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Farmers' Varieties as an Alternative to Climate Smart Agriculture, the Case of Barley (*Hordeum vulgare* L.)

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***Abstract* – Eighty-one barley (*Hordeum vulgare* L.) genotypes were evaluated for seven traits in simple lattice design at Holleta. The overall objective was assessing the potential and the level of phenotypic variability of barley farmers' varieties based on quantitative traits. From this study it was found that the genotypes showed highly significant variation for all the traits. This significant variation coupled with wide range of mean values for most of the traits revealed the presence of variations among the genotypes tested. The farmer variety Accn#16810 yielded significantly higher grain yield than the standard check Cr#41/98. Estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variations were moderately high. The PCV values were only slightly greater than the GCV values. Relatively higher PCV values were exhibited by number of seeds/spikes, grain yield and thousand kernel weight. Number of seeds/spikes showed the highest heritability and moderate to high heritability was observed for days to maturity, thousand kernel weight and days to maturity. D^2 analysis revealed the 81 genotypes grouped into eight clusters. Exploitation of this level of variability in the future breeding activities will end up with the development of varieties which are well adapted the ecological conditions of the target environment.**

***Keywords* – Farmer Varieties, Climate Smart, Barley.**

I. Introduction

Barley (*Hordeum vulgare L.*) was one of the first domesticated crop and is believed to be originated in the Fertile crescent Near East from the wild progenitor *Hordeum* spontaneum over 10,000 years ago (Badr et al., 2000). It is a polypliod crop with most of the species including the cultivated barely (*Hordeum vulgare spp vulgare)* belonging to diploid level (2n = 2x = 14). Besides, tetraploids (2n = 4x = 28) and Hexaploids (2n = 6x = 42) are also frequent (von Bothmer et al., 1995). Worldwide the crop is being grown more than 197 million hectares in 2014 with Russia and Australia being the largest producers (FAOSTAT: http://www.fao.org/faostat/en/ #data/QC accessed June, 25, 2014).

Owing to its geographic, topographic, edaphic and cultural diversity Ethiopia is believed to be origin and diversity of different crops (Vavilov, 1951). Barley in this case has huge variation in the country to the extent considerable number of variants that were not found elsewhere including the place of origin of the crop (Harlan., 1969). This level of diversity has been taken into account to regard Ethiopia as one of the origins and diversity of the crop plants. Despite this, absence of the wild relative of barley in the country made Ethiopia a center of diversity not origin for barley but the debate continued (Harlan., 1969). In Ethiopia, barley is the fifth most important crop both in area and total production (CSA, 2015) after tef, maize, wheat and Sorghum. Out of the total area devoted to barley farmers' varieties constitute 90% (Tesema *et al.*, 2009). This indicates the role farmers' varieties are playing towards the food security of the country. Particularly in this era of climate change farmers varieties are playing an important role since they are capable of withstanding harsh biotic and a biotic stress (Knepffer *et al.*, 2003). Having adaptability or resilience, one of the three pillars for climate smart agriculture, farmers' varieties tend contribute significantly to such a kind of agriculture. To this end, characterization of the potential of these farmers' varieties is quite crucial.

Characterizing and understanding the level of diversity those farmers' varieties of barley entail will be an important step in the conservation and sustainable utilization of the crop. This stems from the fact that farmers' varieties are the major components of the agricultural system found in Ethiopia. Genetic diversity which is most noticeable within a crop species like barley are of visible differences in phenotype. These differences may be of qualitative (row type, kernel color, hulled or naked seeds) and/or quantitative nature (phenological and agronomic characters) (Demissie and Bjornstad, 1996). In Ethiopian Biodiversity Institute gene bank barley constitutes the major holding with more than 15,000 accessions (Adugna, 2011). Despite this huge resource the research effort made on the farmers' varieties still fall short. Hence the current study was initiated with the objective of assessing the potential and the level of phenotypic variability of barley farmers' varieties based on quantitative traits.

II. Material and Methods

The experiment was conducted in the 2013/14 main cropping season at Holleta Agricultural Research Center. It was composed of 80 different farmers' varieties obtained from Ethiopian Biodiversity Institute and one standard check obtained from Holleta Agricultural Research Center. The farmers' varieties were originally collected from four regions (Amhara, Oromiya, SNNP and Tigray) and two zones form each the four regions (Awi and Semien Gondar zone from Amhara; Arsi and Mistrak Wellega from Oromiya; Guraghe and Keficho Shekicho form SNNP; Debubawi and Misrakawi zones form Tigray). Altitudinally the localities from which the accessions were collected ranged from 1700 (Arsi, Dodota) to 3202 (Semein Gondar, Debark).

The experiment was laid out in 9x9 simple lattice design. The plot size was six rows of 2m length with 0.3m row spacing i.e. 1.2 m x 2 m = 2.4 m^2. Planting was done by hand drilling at a rate of (24 g/plot). The plots were fertilized with DAP and Urea fertilizers as per the recommended rate of application for the site. All other experimental factors were applied uniformly to the entire plot. The data collected include days to heading (DH) maturity (DM), plant height (PH), number of tillers (TI), number of seeds per spike (SPS), thousand kernel weight (TKW) and grain yield (GY). The data were subjected to analysis of variance, divergence and principal component analysis using Agrobase, SAS, MINITAB soft wares in the same order. Phenotypic and genotypic coefficients of variation were estimated based on the method suggested by Burton and DeVane (1953). Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis's D^2 statistics (Mahalanobis, 1936) by using SAS software program. Points where local peaks of the pseudo F statistic join with small values of the pseudo t^2 statistic, followed by a larger pseudo t^2 for the next cluster fusion were examined to decide the number of clusters.

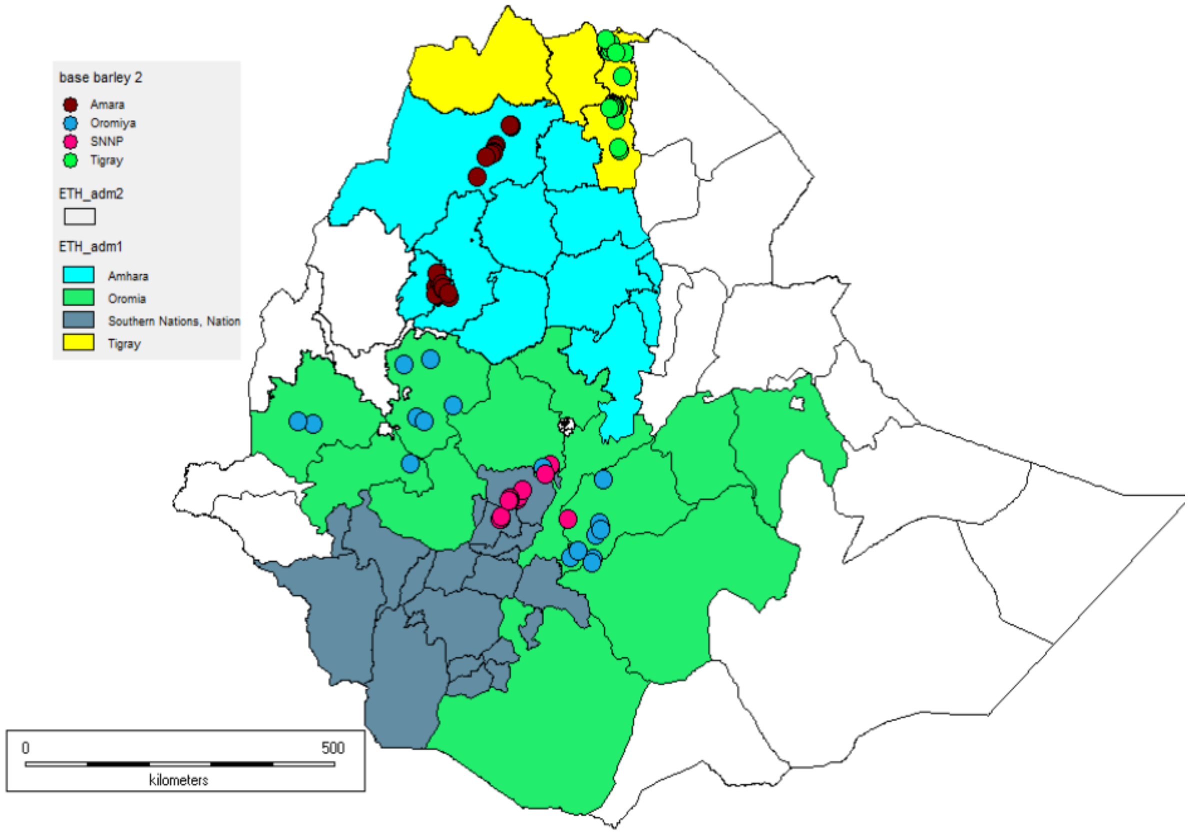

Fig. 1. The geographic distribution of barley farmers' varieties under study.

III. Results and Discussion

Analysis of Variance

The data of the mean values of all experimental unit were subjected to analysis of variance (ANOVA) based on simple lattice design. Significant differences among genotypes ($p<0.01$) were observed for all traits under study except number of tillers. Block effects were found to be significant at ($P<0.01$) only for thousand kernel weight and grain yield (Table 1). This finding is an indicator the presence of huge variability in the studied genotypes for the traits considered and hence could be exploited through selection, since it is an input for successful breeding program. This result was in agreement with the findings of (Matin *et al.,* 2019).

All the accessions included in the experiment showed significantly lower days to mature than the improved variety Cr#41/98. In addition, 48% of the genotypes exhibited below average (110) days to maturity. Comparing the mean grain yield (Kg/ha) of the accessions it was revealed that 18% of the accessions showed significantly higher yield than the improved variety. Furthermore 41% of the genotypes showed above average (2409 kg/ha) grain yield with the top 5% high yielder being Accn# 16810, 16811, 16982 and 16820.

Table 1. Mean squares, mean, range σ^2p, σ^2g, σ^2e PCV and GCV values for the six characters of 80 barley genotypes grown at Holleta (2013/14).

Characters	Replication df = 1	Genotype (G) (df = 48)	Mean	Range	σ^2p	σ^2g	σ^2e	PCV (%)	GCV (%)	h^2
DH	4.84^{ns}	78.96^{**}	66.78	56-79	41.67	37.29	4.38	9.66	9.14	0.89
DM	21.48^{ns}	110.75^{**}	110.66	96-135	63.79	46.95	16.841	7.21	6.19	0.74

PH(cm)	166.02^{ns}	32.58^{**}	113.91	107-128	22.77	9.80	12.965	4.18	2.74	0.43
TI	2.98^{ns}	0.60^{ns}	5.06	4-6	0.599	0.01	0.59	15.30	1.92	0.02
SPS	1.04^{ns}	173.24^{**}	26.91	17-54	91.28	81.95	9.331	35.50	33.64	0.90
TKW	529.93^{**}	300.50^{**}	43.4	25-60	161.45	139.05	22.401	29.27	27.17	0.86
GY(kg/ha)	10297997.7^{**}	929027^{**}	2409.76	1246-4106	620780	308247	312533	32.69	23.03	0.50

DH (days to heading), DM (days to maturity), PH (plant height), TI (fertile tiller), SPS (seeds per spike), TKW (thousand kernel weight), GY (grain yield), σ^2p (phenotypic variance, σ^2g (genotypic variance, σ^2e (environmental variance), PCV (phenotypic coefficient of variation, GCV (genotypic coefficient of variation), h^2 (broad sense heritability)

** = significant at (P<0.01) and ^{ns} = not significant.

It has also been observed that most of the characters showed relatively wider range except for number of tillers. Days to maturity in this case ranged from 96 (Accn# .17255) -134 days (Cr# 41/98). Grain yield on the other hand showed range of 1246 (Accn# 15268) - 4106 (Accn# 16810) kg/ha. The highest σ^2g (308247) and σ^2p (620780) variance were observed for grain yield (Kg/ha) (Table 2). The lowest σ^2g (0.01), σ^2p (0.59) variance were observed for fertile tiller. Except for number of tillers and grain yield the difference between PCV and GCV was very minimal. This suggests the environmental variance had larger contribution in the phenotypic expression of number of tillers and grain yield as compared to the rest of the characters. The higher GCV with higher PCV for seeds per spike, thousand kernel weight and grain yield suggest that there was ample variability in the gene pool and hence there are plenty of choices for genetic improvement through selection with these traits. Moderate to high PCV values were reported by (Yadav *et al.,* 2015).

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability. The heritability estimates in the current experiment varied from 0.02 for fertile tillers to 0.90 to number of seeds per spike. The characters which showed high heritability, suggested that selection based on these traits will be more effective. In addition, these characters governed mainly by additive gene action and could be improved through individual plant selection. Those with low heritability indicated that the characters were highly affected by environment and improvement through selection based on these traits will be difficult (Dinsa *et al.,* 2018).

Divergence Analysis

The D^2 values based on the mean of genotypes resulted in classifying the 80 barley genotypes in to eight distinct clusters (Fig 2). In the cluster analysis it has also been identified that there were two main branches of the eight clusters. The x^2 test for the eight clusters indicated that there was statistically accepted difference at (p<0.05) between clusters except, Cluster II & IV and III &VI (S. Table 1). Cluster II was found to have the largest number of accessions (20) (S. Table 2) and they were from four different altitudinal classes (Fig 3.a) and all the eight administrative zones (Fig 3.b) from which the accessions were collected. Cluster IV was the second largest with 15 accessions from two altitudinal classes and all the zones except Arsi and Semen Gondar. Cluster III and VIII were found to be solitary and were from Agew and Keficho respectively. Cluster V had 14 accessions one of which was the improved variety. The accessions in this cluster were from three altitude classes and having no accession from Misrak Wellega but at least an accession from other zones. Hence, cluster II with the largest number of genotypes from all the altitudinal classes and all the zones fond to be the most diverse cluster. The D^2 statistics has also showed there was significant and high genetic distance among clusters. The maximum genetic distance was found between cluster V and VIII with $D^2 = 466$. The second most divergent clusters were cluster VII and VIII with $D^2 = 452$. The least divergent clusters were cluster III and VI with $D^2 = 9.97$.

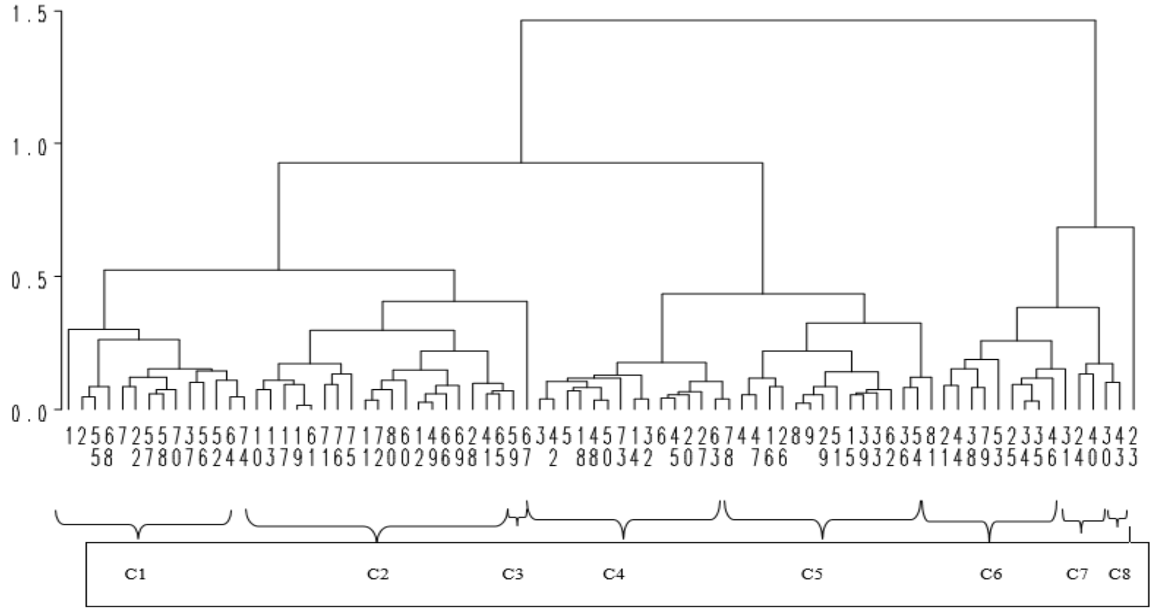

Fig. 2. Seven quantitative characters based dendrogram for 80 barley genotypes tested at Holleta (2013/14).

Each of the eight clusters were found to have their own merit based on the characters under study. Cluster I, II and III for instance were composed of accessions with early maturity types (S. Table 3). Cluster VI had the highest plant height (which is highly linked to biomass yield) and the highest thousand kernel weight. Cluster VII had the largest number of kernel and the second highest grain yield. Cluster VIII had the highest grain yield and the second largest number of seeds per spike. (Kemelew and Alemayehu, 2011) grouped 181 barley landraces in to ten clusters.

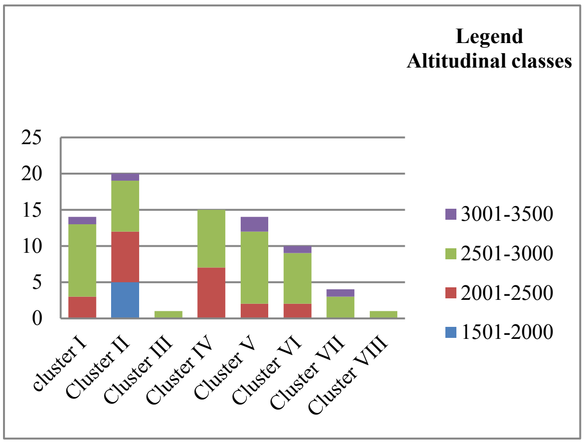

Fig. 3.a No. of accessions in in each cluster from each of the arbitrary altitudinal classes (2013/14).

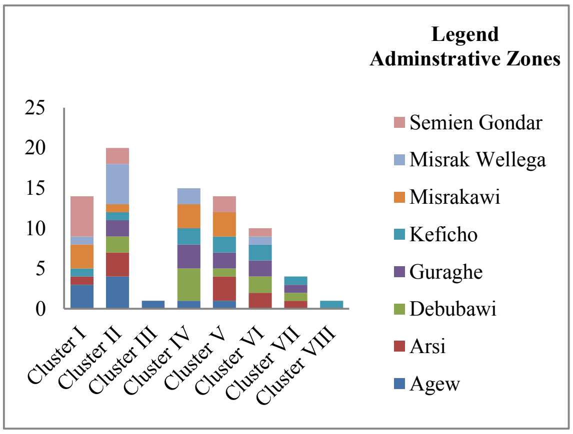

Fig. 3.b No. of genotypes in each cluster from 8 zones.

Principal Component Analysis

In the principal component analysis, the first three PCs with eigen value greater than unity were retained. This analysis revealed that three principal components (PC1, PC2 and PC3) with values of 38.6%, 23.6% and 15.7% in the same order accounted for 77.90% of the total variation (S. Table 4). In the first component number of fertile tillers, days to heading, days to maturity, number of seeds per spike and grain yield had the major contribution for the observed variation in which case number of fertile tillers was negatively correlated with the rest of these traits. Though negatively correlated number of seeds per spike and thousand kernel weight were found to affect the second PC. In the third PC plant height and thousand kernel weight in the respective direction were the main contributors of the variation.

IV. Conclusion

Having covered considerably huge cultivable land farmers varieties are still an important component of Ethiopian agriculture. As it is attested with the present finding still there are farmers' varieties with superior yielding potential. As one of the strategies to withstand the drought challenges early maturing farmers varieties will also be either used as they are or can be used as parental source in the effort of developing superior varieties in the breeding programs. Varieties with superior yield potential and well adapted to the prevailing situation of the area being grown best fit the requirements of the climate smart agriculture.

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Supplementary Data

Table 1. Inter Cluster Distance (D^2) Values 80 Barley Genotypes Tested at Holleta (2013/14).

Cluster		I	II	III	IV	V	VI	VII	VIII
I		0	47.39**	127.89**	16.92*	19.37**	195.05**	122.90**	307.75**
II			0	22.12**	11.91^{ns}	118.17**	52.51**	190.74**	117.04**
III				0	59.08**	238.24**	9.97^{ns}	262.55**	42.74**
IV					0	64.22**	108.26**	155.34**	188.67**
V						0	325.01**	147.79**	465.78**
VI							0	317.95**	16.96*
VII								0	451.56**
VIII									0

Table 2. The Distribution of Genotypes in to Eight Clusters Based on D^2 Analysis for 80 Barley Genotypes Tested at Holleta (2013/14).

Cluster	No. of genotypes	Genotypes
Cluster I	14	15255, 15268, 15275, 16809, 16930, 17206, 17210, 17211, 17212, 17213, 17244, 17253, 17257, 17263,
Cluster II	20	15287, 15405, 16714, 16722, 16738, 16757, 16815, 17143, 17153, 17214, 17216, 17237, 17245, 17250, 17255, 17648, 17651, 17671, 17672, 17690
Cluster III	1	17252,
Cluster IV	15	15270, 15272, 15274, 16732, 16755, 16805, 16814, 16824, 17145, 17149, 17152, 17154, 17242, 17655, 17682,
Cluster V	15	15271, 15277, 15280, 16734, 16736, 16813, 16817, 16863, 16910, 16956, 17151, 17204, 17209, 17240, C41/98
Cluster VI	10	16806, 16812, 16822, 16866, 16908, 16945, 17148, 17150, 17207, 17688,
Cluster VII	4	16811, 16820, 16982, 17146
Cluster VIII	1	16810

Table 3. Cluster Mean Values of Seven Quantitative Characters of 80 Barley Genotypes Tested at Holleta (2013/14).

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
DF	63.86	62.85	26.00	65.20	71.67	73.30	72.50	74.00
DM	105.43	105.25	105.00	110.20	117.07	117.80	118.50	121.00
PH	111.57	114.70	121.00	113.60	112.93	116.10	113.75	112.00
TI	5.43	4.90	5.00	5.53	4.87	4.80	4.50	5.00
SPS	26.36	23.25	34.00	21.27	32.07	28.70	40.50	36.00
TK	39.07	41.55	39.00	42.73	42.87	47.40	43.50	41.00
GY	1499.64	1956.5	2106	2422.33	2798.66	3350.5	3681.25	4106

Table 4. Eigen Vectors and Values of the First Three Pcs of 80 Barley Genotypes Tested at Holleta (2013/14).

	Principal Component		
	PC1	PC2	PC3
Eigenvalue	2.702	1.648	1.098
Variance (%)	38.60	23.60	15.70
Cumulative variance (%)	38.60	62.2	77.90
Traits	Eigen vectors		
DF	-0.536	-0.138	-0.252
DM	-0.531	-0.210	-0.198
PH	-0.066	0.285	0.737
TI	0.290	-0.360	-0.289
SPS	-0.306	0.586	-0.189
TK	-0.146	-0.615	0.434
GY	-0.476	-0.057	0.214