401).

Genetic Advance (GA) was relatively high for spike length (15.59) and number of kernels per spike (11.27) and thousand kernel weight (5.71) and this was coupled with high heritability (Table 2).

DISCUSSION

Ethiopian 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 landraces and crosses 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 grain yield per plot, thousand kernel weight and number of kernels per spike (Table 2) indicating barley genotype and crosses showed inconsistent performances across locations 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 six and two rowed types may be considered during selection. The maximum yield was obtained from the advanced line, Aruso/EH/956 F₂ 8H-6-4 SNR FBC 99G 0003-21 (2.6 t ha⁻¹) which was developed through crossing with Aruso (local) in landrace enhancement program. This indicates the requirement of crossing program with landraces as one option to improve barley yield.

Phenotypic Coefficient of Variability (PCV) and Genotypic Coefficient of Variation (GCV) across locations was relatively high for grain yield per plot, number of kernels per spike, biomass yield per plant and spike weight (Table 3). In addition to this, these characters were accompanied by high heritability (Table 2) expressing the presence of more additive gene effects for possible improvement. Days to maturity showed the least variable trait. Generally, the differences between phenotypic and genotypic coefficient of variability for all the corresponding characters was small indicating that these characters 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). 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 grain yield per plot, number of kernels per spike, spike weight and biomass yield per plant. 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 (Allard, 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 plot, thousand kernel weight and number of kernels per spike.

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_6 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) reported higher heritability for spike length, grain yield and number of spikelets per spike. Low heritability was reported by Ceccarelli (1994), 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).

Genetic advance (GA) was relatively high for spike length (15.59) and number of kernels per spike (11.27) and thousand kernel weight (5.71) 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).

CONCLUSION

This result demonstrates that there exist variability among barley landraces and crosses tested for important quantitative traits indicating high potential for effective crop improvement and/or for further manipulation of the genetic resources through breeding as Ethiopian landraces are good sources of genes for many desirable traits. The advanced line, Aruso/EH/956 F_2 8H-6-4 SNR FBC 99G 0003-21 which was obtained from barley crossing gave highest grain yield (2.6 t ha⁻¹) 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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