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Phenotypic Diversity in Ethiopian Food Barley (*Hordeum vulgare* L.) Genotypes

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Abstract: In Ethiopia, barley (*Hordeum vulgare* L.) is grown primarily for local food and beverage consumption. Keeping in view the inadequate number of improved food-barley varieties adapted to the different agro-ecological zones of Ethiopia, the present study was conducted on thirty six food barley genotypes to estimate the genetic variability, estimate genetic divergence and clustering them into genetically divergent classes. The genotypes were grown in a simple lattice design. Data were collected on 11 morph-agronomic quantitative characters. The results of genotypic path coefficient analysis indicated that biomass and harvest index had the highest positive direct effect on grain yield at Holetta and Debark. Selection for biomass and harvest index would, therefore, be very useful for grain yield improvement at both locations. Genotypes were grouped in to seven clusters which make them divergent. The present study generally implied the presence of significant genetic variability among the tested genotypes.

Key words: Clustering · Ethiopian barley · Path coefficient · Yield · Yield component

INTRODUCTION

Ethiopia is considered as one of the richest genetic resource centers in the world. Crop plants such as coffee and tef (*Eragrostic tef*), are known to originate in Ethiopia [1]. Barley is grown primarily for food and beverage consumption [2] Barley can be cultivated at an altitudes between 1500 and 3500 m.a.s.l, but is predominantly grown between altitudes of 2000m and 3000 m.a.s.l [3]. This wide distribution demonstrates the wide ecological amplitude throughout the country [3, 4, 5]. So far, a lot of work has been carried out and reported on analyzing associations and genetic diversity for morphological trait in Ethiopian germplasm [2, 6]. Yet, the work on breeding for high yielding genotypes of food barley needs attention taking in to account the ever increasing human population. Knowledge regarding the amount of genetic variation in germplasm arrays and genetic relationships between genotypes are important considerations for efficient utilization of germplasm resources [7, 8, 9]. Therefore, a study was conducted in some of the genotypes of food barley for searching desirable attributes, which could be exploited in breeding programmes.

MATERIALS AND METHODS

Genetic Material: Twenty six released and 10 in pipe line food barley genotypes representing the germplasm of the crop were procured from Holeta Agricultural Research Center (HARC) (Table 1). The experiment was conducted from 2010 to 2011 cropping season in 6 x 6 a simple lattice design with two replications at HARC (9° 3'N and 38° 30'E) and Debark Agricultural Research Sub Center (DARSC) (14° 49'N and 37° 75'E). In this field trial, fertilizer was applied with the rate of 41 kg h^{-1} N and 46 kg h^{-1} P_2O_5 and other crop management practices were undertaken as per the recommendation. Each experimental plot measures 2.5m long and 1.2m wide. There were six rows on each plot with 0.2m row spacing. The middle four rows were used ($2m^2$ areas) for data collection. The traits studied were days to heading, days to maturity, grain filling period, biomass yield, grain yield, harvest index, thousand- kernel weight, tiller number $plant^{-1}$, plant height, spike length, kernel number $spike^{-1}$.

Statistical Analysis: The data collected for each trait were subjected to analysis of variance (ANOVA) according to the method described in [10]. LSD was used to separate

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Table 1: Barley genotypes used in the experiment

No.	Genotype	Pedigree (Selection)	Source
1	HB- 1307	EH-1700/F71.B1.63	HARC
2	DIMTU	3369-19	HARC
3	SHEGE	3336-20	HARC
4	TOLESE	TOLESE	HARC
5	EH1642	EH1642	HARC
6	HB-42	-	HARC
7	ARDU12-60B	-	HARC
8	4748-16	MEZEZO	DBARC
9	4731-7	BASO	DBARC
10	MISRACH	KULUMSA1/88	DBARC
11	SHEDEHO	3381-01	SARC
12	YEDOGIT	BI95IN 198	SARC
13	ESTAYISH	218963-4	SARC
14	TRIT	215235-2	SARC
15	AGEGNEHU	218950-08	SARC
16	BENTU	EMBSN5TH	KARC
17	IBCB-5/76/06	-	-
18	MULU	3371-03	AARC
19	SETEGN	3369-17	AARC
20	ABAY	3357-10	AARC
21	TILLA	EMBSN 14/98	AARC
22	GUTA	-	-
23	BIFTU	SHASHO#22 Go-1(sn98B)	SARC
24	DAFO	ARUSO(42)4(sn99G)	SARC
25	DINSHO	WADAGO-4	SARC
26	HARBU	ARUSO	SARC
27	ACC.#220718	-	ICARDA (in pipe line)
28	IBON9163/05	-	ICARDA (in pipe line)
29	IBON9156/05	-	ICARDA (in pipe line)
30	BYT909//05	-	ICARDA (in pipe line)
31	IBON9045/05	-	ICARDA (in pipe line)
32	IBON9090/05	-	ICARDA (in pipe line)
33	IBON9098/05	-	ICARDA (in pipe line)
34	IBYT914/05	-	ICARDA (in pipe line)
35	IBON9114/05	-	ICARDA (in pipe line)
36	IBON9135/05	-	ICARDA (in pipe line)

HARC= Holetta Agricultural Research Center. DBARC= Debre Birhan Agricultural Research Center. SARC= Sirinka Agricultural Research Center. KARC= Kulumsa Agricultural Research Center. AARC= Adet Agricultural Research Center. SARC= Sinana Agricultural Research Center. ICARDA=International Center for Agricultural Research in the Dry Areas

the means. Path coefficient analysis was calculated as the method used by [11]. Clustering of genotypes was performed by NCSS2000 program [12] to group sets of genotypes in to homogenous cluster, to estimate genetic distance between genotype. Mahalanobis's D^2 [13] was used to estimate the genotypic divergence between the cluster in the experimental population. The D^2 analysis was based on the mean values of all yield related traits across locations by using SAS software program [14].

RESULTS AND DISCUSSION

Genotypic Path-Coefficient: Grain yield is a complex outcome of different yield components. Although correlation estimates are helpful in determining the association yield components with a complex trait such as grain yield, but they do not provide exact picture of the significance of direct and indirect contribution of each character towards this trait [15]. Path coefficient analysis is a best way of understanding the contribution of traits to final grain yield and provides important information for improving grain yield through selection of its components [16]. The direct and indirect effects of the 10 grain yield related characters are shown in Table 2.

At Holetta, characters like days to maturity, plant height, spike length, kernel number spike^{-1}, biomass, harvest index and thousand-kernel weight displayed that positive direct effect on grain yield. Among characters,

Table 2: Path coefficients of direct (main diagonal) and indirect effects of the quantitative characters of barley genotypes studied at Holetta 2010/11
Residual=0.0528

Traits	DHE	GFP	DMA	PLH	SPL	PT/PL	KN/SP	BM	HI	TKW	r_g
DHE	-11.25	4.98	5.89	0.025	0.010	0.024	0.076	0.662	0.174	0.043	0.644**
GFP	8.84	-6.34	-2.29	0.004	-0.013	-0.101	-0.062	-0.283	-0.011	0.002	-0.265
DMA	-9.47	2.08	7.00	0.042	0.004	-0.051	0.062	0.763	0.256	0.068	0.752**
PLH	-0.487	-0.392	5.04	0.058	0.011	0.003	-0.006	0.223	-0.216	0.026	-0.134
SPL	-3.86	2.83	0.899	0.022	0.030	-0.004	-0.004	0.113	-0.166	0.021	-0.116
PT/PL	2.56	-6.12	3.44	-0.002	0.001	-0.104	-0.035	0.361	0.282	0.081	0.457**
KN/SP	-8.00	3.65	4.06	-0.003	-0.001	0.034	0.107	0.609	0.266	0.024	0.755**
BM	-8.77	2.11	6.29	0.015	0.004	-0.044	0.077	0.848	0.352	0.059	0.943**
HI	-4.45	0.16	4.08	-0.028	-0.012	-0.067	0.065	0.680	0.438	0.070	0.649**
TKW	-4.81	-0.125	4.72	0.015	0.006	-0.084	0.026	0.493	0.304	0.101	0.649**

*, ** significance at the 0.05 and 0.01 probability levels, respectively.

DHE=Days to Heading, GFP=grain filling period, DMA=Days to Maturity, PLH=Plant Height (cm), SPL= Spike length (cm), PTI/PL=Number of Productive tillers plant^{-1}, NK/SP= Number of Kernels spike^{-1}, BM=biomass (kg h^{-}),^{1} HI= Harvest index (%), TKWt=1000Kernel Weight (g) and r_g = Genotypic correlation coefficients

days to maturity had the highest positive degree of favorable influence on grain yield (7.00), followed by biomass (0.848) and harvest index (0.438). Earlier researches [17] identified that biomass showed direct positive contribution for grain yield in wheat. Similar results are also reported by [18, 19] that days to maturity, kernel number spike^{-1} thousand-kernel weight harvest index showed direct positive effect on grain yield.

Days to heading exerted strong negative influence on grain yield (-11.25) followed by grain filling period (-6.34) and productive tillers (-0.104). However, the indirect effect of days to heading through days to maturity (5.89), days to heading with grain filling period (4.98), days to heading with biomass (0.662) and days to heading with harvest index (0.174) counter balance the negative direct effect of days to heading on grain yield. Therefore, the indirect correlation reduces to favorable effect 0.644. Similarly, grain-filling period was counter balanced through the indirect correlation effect of days to heading (8.84) and reduces the correlation to -0.265. In the same way, productive tillers showed negative direct effect on yield (-0.104), but the indirect correlation effect with days to heading (2.56), days to maturity (3.44), biomass (0.36) and harvest index (0.28) reduces into favorable values on grain yield (0.457).

On the contrary side, the plant height and spike length showed positive direct effect on grain yield (0.058, 0.030 respectively), but the indirect correlations of plant height with days to heading (-0.49), grain filling period (-0.39) and harvest index (-0.22) reduces the correlation to -0.134. Spike length indirectly correlated with days to heading (-3.86) and harvest index (-0.166) due to these, reduces the correlation to -0.166 at Holetta.

The residual effect determines unaccounted variability of the dependent factor (seed yield). Its magnitude 0.0528 indicated that the characters included in the path analysis explained 94.72% of the variation in seed yield. Generally, both the genotypic correlation and path coefficient indicating that, characters like days to maturity, biomass, harvest index and thousand-kernel weight are important primary components for yield improvement (Table 3). The other characters can be considered as secondary components for yield improvement.

At Debark, the genotypic path coefficient analysis (Table 3) displayed that the indirect effects were either positive or negative and lower in magnitude on grain yield. Grain filling period, plant height, productive tiller and kernel number spike^{-1}, biomass and harvest index showed that positive direct effect on grain yield.

Among the direct and positive effects, harvest index and biomass indicated almost equal and the highest direct positive effect on grain yield (0.747, 0.742), respectively. Similarly it was reported that the biomass exerted high positive direct effects on grain yield [20]. These characters also had similar magnitude of direct and indirect correlation. Therefore, direct selection is effective for these characters. If the correlation coefficient between a causal factor and the effect (i.e. grain yield) is almost equal to its direct effect, then correlation explains the true relationship and direct selection through this trait will be effective [21].

The effect of days to maturity on grain yield is direct negative (-0.043). Whereas, the correlation is positive and highly significant due to positive indirect correlation with biomass (0.596) were counter balanced the negative direct

Table 3: Path coefficients of direct (main diagonal) and indirect effects of the quantitative characters of barley genotypes studied at Debark 2010/11cropping season

Residual=0.0851

Traits	DHE	GFP	DMA	PLH	SPL	PT/PL	KN/SP	BM	HI	TKW	r_g
DHE	-0.075	-0.008	-0.029	0.100	-0.022	-0.011	-0.008	0.442	-0.247	-0.015	0.128
GFP	0.006	0.104	-0.029	-0.026	0.017	-0.024	-0.012	0.338	0.136	-0.048	0.461**
DMA	-0.050	0.071	-0.043	0.039	0.006	-0.029	-0.015	0.596	-0.098	-0.042	0.437**
PLH	-0.043	-0.016	-0.010	0.173	-0.113	-0.013	0.006	0.275	-0.427	-0.024	-0.191
SPL	-0.009	-0.009	0.001	0.105	-0.186	0.037	0.019	0.155	-0.203	-0.008	-0.098
PT/PL	0.010	-0.029	0.015	-0.026	-0.081	0.086	0.008	-0.019	-0.099	0.012	-0.123
KN/SP	0.014	-0.032	0.016	0.028	-0.088	0.018	0.040	-0.120	0.159	0.005	0.040
BM	-0.044	0.047	-0.035	0.064	-0.039	-0.002	-0.006	0.742	-0.047	-0.041	0.637**
HI	0.025	0.019	0.006	-0.099	0.051	-0.011	0.008	-0.047	0.747	0.032	0.730**
TKW	-0.018	0.081	-0.029	0.066	-0.025	-0.017	-0.003	0.497	-0.389	-0.062	0.101

*, ** significance at the 0.05 and 0.01 probability levels, respectively.

DHE=Days to Heading, GFP=grain filling period, DMA=Days to Maturity, PLH=Plant Height (cm), SPL= Spike length (cm), PTI/PL=Number of Productive tillers plant^{-1}, NK/SP= Number of Kernels spike^{-1}, BM=biomass (kg h^{-1}), HI= Harvest index (%), TKWt=1000Kernel Weight (g) and r_g = Genotypic correlation coefficients.

Table 4: Distribution of 36 barley genotypes in different cluster groups studied at Holetta and Debark in 2010/11 crop season

Clusters							
CL-I	CL-II	CL-III	CL-IV	CL-V	CL-VI	CL-VII	Solitary genotypes
Setegn	4731-7	Yedogit	Shege	IBON9156/05	HB 1307	Dimtu	IBCB-5/76/06
Dafo	Misrach	Tilla	Tolese	IBYT 909/05	IBON9045/05	HB42	Abay
	Trit		EH1642	IBON9090/05		Ardu12-60B	Guta
	Agegnehu		4748-16	IBON9098/05		Acc.#22078	Harbu
	Bentu		Shedeho	IBYT 914/05			IBON9163/05
	Dinsho		Estayish	IBON9114/05			
			Mulu	IBON9135/05			
			Biftu				

effect of days to maturity on grain yield and reduces the correlation to 0.437. Similarly, the direct effect of days to heading, spike length and thousand-kernel weight with grain yield was negative, but the indirect correlations with biomass counter balance and reduced the direct negative influences of days to heading, spike length and thousand kernel weight on grain yield. Since the direct effect is negative the direct selection for this trait to improve yield will be undesirable.

In the case of Debark, the residual (0.0851) indicates that characters which are included in the genotypic path analysis explained 91.49% of the total variation in seed yield. In general, it is logical to conclude that harvest index, biomass and grain filling period were the major contributors to grain yield. Since, these three characters had high correlation and high direct effect thus direct selection for these three characters should be concern for the plant breeder.

Genetic Clustering: The results of cluster analysis for genetic diversity of 36 barley genotypes studied at Holetta and Debark are presented in Table 4 and Fig. 1. The genotypes were grouped in a particular cluster on the basis of morphological trait similarities, thus representative accessions from a cluster of particular group could be chosen for hybridization program. Some potentially important traits have been identified and these can be exploited for specific trait improvement. Cluster diagram based on Euclidian dissimilarity using group average method categorized the genotypes into 7 clusters. Cluster I consisted of two genotypes, cluster II six, cluster III two, cluster IV eight, cluster V seven, cluster VI two and cluster VII four genotypes. The number of accessions per cluster varied from two genotypes in cluster III and I to eight genotypes in cluster IV. Distribution pattern of all the genotypes into various clusters showed the presence of considerable genetic divergence among the genotypes for most of the traits studied.

Genotypes included in the first cluster were 5.5% out of the total genotypes. Undir this cluster genotypes had early heading, high number of productive tillers and less amount of kernel number per spike. The second cluster included 16.6% of the genotypes. The cluster mean showed that genotypes grouped here showed smaller number of productive tillers, grain yield and thousand-kernel weight. Cluster III was composed of 5.5% of all the genotypes. In this cluster, genotypes showed early maturity with high harvest index in common.

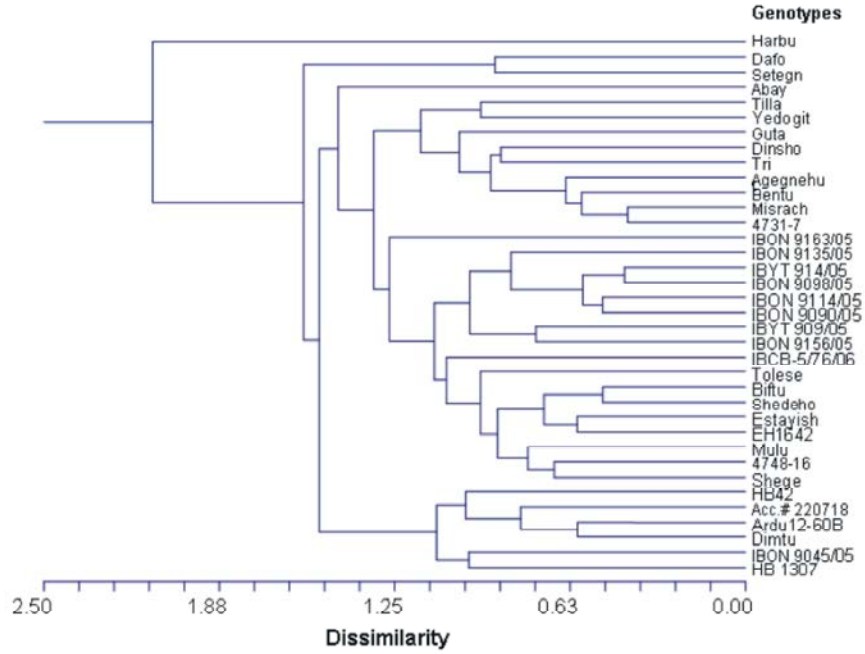

Fig. 1: Dendrogram depicting the genetic relationship of released and in pipeline food barley genotypes based on morphological characters evaluated at Holetta and Debark in 2010/11

Table 5: Cluster wise mean values of characters released and pipeline, food barley genotypes (above number) and the difference between each cluster with the total mean (below number) studied at Holetta and Debark 2010/11 crop season

Clusters	DHE	GFP	DMA	PLH	SPL	PT/PL	KN/S	BM	GY	HI	TKW
I	66.0	54.1	120.1	93.4	7.8	5.5	32.4	8843.7	3095.1	33.0	37.5
M/diff	-4	7.2	3.1	-4.2	-0.1	0.1	-9.0	-434.0	55.1	0.7	3.2
II	69.9	45.5	115.5	98.8	7.5	4.5	37.8	7958.3	2695.2	33.3	34.7
M/diff	-0.1	-1.4	-1.5	1.2	-0.4	-0.9	-3.6	-1319.4	-344.8	1.0	0.4
III	67.1	47.1	114.3	94.4	7.2	5.5	42.1	6875.0	2823.7	44.4	36.1
M/diff	-2.9	0.2	-2.7	-3.2	-0.7	0.1	0.7	-2402.7	-216.3	12.1	1.8
IV	73.9	44.5	118.3	100.6	7.9	4.8	43.3	9953.1	3608.5	36.3	35.9
M/diff	3.9	-2.4	1.3	3.0	0	-0.6	1.9	675.4	568.5	4.0	1.6
V	73.8	45.7	119.5	88.5	7.5	4.9	46.6	10473.2	4514.1	43.5	37.5
M/diff	3.8	-1.2	2.5	-9.1	-0.4	-0.5	5.2	1195.5	1474.1	11.0	3.2
VI	75.7	50.1	125.8	100.5	7.6	4.7	42.0	12125	4625.8	38.3	44.8
M/diff	5.7	3.2	8.8	2.9	-0.3	-0.9	0.6	2847.3	1585.8	6.0	10.5
VII	79.7	45.9	125	111.2	8.2	4.8	44.3	11106.3	3889.9	35.1	40.6
M/diff	9.7	-1.0	8.7	13.6	0.3	-0.6	2.9	1828.6	849.9	2.8	6.3

M/diff= Mean difference between cluster mean and the mean of all genotypes. DHE=Days to Heading, GFP=grain filling period, DMA=Days to Maturity, PLH=Plant Height (cm), SPL= Spike length (cm), PTI/PL=Number of Productive tillers plant^{-1}, NK/SP= Number of Kernels spike^{-1}, BM=biomass (kg h^{-1}), HI= Harvest index (%), TKWt=1000Kernel Weight (g) and r_g= Genotypic correlation coefficients.

Table 6: Mahalanobis distance between groups of barley genotypes studied at Holetta and Debark

Clusters	I	II	III	IV	V	VI	VII
I	-	35.88***	62.86***	82.51***	205.82***	137.14***	135.73***
II		-	55.15***	49.52***	179.78***	136.22***	112.76***
III			-	75.88***	177.21***	180.82***	174.70***
IV				-	51.97***	45.58***	41.58***
V					-	46.59***	79.77***
VI						-	20.43*
VII							-

X^2=18.31, 23.31 and 29.59 at 5%, 1% and 0.1% probability level respectively

Genotypes included in cluster four were 22.2% of the total genotypes. Here early grain filling was peculiar characteristics that discriminated the genotypes from the rest. Cluster V accounted 19.4% of the total genotypes in which plant height showed large difference among clusters in addition to kernel number spike^{-1}. The genotypes grouped in this cluster had short plant height with high kernel number spike^{-1}. Cluster VI included 5.5% of the total genotypes. In this cluster biomass, grain yield, thousand-kernel weight and days to maturity registered maximum cluster mean values. Hence, genotypes were grouped based on high biomass, high grain yield, high thousand-kernel weight and late matured genotypes. Cluster VII took account of 11.1% of the total genotypes. In this cluster, days to heading and spike length had maximum cluster mean values. Therefore, genotypes grouped in this cluster were seen taking longer days for heading with long spike length.

Generally, mean values of each traits in each clusters indicated that different breeding purposes. The mean of days to heading i.e., a criterion for early maturity in the first cluster was significantly lower than the total average (Table 5). Therefore, these genotypes can be used for breeding programs to develop early maturity varieties. Similarly the mean of grain filling period in the fourth cluster was significantly lower than the overall mean average. As a result, these genotypes could be important for short grain filling period breeding programs. Therefore, breeders could select genotypes based on their cluster mean difference to improve grain yield. Generally, genotypes grouped under cluster V and VI were found to be high grain yielder.

Genetic Distance Between Clusters: Divergence analysis is usually performed by using D^2 techniques of Mahalanobis to classify the diverse genotypes for hybridization purpose [13]. The genetic improvement through hybridization and selection depends upon the extent of genetic diversity between parents. The paired D-square value was computed based on the pooled mean of the genotypes. Based on the D-square value genotypes were grouped in to seven (Table 6). The T-test of the clustered group revealed that there is statistically approved difference between the paired clusters.

The X^2-test for the seven clusters indicated that there was statistically significant difference among all the clusters. The highest average inter cluster distance was recorded between cluster I and cluster V (D^2=205.82) followed by between cluster III and cluster VI (D^2=180.82), between cluster II and cluster V (D^2= 179.78), between cluster III and V (D^2=177.21) and between cluster III & VII (D^2 =174.7) which revealed that these clusters were genetically more divergent from each other (Table 6).

Crosses involving parents belonging to most divergent clusters would be expected to manifest maximum heterosis and wide variability in genetic architecture [22]. In the present study, clusters I, II and III were the most divergent from clusters V, VI and VII. However, the chance of getting segregants with a high yield level is quite limited when one of the clusters has a very low yield level [23]. Among clusters, cluster II and III had the lowest mean performance in yield and other important characters. This indicates that the chance of getting segregants with high yield is limited from crosses with other clusters.

The selection of parents should also consider the special advantages of each cluster and each genotype within a cluster depending on specific objectives of hybridization [24, 25]. Thus, in view of the present result, crosses involving cluster I with cluster V, VI and VII would be suggested to exhibit high heterosis and could result in segregants with higher grain yield. The present study revealed the presence of significant genetic variability among the tested genotypes. Thus, there is an opportunity to improve yield through hybridization of genotypes from different clusters and subsequent selection from segregating advanced generations.

CONCLUSIONS

The present study generally showed the presence of significant genetic variability among the tested genotypes. Thus, there is an excellent opportunity to bring about improvement through direct selection and hybridization that involves crossing of genotypes from different clusters.

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