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Genetic Variability of Ethiopian Barley (*Hordeum Vulgare* (L.)) Genotypes for Yield and Yield Related Traits

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Abstract: The existence of genetic diversity is very essential in identifying possible genotypes for further crop improvement. One hundred thirty-five landrace barley accessions and three released varieties were evaluated for their genetic variability and the preliminary performance for agronomic importance traits using augmented block design during the 2019 main cropping season under rain-fed condition. Data were recorded from nine quantitative characters and analysis of variance indicated the presence of significant variations at ($P < 0.01$) between the tested genotypes for days to 50% flowering, number of tillers per plant, spikelet per spike and thousands seed weight. The phenotypic and genetic coefficients of variations ranged from 11.19 to 38.84% and 3.77 to 33.87%, respectively. Both coefficients of variations had high values for the number of spikelets per spike, number of kernels per spike and grain yield. Broad sense heritability ranged from 11.35% to 98.01% and all traits had high heritability except plant height which had low heritability. Also, the genetic advance as per cent of mean ranged from 2.6 (plant height) to 67.35% (kernel per spike), respectively. Generally, the study revealed the existence of a wide range of variability among the studied barley genotypes which has paramount importance for further exploitation of genotypes for their important traits to enhance the breeding program of barley in the country.

Keywords: Heritability, *Hordeum Vulgare*, Quantitative Traits, Productivity, Variability

1. Introduction

Ethiopia is the primary and secondary gene centre for various crop species, including barley. Barley introduced in Ethiopia centuries ago and since then adapted and developed wide genetic diversity [1]. The variety in soil, climate, altitude and topography, together with geographical isolation for long periods considered the key factors inducing the large diversity in Ethiopian barley [2]. Social features also play a significant role in diversification. Thus, morphological, biochemical and molecular assemblies in Ethiopian barley are the overall effect of accumulated long-term mutations, hybridization, gene recombination and natural as well as human selection in heterogeneous environments [3].

It is one of the oldest cultivated crops in Ethiopia and has been grown for at least 5000 years [4]. The total area covered by barley in Ethiopia is 811,782.08 hectares and total annual production of about 1,767,518.447 tons with the productivity of 2.177 ton ha⁻¹ in the 2018/2019 main cropping season and it is the fifth most important cereal crop next to *teff*, wheat,

maize and sorghum in terms of area coverage and production, in a given order [5]. Barley can be grown at altitudes ranges of 1500 and 3500 m but is mostly grown between altitudes of 2000 and 3000 m above sea level [6]. In Ethiopia, barley produces in two harvests per year including the main rainy (June to September) and the short rainy (March to April) seasons [7].

Availability of proper genetic resources is very vital for any crop improvement and their evaluation for various agronomic traits. The assessments of the extent of genetic variation among and within populations are valuable to do more effective and efficient genetic improvement [8]. Genetic diversity assessment can be used to evaluate the extent of variability in a given genetic resource and used to identify parental lines for hybridization and introgression of desired genes into the available genetic base [9, 10].

Ethiopian Biodiversity Institute collected and conserved about 17,000 barley accessions which are 20.7% of the total crop plant accessions preserved in its gene bank. The collections were representative of the major barley growing

regions of the country which covers a wide range of agro-ecological conditions. Among barley accessions conserved in a gene bank, 5003 accessions were characterized by researchers and further 12,004 barley accessions are yet to be screened for their potentially useful traits to address constraints observed in the barley improvement research program in the country which is of paramount importance in increasing the production and productivity of barley to enable the food security struggle of the country. Therefore the study aimed to assess the extent of genetic variability of the barley genotypes and evaluate the preliminary performance of genotypes for agronomic importance traits which will serve to expand varietal choice options for researchers in developing barley cultivars with better agronomic performances.

2. Materials and Methods

2.1. Description of the Study Area

The experiment was conducted at Ethiopian Biodiversity Institute Arsi Negelle research site, West Arsi Zone of

Oromia Region during the 2019 main cropping season under rain-fed condition. The research site is located 7°19'22" N latitude and 38°39'20"E longitude with an altitude of 19330 m above sea level. The site is characterized with mean annual minimum and maximum temperature of 6.8°C and 27.2°C, respectively. The area's rainfall also ranged from 250 to 750 mm per annum. The soil of the experimental site was sandy loam [11].

2.2. Experimental Materials and Design

The plant materials used in this study consist of 135 barley accessions that were collected from different agroecology of the country ranging from 1500 to 2500 m above sea level and conserved in the Gene Bank of Ethiopia Biodiversity Institute. Three released varieties (HB-1963, HB-1964 and IBON-173/03) obtained from the Kulumsa Agricultural Research Centre were included as standard checks. These checks were selected from released varieties commonly grown around the experimental site and the total genotypes used in the study are presented in table 1.

Table 1. List of barley accessions and checks variety used for the study.

S/N	accession number										
1	3630	24	3671	47	3756	70	3781	93	3896	116	3969
2	3631	25	3672	48	3757	71	3783	94	3917	117	3970
3	3632	26	3673	49	3758	72	3834	95	3940	118	3971
4	3633	27	3680	50	3759	73	3835	96	3941	119	3972
5	3634	28	3681	51	3760	74	3836	97	3942	120	3973
6	3638	29	3682	52	3761	75	3837	98	3943	121	3975
7	3653	30	3682	53	3762	76	3838	99	3944	122	3976
8	3654	31	3682	54	3763	77	3840	100	3946	123	3980
9	3655	32	3682	55	3764	78	3841	101	3947	124	3981
10	3656	33	3682	56	3765	79	3842	102	3948	125	4048
11	3657	34	3682	57	3767	80	3843	103	3949	126	4049
12	3658	35	3682	58	3769	81	3844	104	3955	127	4050
13	3659	36	3682	59	3770	82	3845	105	3956	128	4111
14	3660	37	3682	60	3771	83	3846	106	3957	129	4112
15	3662	38	3682	61	3772	84	3847	107	3958	130	4113
16	3663	39	3682	62	3773	85	3848	108	3959	131	4114
17	3664	40	3682	63	3774	86	3849	109	3960	132	4115
18	3665	41	3682	64	3775	87	3850	110	3961	133	4116
19	3666	42	3682	65	3776	88	3851	111	3964	134	4117
20	3667	43	3682	66	3777	89	3852	112	3965	135	4118
21	3668	44	3682	67	3778	90	3853	113	3966	136	HB-1963
22	3669	45	3682	68	3779	91	3854	114	3967	137	HB-1964
23	3670	46	3682	69	3780	92	3855	115	3968	138	IBON-173/3

The experiment was laid down in augmented block design. The three checks were replicated in each block. Each genotype was sown on 4 rows x 0.2m x 2m (1.6 m²) plot size and accommodated four rows of 2 m length with 20 cm distance. The distance between plots and blocks was 0.5 m and 1 m respectively. The genotypes were sown on 23 July 2019. 100 kg ha⁻¹ Diammonium Phosphate (DAP) and 80 kg ha⁻¹ Urea were applied during sowing. Other management practices were applied as recommended for the site.

2.3. Data Collection

All phenological and morphological data were recorded

according to [12] barley descriptor list. Data of phenological traits, grain yield and thousand kernel weight were collected on plot bases while data for the number of tillers per plant (count), plant height (cm), spike length (cm), Spikelet per spike (count), and Kernels per spike (count) were collected from 20 randomly selected and tagged plants.

2.4. Statistical Analysis

2.4.1. Analysis of Variance

Analysis of variance was analyzed for all agromorphology traits using R statistical software (version 4.0.4; augmentedRCBD package [13]). The mean performance of

genotypes comparison was done following the significance of mean squares using Duncan's Multiple Range (DMRT) at $P < 0.05$.

2.4.2. Estimation of Genetic Variability Components

The phenotypic and genotypic variability of 138 barley genotypes for each quantitative trait was estimated as phenotypic and genotypic variances and coefficients of variation. The genotypic variance was estimated according to the method suggested by Burton and Devane [14] considering mean square expectations from the analysis of variance. The analyses were done using R statistical software (version 4.0.4; augmentedRCBD package [13]). According to Sivasubramaniah and Menon [15], PCV and GCV values were categorized as low (0-10%), moderate (10-20%) and high ($\geq 20\%$).

2.4.3. Heritability and Genetic Advance

Broad sense heritability was estimated using the formula adopted by Falconer [16]. The heritability was categorized as low, moderate and high as suggested by Johnson *et al.* [17]. Genetic advance in the absolute unit (GA) and per cent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated following the methods illustrated by Falconer [16] and was categorized as low, moderate and high.

3. Results and Discussion

3.1. Analysis of Variance

The analysis of variance of the nine quantitative traits indicated the presence of significant variations at ($P < 0.01$) between the tested genotypes for days to 50% flowering, number of tillers per plant, spikelet per spike and thousands seed weight. Traits like 75% maturity and grain yield were significant at ($P < 0.05$). However, plant height, spike length and kernels per spike were not significant differences in genotypes. Significant variations were observed at ($P < 0.01$) among accessions for days to 50% flowering, number of

tillers per plant, spikelet per spike, kernel per spike and thousands seed weight. Besides, days to 75% maturity, spike length and grain yield showed significant variation between accessions at ($P < 0.05$). Highly significant ($P < 0.01$) difference between accessions vs checks for number of tillers per plant, spikelet per spike, kernel per spike, thousands seed weight and grain yield. No significant difference was observed for days to 50% flowering and days to 75% maturity in accessions vs checks; and number of tillers per plant between checks (Table 2).

The mean value of genotypes for days to 50% flowering and days to 75% maturity ranged from 38 to 86 and 76 to 125 days, respectively. Accession 3774 showed significantly earliness in 50% flowering while 3670, 3671, 3672, and 3696 showed significantly delayed flowering. Having such a wide variation of phenology traits would help to select or develop early maturing barley genotypes which can escape drought and can be cultivated in drought-prone areas of Ethiopia. Also, those delayed accessions could be used for areas that have prolonged rainfall season.

Accessions 3783, 3665, 3755, 3663 and 3759 had the highest numbers of tillers per plant whereas accessions 4113, 3965, and 4118 had the lowest numbers of tillers per plant. The lowest grain yield was estimated from accessions number 3688, 3847 and 3681. On the other hand, the highest grain yield was harvested from the accession numbers 3753, 3754, 3630 and 3660. Accession 3689 showed the lowest thousand grain weight, kernel per spike, spikelet per spike. On the other hand, genotypes 3837, 3673, 3965, and 3971 showed the highest mean values for spike length, thousand seed weight, kernel per spike and spikelet per spike, respectively. The present study showed that the presence of variations among barley genotypes for phonological and important agronomic traits. Having a wide range of genetic variation in mean values show the presence of high variability for these traits and thus offering greater scope for selecting desirable genotypes.

Table 2. Mean square values of the nine quantitative traits of 135 barley accessions along with the three standard checks.

Traits	Mean square					Error (DF 8)	Mean	CV (%)
	Block (DF 4)	Genotypes (DF 137)	Accessions (DF 134)	Checks (DF 2)	Accessions vs Checks (DF 1)			
Days to 50% flowering	4.73	73.9**	82.16**	210.2**	1.13 ^{ns}	2.28	58.86	2.6
Days to 75% maturity	24.17	158.56*	192.63*	88.8 ^{ns}	2.32 ^{ns}	49.22	94.37	7.4
Plant height (cm)	17.39	44.68 ^{ns}	26.7 ^{ns}	573.99*	1460.58*	77.67	93.96	9.4
Number of tillers per plant	0.054	0.66**	0.95**	0.029 ^{ns}	3.07**	0.1	4.91	6.6
Spike length (cm)	0.32	1.09 ^{ns}	1.37*	4.85**	3.90*	0.39	7.78	8.1
Spikelet per spike	0.74	50.02**	84.47**	13.1*	261.4**	2.48	29.86	5.3
Number of kernels per spike	0.74	2.494 ^{ns}	91.99**	13.12*	527.47**	1.83	28.03	4.8
Thousand seed weight (gm)	7.55	56.11**	30.42**	153.3***	786**	5.69	42.6	5.6
Grain yield (kg ha ⁻¹)	23.94	145.24*	146.3*	29.92	937.6**	34.25	31.36	18.7

*, **, ns= Significant at ($p < 0.05$), ($p < 0.01$) and non-significant, respectively. DF= Degree of freedom, CV= Coefficient of Variation (%), genotypes= accessions + checks.

3.2. Estimates of Variability Components

3.2.1. Phenotypic and Genetic Coefficient of Variations

The Phenotypic coefficient of variation (PCV) and

genotypic coefficient of variation (GCV) values ranged from 11.19 to 38.84% and 3.77 to 33.87%, respectively (Table 3). The lowest PCV and GCV values were estimated for plant height while the highest values for PCV and GCV were estimated for grain yield. According to Sivasubramaniah and

Menon [15], PCV and GCV could be categorized as low (<10%), moderate (10-20%) and high (> 20%). The number of spikelets per spike, number of kernels per spike and grain yield had high values for both coefficients of variations. The PCV and GCV values for these traits ranged from 30.42 to 38.84% and 29.97 to 33.87, respectively.

Days to 50% flowering; days to 75% maturity, number of tillers per plant, spike length, thousand seed weight had moderate GCV ranging from 11.84 to 18.59%. Also, days to 50% flowering; days to 75% maturity, plant height, number of tillers per plant, spike length, thousand seed weight had moderate PCV values ranging from 11.19 to 19.7%. The magnitude of the differences between GCV and PCV values was low <5% for all traits except plant height (7.42). High phenotypic and genotypic coefficient of variation for studied traits indicates the existence of immense inherent variability that remains unaltered by environmental conditions among the genotypes, which in turn is more useful for exploitation in selection and hybridization programs.

3.2.2. Heritability and Genetic Advance

Heritability values help predict the expected progress to be achieved through the process of selection. Heritability in a broad sense (H^2) ranged from 11.35% (plant height) to 98.01% (kernel per spike) (Table 3). As suggested by Johnson *et al.*

[17], heritability values are categorized as low (<30%), moderate (30-60%) and high (>60%). Based on this classification, all traits had high heritability except plant height which had low heritability. High heritability estimated for days to 50% flowering, days to 75% maturity, number of tillers per plant, spike length, spikelet per spike, number of kernels per spike, thousand seed weight and grain yield. Heritability tells us the possibility and extent to which improvement can be brought through selection. It is also a good index of the degree of transmission of the characters from parents to their offspring. The most important purpose of the heritability estimation in the genetic study of quantitative traits is its predictive role to indicate the trustworthiness of the phenotypic value as a guide to breeding value [16]. The genotypic coefficient of variation along with heritability estimates provides reliable estimates of the amount of genetic advance to be expected through phenotypic selection [18].

The genetic advance as per cent of mean ranged from 2.6 to 67.35% for plant height and kernel per spike, respectively (Table 3). According to Johnson *et al.* [17], the range of genetic advance as per cent mean classified as low (<10%), moderate (10-20%) and high (>20%). Accordingly, all the traits had high genetic advance as percent of mean at 5% selection intensity except low for plant height.

Table 3. Estimates of variability components for nine quantitative traits of 138 barley genotypes.

Traits	Range	Mean	SE	σ^2_g	σ^2_e	σ^2_p	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
Days to 50% flowering	39-86	58.88	0.79	79.88	2.28	82.16	15.18	15.39	97.22	18.18	30.87
Days to 75% maturity	76 -126	94.41	1.12	143.42	49.22	192.4	12.69	14.70	74.45	21.32	22.58
Plant height (cm)	64.1-115.3	85.85	0.78	10.49	81.94	92.43	3.77	11.19	11.35	2.25	2.60
Number of tillers per plant	2.63-7.45	4.95	0.08	0.85	0.10	0.95	18.59	19.7	89.00	1.79	36.18
Spike length (cm)	4.74-10.88	7.82	0.11	0.98	0.39	1.37	12.66	14.99	71.32	1.73	22.06
Spikelet per spike	13.07-53.97	30.21	0.77	81.99	2.48	84.47	29.97	30.42	97.06	18.4	60.92
Number of kernels per spike	13.53-49.2	28.79	0.81	90.17	1.83	91.99	32.98	33.31	98.01	19.39	67.35
Thousand seed weight (g)	21.13-56.27	42.00	0.51	24.73	5.69	30.42	11.84	13.13	81.29	9.25	22.02
Grain yield (quintals ha ⁻¹)	6.9-63.19	30.78	1.01	108.70	34.25	142.9	33.87	38.84	76.04	18.75	60.92

SE = Standard Error, σ^2_p = Phenotypic Variance, σ^2_g = Genotypic variance, σ^2_e = Error variance, PCV= Phenotypic Coefficient of Variation, GCV = Genotypic Coefficient of Variation, H^2 (%) = Broad-sense heritability in percent, GA= Genetic Advance and GAM (%) = Genetic Advance as percent of the Mean.

Days to 50% flowering, days to 75% maturity, number of tillers per plant, spike length, spikelet per spike, kernels per spike, thousand seed weight and grain yield had high heritability and genetic advance as per cent of mean. However, plant height had low heritability and genetic advance as a per cent of the mean. High heritability coupled with high genetic advance as per cent of the mean was more valuable in predicting the effect of selection than considering heritability estimates alone. Heritability estimates along with genetic advance provide better information than each parameter alone [17].

The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action [19]. Similar findings were reported by Hailu *et al.* [20] that low heritability <20% and low% mean GA <10% for plant height, high broad-sense

heritability >60% for days to maturity, high genetic advance >20% for grain yield. Also similar result reported high heritability for grain yield and days to maturity [21]. In any crop improvement program, genetic gains require high heritability of important agronomic traits 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 genotypes.

4. Conclusion

One hundred thirty-eight barley genotypes were evaluated for nine quantitative traits to assess the extent of variability and performance for these traits. The analysis of variance showed significant variation among genotypes for all quantitative traits except for plant height, spike length and number of kernels per spike. Phenotypic and genetic

coefficients of variations values were high for spikelet per spike, kernel per spike and grain yield and both had moderate values for days to 50% flowering, days to 75% maturity, number of tillers per plant, spike length, and thousand seed weight. The differences between the values of genetic and phenotypic coefficient of variations were low <5% for all these traits except plant height. Besides, both heritability and genetic advance as per cent of mean values were high to most of the traits which provide better information than each parameter alone. The results of this study revealed the presence of wide variation among barley genotypes for important traits indicating the potential for effective improvements and further manipulation of the genetic resources. This could be the nature of farmer's varieties because of their better adaptive traits to available environmental conditions which have important implications for sustainable crop production.

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