International Journal of Science and Research (IJSR)
ISSN (Online): 2319-7064

Genetic Variability in Barley (*Hordeum vulgare* (L.)) Landrace Collections from Southern Ethiopia

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Abstract: ***Landraces are the major genetic resources of cultivated barley in Ethiopia. Two hundred seven accession and 18 released varieties were laid out in 15by15 simple lattice design and were planted in 2008 main cropping season at Kokate. The objectives of the study were to conduct the morphological characterization and to determine the nature and degree of variability in morpho- agronomic traits of the barley landrace collections from southern Ethiopia. A plot size of two rows each 2.5m long and spaced 0.2m apart was used. Analysis of variance showed highly significant differences among the tested genotypes for all traits considered in the study, indicating the presence of genetic variability in the traits and a wide range was observed in the morpho-agronomic traits. Grain yield varied between 436 and 375.5 kg/ ha, plant height from 44.95 to 94.1 cm, days to maturity between 92 and 131, and days to heading between 57 and 94. Twelve genotypes out yielded the best released variety, Dafo. These can be released as new varieties or can be used in crosses for further breeding work. Phenotypic coefficient of variation ranged from 8.77 for days to maturity to 63.49 for susceptibility to lodging, while genotypic coefficient of variation ranged from 7.98 to 60.03, for the same traits. High heritability and high genetic advance as the percent of the mean were observed for susceptibility to lodging, flag leaf width, spikelets per spike and grain yield per plant. Relatively rapid progress can be achieved in these traits through selection. The clustering of genotypes based on 10 quantitative traits revealed existence of divergence among genotypes. Ten distinct clusters of different sizes were formed.***

Keywords: Hordeum vulgare, Landrace, Variability, Clustering Morpho-agronomic characters

1. Introduction

Barley is one of the most important traditional crops and landraces form is the major genetic resources of cultivated barley in Ethiopia (Lakew and Assefa, 2011). It occupies about 948,107.0 hectares of land with total production of 1,585,286.9 tones (CSA, 2011). This gives a productivity of about 1.67 tonnes / ha almost half of the world productivity. It is used in many traditional foods and making local beverages. The straw is good for animal feed during the dry season and it is also a useful material for thatching roofs of houses and for use as bedding (Kersie and Goitom, 1996; Bekele *et al*., 2005). Barley breakfast foods and snacks are increasingly made available, driven by recent findings, which show that barley fiber contains beta- glucans and tocotrinols, chemical agents known to lower serum cholesterol levels (Burger *et al.,* 1981; Anderson *et al.,* 1991; Asfaw, 2000).

The long history of barley cultivation and the diverse agro-ecological zones and the diverse cultural practices have resulted in a country renowned for its large number of farmers' varieties (landraces) and traditional agricultural practices (Bekele *et al*., 2005). The existence of genetic diversity has special significance for the maintenance and enhancement of productivity in agricultural crops in a country like Ethiopia, which is characterized by highly varied agro-climates and diverse growing conditions (Worede, 1993; Worede *et al.*, 2000; Brush 2000).

Landraces are still the backbone of agricultural systems in many developing countries, mainly in marginal environments and are characterized by high genetic heterogeneity, good adaptation to local environment conditions and by low productivity (Ceccarelli and Grando, 1996).These landraces have developed abundant patterns of variation and would represent a largely untapped reservoir of useful genes for adaptation to biotic and abiotic stresses (Nevo, 1992; Brush, 1995). Therefore, characterization of landraces and knowledge on the pattern of variation for important morpho-agronomic traits is needed for a proper management and a better exploitation of this gene pool (Jain *et al*., 1975; Assefa, 2003).

According to Asfaw (2000), there exists at a higher level of barley diversity in southern Ethiopia but this was not well studied and documented. Landraces need to be evaluated, characterized and properly documented so that well defined sets of samples with specific combinations of desirable traits can easily be retrieved and used in breeding programs (Gebrekidan, 1982). In this regard, a considerable number of characterization and diversity studies have been conducted and documented on barley landrace collections from northern and central Ethiopia barley (Asfaw, 1988, 1989; Demissie, 1996; Fassil *et al*., 2001; Assefa, 2003; Abay *et al.*, 2009; Tanto *et al.,* 2009; Assefa *et al., 2010*). However, barley collections from southern Ethiopia have not been extensively studied and characterized and the diversity within this material is not known. Hence, this work was done with the objectives to conduct the morphological characterization and to determine the extent and nature of variability in morpho- agronomic traits of the barley landrace collections of southern Ethiopia.

2. Materials and Methods

2.1 Description of the Experimental Area

The experiment was conducted at Kokate sub center located in Soddo Zuria Woreda of Wolaita Zone. Kokate is located at the coordinates of 6^0 52'43. 9''N and 37^0 48'22.1''E. and has an elevation of 2161 meters above sea level. The ten years (1999- 2008) mean annual rainfall of the area is 1352.11 mm. The ten years (1999- 2008) mean minimum

and maximum annual temperatures are 14.5^{0}c and 25.3^{0}c, respectively. The soils of the site are classified as dystric Nitosols (EMA, 1988), which are formed from basaltic parent materials. The soils are highly weathered, well drained, deep, highly leached and acidic with low organic carbon, nitrogen and phosphorus content (Kelsa *et al*., 1996). The pH of the soil is 5.1 to 5.6 (strong to moderately acidic); CEC is 24.1 to 26.65 cmol (+) / kg soil (medium to high); organic matter content is 0.764 to 3.47 % (very low to medium) and total N ranges from 0.056 to 0.182 % (low to medium) (Esayas and Ali, 2006).

2.2 Genotypes Studied

The materials for this study consisted of a total of 225 genotypes of which 207 are landraces (accessions) collected from various agro-ecological zones in southern Ethiopia and 18 released varieties. The landraces were collected and maintained by Awassa Agricultural Research Center. The original samples were collected from farmers' stock and village markets.

2.3 Experimental Design and Cultural Practices

The 207 accessions and 18 released varieties were laid out in 15 by 15 simple lattice design and were planted in 2008 main cropping season at Kokate. The lay out and randomization of the materials were carried out based on the standard procedures suggested by Cochran and Cox (1957). A plot size of two rows each 2.5m long and spaced 0.2m apart was used. The spacing between plots and blocks was 0.4m and 1m, respectively. At planting the seeds were drilled in rows at the rate of 85 kg per hectare. Nitrogen and phosphorous fertilizers were applied at the rate of 78.56 kg/ha Urea and 54.76 kg/ ha DAP at planting. To control broad leaf weeds the herbicide 2, 4-D, was applied four weeks after planting at the rate of 1 liter per 200 liter of water per hectare followed by two hand weedings.

2.4 Data Collected

Data were taken according to the International Plant Genetic Resources Institute descriptor for barley (IPGRI, 1994). Eleven quantitative data (five plant based and six plot based) were recorded by measuring or weighing. Ten plants (spikes) were selected randomly at heading (five plants from each row) and tagged with thread and all the necessary plant-based quantitative data were collected from these plants. Plant-based data included flag leaf width, plant height, number of spiklets per spike, head (spike) length and yield per plant. Flag leaf width was recorded at dough stage (Sarkar, *et al*., 2002) and visual evaluation was made at the place where leaf width was maximum (1 narrow leaves, 2 intermediate and 3 broad leaf). All other data were recorded at harvest (plant height, number of spiklets per spike and head length of the main stem). Yield per plant was taken from 10 heads (randomly selected and averaged).

Those data collected on plot basis were: days to heading, and maturity, susceptibility to lodging, thousand seed weight, scald susceptibility and grain yield per plot. Days to heading (days from sowing to the day when at least 50% of the heads are fully exerted from the boot), days to maturity (days from sowing to the day when 95% of the heads have matured), susceptibility to lodging (visually assessed on 0-9 scale, where 0 indicates no lodged plants, subsequent scales describing increasing lodging and 9 very highly lodged).For thousand seed weight, 500 barley grains were counted and weighed then multiplied by two to obtain thousand seed weight; scald **(***Rhynchosporium secalis* (Oud.) J.) **s**usceptibility was visually assessed on 0-9 scale (where 0 indicates absence of visible scald lesions, scale 1 a few isolated lesions on lowest leaves only, and the subsequent scales describe increasing scald severities ending with scale 9 for very severe infection all over the plants). Yield per plot was taken from the two rows and moisture was adjusted to 12.5%. While the yield for 10 randomly sampled plants were taken at harvested per plot.

2.5 Statistical analysis

2.5.1 Analysis of Variance (ANOVA) and Estimation of Variability Parameters

ANOVA of the tested genotypes was conducted both for the simple lattice and randomized complete block design (RCBD) for the quantitative data. For the estimation of variance components of the various sources of variation, RCBD ANOVA was used (Table 1). The SAS computer software (SAS, 1994) was employed for the analysis of variance to estimate the variance components, phenotypic coefficients of variation (PCV) , genotypic coefficients of variation (GCV), heritability and genetic advance. Variance components were computed only for traits where significant difference existed between the accessions. The released varieties were removed for this analysis.

Table 1: Form of analysis of variance of table for each quantitative character

Source of variation	*Df*	*MS*	*EMS‡*
Replication	r-1	MSr	
Accessions	a-1	MSa	$\sigma^2_e + r\sigma^2_g$
Error	(r-1) (a-1)	MSe	σ^2_e

Genotypic variance ($\sigma^2 g$) = (MSa – Mse)/r; ‡EMS – Expected Mean Square; Error variance (MSe) = $\sigma^2 e$;
Where r = number of replications; a = number of accessions; MSr = mean square of replication; MSa = mean square of accessions; MSe =mean square of error; $\sigma^2 g$ = genotypic variance; $\sigma^2 e$ = error variance; $\sigma^2 p$= phenotypic variance= $\sigma^2 g + \sigma^2 e / r$

2.5.2 Phenotypic and Genotypic Coefficients of Variation

Phenotypic (PCV) and genotypic coefficients of variations (GCV) were estimated according to Burton (1951) as

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

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

Where $\bar{X}$ = mean value of the trait;

$\sigma^2 p$ = phenotypic variance of the character; $\sigma^2 g$ = genotypic variance of the character; PCV= Phenotypic coefficient of variation; GCV= Genotypic coefficient of variation

Heritability in broad sense (H^2): was calculated according to Allard (1960) as:

$$H^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

2.5.3 Clustering

Cluster analysis is a numerical classification technique that defines groups of clusters of individuals. Quantitative characters were subjected to cluster analysis so as to determine the similarity among the accessions. Clustering was done using proc cluster of SAS and the average linkage option was used. Genetic distance between clusters was calculated using the generalized Mahalanobis's D^2 statistics. The D^2 is defined as:

$D^2ij = (\overline{X}\,i - \overline{X}\,j)^1 (\overline{X}\,i - \overline{X}\,j)$

Where D^2ij =the distance between any two groups i and j; $\overline{X}\,i$ and $\overline{X}\,j$ the vector mean of the traits for the i^{th} and j^{th} groups respectively.

3. Results and Discussion

3.1 Analysis of Variance

Since the efficiency of lattice over RCBD was not very high (Table not shown), it was decided to partition various source of variation following RCBD ANOVA; moreover estimation of variance components is easier in RCBD. Analysis of variance indicated that there were very highly significant differences (P<0.001) among the genotypes for all traits (Table 2), indicating the presence of genetic variability in the characters studied. Similarly, previous studies on collections of barley landraces from other regions indicated that significant variations existed for many of these traits like plant height, days to heading, thousand grain weight and scald severity (Alemayehu and Parlevliet, 1997) and for days to maturity, spike length, seeds per spike, heads per square meter and grain yield per spike (Assefa, 2003). Lakew *et al*. (1997) also reported large amount of variation between populations for days to heading, maturity and plant height.

Table 2: Analysis of variance for 11 quantitative traits of 225 barley genotypes grown at Kokate in 2008

Mean square	*Source of Variation*			
	Replication	*Genotype*	*Error*	*CV%*
DF	1	224	224	
DH	3.380	120.483***	21.353	6.15
DM	10.276	95.67***	33.584	5.14
LOD	0.320	1.501***	0.159	29.25
TSWT	154.645***	48. 298***	15.381	9.64
SCALD	19.220***	1.154***	0.698	43.55
FLW	6.242	0.435***	0.144	18.89
PLH	882.560***	172.102***	65.309	10.63
SGS	94.302***	16.628***	3.937	14.15
HL	0.987	1.936***	0.798	10.93
YGPP	0.181	0.112***	0.052	19.25
YKPH	1408.04	701040.0***	79234.6	17.78

*** =Significant at 0.1%; CV % = coefficient of variation; DH=days to heading; DM= days to maturity; LOD susceptibility to lodging; TSWT= thousand seed weight (gm); SCALD= susceptibility to scald; YKPH= yield kg/h; FLW=flag leaf width; PLH= plant height (cm); SGS= number of spikelet groups per spike; HL= head length (cm); YGPP=yield gram per plant; YKPH= yield kilogram per hectare.

3.2 Estimation of Variability Parameters

3.2.1 Range and Means

A wide range of values were observed in morpho-agronomic traits of the studied barley genotypes (Table 3). Grain yield exhibited the widest range (436 –3752.5 kg/ ha) followed by plant height (44.95 – 94.1 cm), days to maturity (92 – 131) and heading (57 – 94). Similarly, Alemayehu and Parlevliet, (1997) reported 62- 97 days and 70.5- 112.2 cm for heading and plant height, respectively. Lakew *et al* (1997), also reported a wide range of variation for days to heading (96-116), maturity (137-174), plant height (80 - 140 cm) and grain yield (4202- 5705 kg/ha) while the experiment was conducted at Sheno. In this study, the genotypes had broad range of maturity period. The early maturing genotypes reached physiological maturity in 92 days while the late maturing accessions took 131 days to mature**.**

Table 3: The observed variation in morpho-agronomic characters

Character	*Range (min to max)*	*Range unit*
Days to heading	57 – 94	37.0
Days to maturity	92 – 131	39.0
Lodging 0-9 scale	1 - 7	6.0
Thousand seed weight(g)	30 - 52.5	22.5
Scald 0-9 scale	1- 5	4.0
Flag leaf width	1 – 2.95	1.95
Plant height (cm)	44.95 – 94.10	49.15
Spikelet per spike	10 – 42	34
Head length (cm)	4.85 - 10.25	5.4
Yield gram per plant (g)	0.62 - 2.2	1.58
Yield kg/ha	436 – 3752.5	3316.5

3.2.2 Phenotypic and Genotypic Variations

Estimates of phenotypic and genotypic coefficients of variations , broad sense heritability (H^2), genetic advance in original units (GA) and percent of the mean (GAM %) for the present study are shown in Table 4a and b. Phenotypic and genotypic coefficient of variation varied between 8.77-63.49 and 7.98 - 60.03, respectively. The lowest PCV and GCV (8.77 and 7.98), respectively were obtained for days to maturity while the highest PCV and GCV values (63.49 and 60.03), respectively were obtained for susceptibility to lodging, respectively. For most of the traits studied, phenotypic coefficient of variation was slightly higher than the corresponding genotypic coefficient of variation. The relative narrow gap between the corresponding PCV and GCV values for all traits indicated small environmental effects on these parameters. PCV and GCV values of roughly more than 20% are considered to be high, and values less than 10% low and values in between as medium (Deshmukh *et al*., 1986). Accordingly, susceptibility to lodging and susceptibility to scald had high PCV values.

In this study susceptibility to lodging and scald had a high PCV and GCV values but flag leaf width, spikletes per spike, days to heading, head length, thousand seed weight, plant height and yield per plant displayed moderate values of PCV

whereas days to maturity had the lowest PCV value (Table 4a). Susceptibility to lodging and scald had the highest value and yield per plant, spikelet per spike and flag leaf width exhibited moderate GCV values, but days to heading and maturity, head length, plant height, and thousand seed weight showed lowest GCV value. This is in agreement with the finding of Assefa (2003) who reported lowest GCV values for days to heading, maturity, plant height and the highest GCV values of 17.91 and 20.5 at two locations, Keyit and Sheno, respectively were recorded for grain yield per spike.

3.2.3 Estimates of Heritability and Expected Genetic Advance

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally helpful in predicting gain yield under selection than heritability estimates alone (Singh, 1993). In this study, broad sense heritability (H^2) estimate varied from 40% for susceptibility to scald to 89% for susceptibility to lodging (Table 4b). In the whole, susceptibility to lodging, days to heading and maturity, and spikelet per spike demonstrated high heritability estimates (>75%). Similarly, Assefa (2003) reported higher value of heritability for days to maturity, spike length and number of seeds per spike.

Heritability estimates is used in conjunction with selection differential (Rasmusson and Glass, 1967), and heritability is accompanied with a good level of GCV (Burton and De Vane, 1953) to predict advance from selection for testing program is essential.

Table 4a: Estimates of means, variance components, PCVand GCV for 10 traits of barley genotypes at Kokate, 2008

Traits	*Means ± SE*	$\sigma^2 g$	$\sigma^2 p$	*PCV (%)*	*GCV (%)*
DH	75.12 ± 4.62	49.57	60.24	10.33	9.37
DM	112.83± 5.8	81.04	97.84	8.77	7.98
LOD	1.36 ± 0.40	0.67	0.75	63.49	60.03
TSWT	40.67 ±3.92	16.46	24.15	12.08	9.98
SCALD	1.92 ±.0.84	0.23	0.58	39.61	24.90
FLW	2.01 ±0.38	0.15	0.22	23.25	19.03
PLH	76.03 ±8.08	53.39	86.05	12.20	9.61
SGS	14.02 ± 1.98	6.34	8.31	20.57	17.97
HL	8.17 ± 0.89	0.57	0.97	12.04	9.24
YGPP	1.19 ±0.22	0.03	0.06	19.94	14.57

SE= standard error; $\sigma^2 g$=genotypic variance $\sigma^2 p$= phenotypic variance; PCV **(%)**=phenotypic coefficient of variation; GCV **(%)** =genotypic coefficient of variation; H^2 =heritability; GA= genetic advance; GAM (%)=genetic advance as percentage of mean; DH=days to heading, DM= days to maturity; LOD= susceptibility to lodging; TSWT= thousand seed weight (gm); SCALD= susceptibility to scald; FLW=flag leaf width; PLH= plant height (cm); SGS= number of spikelet groups per spike; HL= head length (cm); YGPP=yield gram per plant

An estimate of genetic advance as percent of the mean is presented in Table 4b. It ranged from 14.59% for head length to 116.92% for susceptibility to lodging. Among the traits with relatively high heritability, only susceptibility to lodging, flag leaf width and spikelet per spike combined higher values of GCV and heritability. Accordingly, these three traits had higher values of genetic advance expressed as percentage of the mean with values of 116.92%, 32.34% and 32.09%, for susceptibility to lodging, spikelet per spike and flag leaf width, respectively. Assefa (2003) reported higher values of GCV combined with higher values of heritability which resulted in higher genetic advance as percentage of mean for seeds per spike (21.7%), spike length (21.7%), number of heads per square meter (30%), and grain yield per spike (30 %).

Table 4b: Estimates H^2, GA and GAM for 10 traits of barley genotypes at Kokate, 2008

Traits	H^2	*GA*	*GAM (%)*
DH	0.82	13.16	17.51
DM	0.83	16.88	14.96
LOD	0.89	1.60	116.92
TSWT	0.68	6.90	16.97
SCALD	0.40	0.62	32.25
FLW	0.67	0.64	32.09
PLH	0.62	11.86	15.60
SGS	0.76	4.53	32.34
HL	0.59	1.19	14.59
YGPP	0.53	0.26	21.92

DH=days to heading; DM= days to maturity; LOD= susceptibility to lodging; TSWT= thousand seed weight (gm); SCALD= susceptibility to scald; FLW=flag leaf width; PLH= plant height (cm); SGS= number of spikelet groups per spike; HL= head length (cm); YGPP=yield gram per plant; H^2 =heritability; GA= genetic advance; GAM (%) =genetic advance as percentage of mean.

In this study, traits such as susceptibility to lodging, flag leaf width, spiklete per spike and grain yield per plant coupled with relatively high values of GCV, heritability and genetic advance as percentage of mean, are the most important traits which can easily be improved by selection. According to Panse (1957) cited by Legesse (2007), higher heritability coupled with high genetic advance as percent of mean suggest that the traits are controlled by additive gene action. Therefore, this study indicated that the environment had less influence on susceptibility to lodging, flag leaf width, spikelet per spike, yield per plant and relatively rapid progress can be made in these traits through plant breeding.

3.2.4 Cluster Analysis Based on Quantitative Traits

The plot of the Pseudo-F against the number of clusters (SAS, 2000) suggests that about 10 clusters would be an appropriate classification for the 225 barley genotypes (207 accessions and 18 checks) (Fig. 1). The cluster grouping is given in Table 5 and the dendrogram is depicted on Fig. 2.

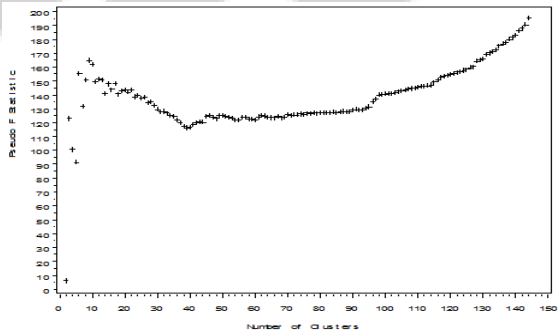

Figure 1: Plot of the Pseudo-F against the number of clusters

The majority of the genotypes (202 or 89.8%) were classified into the five clusters (56, 46, 34, 35 and 31 genotypes in clusters I, II, III, IV and V, respectively. Other clusters had from 1 up to 8 members. Clusters IX and X consisted of solitary genotypes, Entry 39 (Acc 30/2006) and Entry 95 (Accession 64/1/1/2006), respectively. The unique nature of accession 64/1/1/2006 that has five to eight small branched heads leads high number of spikelet groups per spike unlike other clusters.

Table 5: Pattern of clustering of 225 barley genotypes based on 10 quantitative traits grown at Kokate, 2008

Cluster	*N*	*Entries code*
I	56	7, 8, 10, 25, 30, 31, 43, 45, 46, 47, 50, 58, 60, 61, 64, 65, 66, 67, 68, 69, 70, 71, 73, 77, 78, 98, 105, 106, 108, 111, 112, 114, 115, 120, 122, 123, 125, 128, 129, 133, 134, 137, 140, 141, 143, 145, 148, 149, 150, 152, 157, 162, 186, 210, 212, 217
II	46	3, 33, 40, 41, 52, 54, 55, 56, 57, 72, 74, 75, 80, 82, 83, 89, 91, 92, 96, 97, 101, 102, 109, 110, 144, 146, 156, 159, 160, 169, 175, 180, 184, 187, 188, 197, 199, 202, 203, 205, 206, 208, 211, 221, 222, 225
III	34	26, 35, 79, 84, 85, 116, 161, 164, 165, 166, 168, 170, 171, 172, 173, 176, 177, 178, 179, 181, 182, 183, 189, 190, 191, 192, 193, 194, 195, 207, 214, 216, 220, 223
IV	35	4, 6, 9, 11, 13, 14, 15, 16, 17, 18, 19, 21, 22, 27, 29, 44, 86, 87, 88, 90, 119, 126, 127, 130, 132, 135, 142, 155, 163, 174, 185, 196, 204, 213, 224

In Table 6, frequency of accessions of the various zones in a specific cluster is given. This was done to see if accessions from one zone group into the same cluster. Although many clusters contain accessions from different regions, a significant number of accessions of many clusters come from one or two zones (Table 6).

Table 6: Distribution of accessions of the various zones into the 10 clusters

Zone	*Cluster*									
	I	II	III	IV	V	VI	VII	VIII	IX	X
Amaro	1	2	0	1	0	0	0	1	0	0
Bench	1	3	1	1	0	0	0	0	0	0
Dawro	1	4	0	1	4	0	0	0	0	1
Gamog	**21**	**14**	2	1	**14**	2	0	1	1	0
Gedeo	4	0	0	0	1	0	2	1	0	0
Guji	1	0	1	2	2	0	0	0	0	0
Gurgage	2	0	0	2	0	0	1	0	0	0
Hadiya	**12**	2	1	2	1	3	2	1	0	0
Kembata	2	2	0	0	0	0	0	0	0	0
Keffa	1	4	**15**	2	0	1	0	0	0	0
Rel. Var	3	4	4	2	2	2	0	3	0	0
Sheka	0	0	**6**	0	0	0	0	0	0	0
Sidama	3	1	0	**13**	5	0	0	0	0	0
Siltie	4	0	0	3	1	0	1	0	0	0
Wolayita	0	3	2	3	0	0	0	0	0	0
Yem	0	7	2	2	1	2	0	0	0	0
Total	**56**	**46**	**34**	**35**	**31**	**8**	**6**	**7**	**1**	**1**

For example, Clusters II, and V with a total number of 56 and 46 genotypes, each has 21 and 14 accessions from Gamo Gofa. Frequency of accessions from other zones is very low in these two clusters. A maximum of 7 accessions from Yem are grouped into cluster II. Out of the 56 Gamo Gofa accessions 35 (62.5%) belong to the two clusters, II and V. So these two clusters can be designated as Gamo Gofa Clusters. Indeed the distance between them is the minimum, 12.34 (Table 7). The minimum and maximum distances between pairs of clusters in Table 7 are 12.71 (between clusters I and V) and 47.0 (between clusters III and VII). Clusters II and V also join into one cluster at the lowest distance (Fig.2, the dendrogram). The large overlap of members of these three clusters in the Can I and Can II plane of the discreminant analysis on Fig. 3 also conform this. The means of the 10 clusters are presented in Table 8.

Table 7: Distance matrix for 10 clusters formed by 225 genotypes

	A	B	C	D	E	F	G	H	I	J
A	0									
B	18.3	0								
C	33.6	16.1	0							
D	13.6	24.2	36.1	0						
E	12.7	12.3	26.1	15.3	0					
F	24	13.2	16.8	23	15.2	0				
G	14.8	31.6	47	24.3	26.7	38.6	0			
H	19.6	18.1	30.9	32.3	23.1	30.2	24.1	0		
I	32	16.3	17.4	39.3	25.9	26.1	42.4	21.9	0	
J	30.9	31	40	31.3	25.7	34.1	39.2	36	36.7	0

Cluster III lies at the opposite side (furthest from) of clusters II, V and IV. Thirteen of the 34 accessions of cluster III come from Keffa. The other six accessions of this cluster come from Sheka, which is adjacent to Keffa. The two zones in the western end of SNNPRS were in fact considered as one big administrative zone – Keffa-Sheka zone. So cluster III can be designated as Keffa-Sheka cluster.

Cluster IV contains 13 of the 35 accessions that come from Sidama and this cluster can be called a Sidama Cluster. Other members of cluster IV also come from adjacent Siltie and Wolayita zones. Since other clusters (VI, VII and VIII, contain eight, seven and 11 accessions, respectively, we can conclude that there are three main groups here, Clusters II and V of Gamo Gofa, cluster III of Keffa-Sheka in the western end of SNNPRS, and cluster IV of Sidama and adjacent zones in the eastern end of SNNPRS. Indeed the large distance between cluster III and IV (Fig. 2 & 3) reflects the geographic distance between the two regions. On the dendrogram also the two clusters III and IV join each other at the longest distance, at almost the end of the clustering process.

The pair wise generalized square distances (D^2) between the clusters (Table 7) showed that the distance between most of the clusters was big. For example the distance between clusters III and VIII was 47.0. Mehalanobis distance between clusters VII and IX was 42.4 indicating divergence between the genotypes that belong to different clusters.

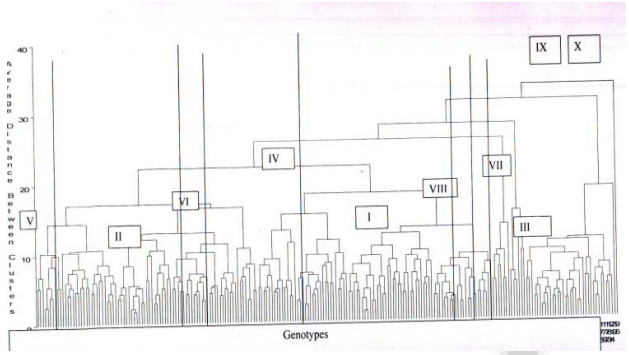

Figure 2: Dendrogram of the distribution of the accessions and checks into 10 clusters

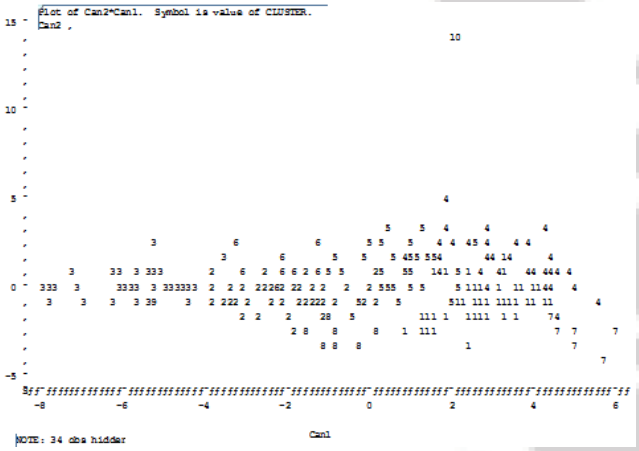

Figure 3: Scatter diagram of members of the 10 clusters in Can 1- Can 2 Plane of the Discriminant analysis

So clustering has revealed similarities of accessions collected from adjacent zones and dissimilarities of accessions collected from regions geographically located apart. The exchange of barley genotypes seems to be more frequent between adjacent zones than that between regions very far from each other.

The fact that some accessions do not follow the general rule outlined above may witness the fact that some genotypes can be shared by regions very far apart. For example two genotypes from Gamo Gofa were grouped into cluster III, the Keffa-Sheka cluster. It is also worth to note that cluster I contains 21.43 % of the accessions from Hadiya, those were classified into Gamo-Gofa which is far from Hadiya. The Hadiya accessions were also scattered over almost all clusters – Cluster II to Cluster VIII. The same is true about the few accessions representing zones such as Amaro, Bench, Dawro, Gedeo, Guji and Gurage. This might witness the fact that some genotypes are scattered through a large ecological zone. People exchange genetic material over larger distances.

Cluster means are presented in Table 8. The solitary cluster IX consisting of entry 39 (Acc 30/2006) is the earliest maturing genotype and took 63 days to head and 95 days to mature. It also had a score of scald 1.5 on the 0 to 9 scale, where 9 is the most susceptible, i.e., it was one of the most resistant accessions. It also gave a reasonable grain yield per plant, 1.24 grams. Cluster III is the other cluster that included genotypes that are early in maturity.

Table 8**:** The means of the 10 clusters based on 10 quantitative traits of 225 genotypes

CLUS	DH	DM	LODG	TSWT	Scald	FLW	PLH	SGS	HL	YGPP
1	80	118	1.1	40.6	2.2	2.2	67.9	13	8	1.1
2	70	107	1.6	39.5	1.7	1.8	77.3	14	8.1	1.2
3	65	97	1.9	42.7	1.5	1.5	88.4	13	8.6	1.1
4	86	124	1.1	44.2	2	2.4	78.2	15	8.2	1.3
5	74	118	1.4	36.9	2.3	2.2	77.9	16	8.5	1.4
6	68	113	1.8	45.4	1.7	1.6	87	12	9	1.1
7	86	122	1	38.7	1.8	2.2	54.8	12	6.9	1
8	70	104	1.1	36.5	1.4	1.7	59.6	14	6.7	1
9	64	95	1	30.2	1.5	1.2	77	16	7.4	1.2
10	75	118	1	34.2	3	2.2	76.8	42	7.9	1.2

Cluster X also consisted of a single accession – Acc 64/1/1/2006 (entry 95). It was the most susceptible to scald with a score of 3.0.

Clusters III and VI consisted the tallest genotypes with plant height of about 87 cm. Genotypes of both clusters headed early, 65 and 68 days, respectively, but genotypes of cluster VI matured late, consequently having long grain filling period. They produced bigger seeds with the highest thousand grain weight of 45.4 grams. The second highest thousand grain weight was obtained from genotypes of cluster IV (44.17 grams). Genotypes of cluster III produced thousand grain weights of 42.7 grams. The lowest thousand grain weight of 30.2 grams was obtained from Acc 30/1/2006 of cluster IX. This entry had the third highest number of spikelet per spike (15.8).

Members of clusters VII and VIII were dwarf genotypes with plant height of 54.8 and 59.6 cm. Cluster IV had the latest maturing genotypes which matured in 124 days.

Clusters I, II and V had intermediate values in almost all traits, although genotypes of cluster V gave the highest grain yield per plant of 1.36 grams per plant. The lowest grain yield per plant was obtained from members of clusters VII and VIII (0.95 and 0.98 grams per plant, respectively). The following table 9a and b shows the 12 highest yielding accessions and the clusters they belong to. The high yielding 12 genotypes are found in cluster II, III, IV and V, among which five are (41.67%) in cluster IV, three (25%) in cluster II, two (16.67%) each in cluster III and IV.

Table 9a: The 12 highest yielding accessions and the clusters they belong to

Acc No	*DH*	*DM*	*LOD*	*Scald*	*TSWT*	*YKPH*	*Cluster*
1	74	119	1	2	39.3	2858	V
3	74	113	1	1.5	46.9	2869	II
4	83	124	1	2.5	45	3294	IV
11	86	125	2	1.5	46.6	2730	IV
14	87	128	1	1	44	3139	IV
15	88	131	1	1	46.1	3524	IV
24	78	128	1	3.5	44.4	2751	V
29	80	119	1	4.5	51.7	2710	IV
33	69	108	2	1.5	33.3	2729	II
35	66	102	5	2	45.4	3100	III
84	68	100	1	1.5	43.3	2719	III
208	72	99	2	1.5	44.7	3753	II
Dafo	65	95	7	1.5	39	2684	I

DH=days to heading; DM= days to maturity; LOD susceptibility to lodging; TSWT= thousand seed weight (gm); SCALD= susceptibility to scald; YKPH= yield kg/h;

Table 9b: The 12 highest yielding accessions and the clusters they belong to

Acc No	*FLW*	*PLH*	*SGS*	*HL*	*YGPP*	*Cluster*
01	2.60	84.10	20	8.60	1.775	V
02	1.90	77.70	13	7.70	1.055	II
03	2.50	89.30	16	8.40	1.380	IV
08/1	2.55	83.00	15	7.15	1.670	IV
11	2.35	76.25	15	6.95	1.610	IV
12	2.65	85.50	16	8.25	1.620	IV
20	2.25	81.75	15	7.15	1.320	V
23	2.90	83.05	13	9.25	1.200	IV
27	1.30	81.35	12	8.55	1.005	II
28	1.00	87.50	12	8.15	1.015	III
59	1.85	90.15	13	10.25	1.110	III
159	2.05	83.40	16	8.20	1.340	II
Dafo	1.1	88.3	14	7.0	1.22	I

FLW=flag leaf width; PLH= plant height (cm); SGS= number of spikelet groups per spike; HL= head length (cm); YGPP=yield gram per plant; YKPH= yield kilogram per hectare.

Crossing of elite accessions from distant clusters is expected to produce transgressive segregants which surpass both parents. Hence, maximum variation in the subsequent generations is expected from crosses that involve parents from the clusters characterized by maximum inter-class distances, the crossing of the highest yielding genotype from different clusters is expected to produce useful segregants. Therefore pedigree selection in segregating generations of these crosses seems to give promising results. For example crossing entries 33 and 208 of cluster II with entries such as 4, 11, 14, 15, 29 of cluster IV is expected to produce interesting segregants. Crossing Accessions in cluster III (Acc-28/2006, Acc-59/2006) with those in cluster V (Acc-01/2006, Acc-20/2006), is also expected to give high yielding crosses.

Twelve genotypes out yielded the released variety Dafo and gave more than 2700 kg/ha. These include Acc-01, 02, 03, 08, 11, 12, 20, 23, 27, 28, 59, and 159 (Table 9a and b). The highest mean yield (3752.5 kg/ha) was recorded for the genotype Acc-159 whereas Acc-103/1 gave lowest yield (436 kg/ ha). The best accession Acc-159 had 39.8 percent yield advantage over the best check Dafo. All 12 accessions were collected from an altitude 2000 to 3000 masl. Among these six were from Sidama, two each from Guji and Gamgofa, one each from Wolaita and Yem, this indicated that potential areas for barley production are located an altitude between 2000 to 3000 masl. The released variety Dafo (2683.80) gave the best yield among the 18 released varieties even better than the recently released variety Gabula (1211 kg/ha).

These high yielder accessions are medium to late maturing types and took 99 to 131 days to mature (Table 9a). The broad difference among the barley landraces tested would provide ample opportunities for the genetic improvement of the crop through selection directly from the landraces and/ or following trait recombination through hybridization of desirable traits.

Due to the disproportional representativeness of barley accessions from the three altitudinal region (14, 97, and 96 from I, II and III) the composition of the ten clusters is not so distinct as it was for the zones (Table 10).

Table 10: Distribution of the accessions from the 3 altitudinal classes into 10 clusters

Altitude	Clusters									
	I	II	III	IV	V	VI	VII	VIII	IX	X
I	2	4	6	2	0	0	0	0	0	0
II	17	26	22	9	11	7	1	2	1	1
III	34	12	2	22	18	1	5	2	0	0
Total	**53**	**42**	**30**	**33**	**29**	**8**	**6**	**4**	**1**	**1**

Altitude 1= less than 2000 masl,; Altitude 2= between 2000 and 2500 masl and Altitude 3= between 2500 and 3000 masl

4. Conclusion

Analysis of variance showed highly significant differences among the tested genotypes for all 11 quantitative traits, indicating the presence of genetic variability in the traits studied. A wide range of values had been observed in morpho-agronomic traits of the studied barley genotypes .Grain yield exhibited the widest range (436 – 3752.5 kg/ ha) followed by plant height (44.95 – 94.1 cm), days to maturity (92 – 131), and heading (57 – 94). Twelve genotypes out yielded the best released variety (Dafo) indicating the possibility of identifying superior genotypes for release or the presence of broad difference among the barley landraces tested that would provide ample opportunities for the genetic improvement of the crop through genetic recombination by hybridization of genotypes with desirable traits**.**

High heritability and high genetic advance as percent of the mean were observed for susceptibility to lodging, flag leaf width and spikelet per spike. This indicates that these traits are governed by additive genetic action. Relatively rapid progress can be achieved through selection.

The clustering patterns of the accessions based on 10 quantitative traits grouped into 10 distinct clusters of different sizes. The maximum inter-cluster distance (D^2 = 47) was noticed between cluster III and VII followed by VII and IX (D^2 = 42.39) and III and X (D^2 = 39.96) suggesting diversity between these groups. There is also high inter-cluster distances between high yielding genotypes of cluster II and IV (D^2= 24.16). Hence, maximum variation in the subsequent generations is expected from crosses that involve parents from the clusters characterized by maximum inter-class distances. The crossing of the highest yielding genotype from different clusters is expected to produce useful segregants. For example crossing entries 33 and 208 from cluster II with entries such as 4, 11, 14, 15, 29 from cluster IV is expected to produce interesting segregants.

In the future head-to-row selection (pure line selection) will be conducted i.e. each spike will be planted in each row and

for comparison standard checks from early and late materials will be used. The best performed materials from both sets will be promoted to the next step and tested across locations in southern high lands. Then high yielder and wide adaptable genotypes will be released and recommended for end users.

5. Acknowledgement

The authors are grateful for the financial support provided by Southern Agricultural Research Institute, SARI, Ethiopia and Canadian International Development Agency (CIDA) / University Partnerships in Cooperation and Development (UPCD) Project, Hawassa, Ethiopia. We also appreciate Dr Tenaw Workayehu for reviewing the manuscript.

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