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Study on malting barley genotypes under diverse Agroecologies of north western Ethiopia

Muluken Bantayehu

Adet Agricultural Research Center, P. O. Box 08, Bahirdar, Ethiopia.

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The study was conducted with the objectives to determine the magnitude effect of genotype, environment, and their interactions on economically important traits and identify stable malt barley (*Hordeum distichon* L.) genotypes. Combined analysis of variance indicated that the main effects due to environment, genotype and GxE interaction were highly significant for grain yield and economically important malting quality triats indicated that development of both specific and wide adaptable varieties are essential. The GxE interaction of grain yield was further partitioned using AMMI and it showed the first two IPCA axes explained most of the sum of squares. According to stability analysis measures genotype G1 was the most stable whereas G13 showed specific adaptation in low potential environments. Protein content and seed size variability measures revealed G9 and G11 in protein content and G1 and G11 in seed size, respectively as the least varying genotypes across environments.

Key words: GxE interaction, kernel protein content, malting barley, stability analysis.

INTRODUCTION

Barley (*Hordeum distichon* L.) is an important grain crop in Ethiopia. It has diverse ecologies being grown from 1800 to 3400 m altitude in different seasons and production systems. In the highest altitudes, barley is grown as a sole crop. The total area covered by the crop is about one million hectares with a total annual production of 1.3 million tons (CSA, 2005). Northwestern high and mid altitudes belong to the major barley producing areas however all of the produce is used for food purpose. On the other hand, breweries have been setup in the country, which require lots of malt annually. Majority of their requirement is obtained from import. Since malting barley is a new crop to the northwestern Ethiopia, information is unavailable about cultivar performance across diverse environments. The performance of malting barley grain yield and quality characteristics depends greatly on environmental conditions, which results in differential expression of grain quality from environment to environment (Verme and Nagaragam, 1996). The genotype by environment interaction is another important aspect in affecting performance of genotypes across diverse environments. The GxE interaction arises when there is differential response of genotypes in environmental changes. It reduces the correlation between the genotype and phenotype, hindering the genetic potential of the cultivar (Kang and Gorman, 1989). Selection of stable genotype is described as one of the strategies to reduce GxE interaction effect. High yield stability refers to a genotype's ability to perform consistently, whether at high or low yield levels, across a wide range of environments. According to Finlay and Wilkinson (1963), yield response and stability are heritable and can be measured. Lin et al. (1986) have described nine parametric stability statistics. Among them, are conventional coefficient of variation (CV_i), variance of genotypes across environments

E-mail: mulban7@yahoo.com. Tel: 0911833047. Fax: +2510583380235.

(Si^2), Finlay and Wilkinson (1963) regression coefficient (b_i), Eberhart and Russell (1966) deviation from regression (S_{di}^2), Shukla's (1972) stability variance (σi^2) and Wricke's (1962) ecovalence (W_i^2) are parametric stability measures of genotypes.

The objectives of this paper were to: i) assess phenotypic performance of malting barley genotypes across northwestern Ethiopia, ii) determine the magnitude of effect of genotype, environment, and their interaction on yield and quality traits, and iii) to identify stable genotype in grain yield and consistence performance in protein content and seed size across environments.

MATERIALS AND METHODS

Field experiment

The field experiment was carried out with 20 advanced malting barley genotypes; EH1609-F5.B3-10 (G1), 37622 (G2), 118173 (G3), Bekoji sel-8 (G4), 118007 (G5), EH1510-F6.10H.3 (G6), 108932 (G7), 118173 (G8), 118146 (G9), EH1746-F6.B2-109 (G10), EH1606-F5.B2-7 (G11), EH1601-F5.B2-2 (G12), EH1603-F5.B1-4 (G13), EH1612-F5.B3.13 (G14), HB1533-sels (G15), and Miscal-2 (G16), Miscal-1 (G17), HB-242-sels (G18), along with standard checks; HB-52 (G19) and HB-120 (G20). The experiment was conducted under rainfed conditions in four locations that represent different barley growing agro-ecologies during three growing seasons (2004, 2005, 2007) where E1 = Adet-2004, E2 = Adet-2005, E3 = Adet-2007, E4 = Debretabor-2004, E5 = Debretabor-2005, E6 = Debretabor-2007, E7 = Dabat-2004, E8 = Dabat-2005, E9 = Adet-2007, E10 = Laygaint-2004, E11 = Laygaint-2005 and E12 = Laygaint-2007. At each location, the genotypes were planted in a randomised block design in three replicates. Sowing was done by hand in plots of 3 m^2 with six rows measuring 2.5 and 0.2 m within row spacing. Fertiliser application was 41 kg N ha^{-1} and 46 kg P_2O_5 ha^{-1} at planting. The four middle rows with an area of 2 m^2 were harvested.

Data collected

Harvesting and data collection were done from the four central rows. Yield data was recorded on clean, dried samples and plot yields were adjusted to 12.5% moisture level and converted to kilogram per hectare. Thousand kernels were counted by using electronic seed counter and weighted (g). Every sample was measured in standard hectoliter and then weighted to know their hectoliter weight. Germination energy in percent was determined from 100 seeds germinated in a petridish after 120 h. Two hundred seeds were soaked in a flask with 0.3M H_2O_2 (hydrogen peroxide) and counting after 24 h and converted to percentage to determine germination capacity. Seed size test was carried out using 2.2, 2.5, 2.8 mm size sieves and proportion of the seed trapped by each sieves were weighted and converted to percentage. Eight gram samples from each plot were grounded and 5.0 g flour was placed in moisture dishes and was oven dried for 1 h at 100°C. Percent moisture was determined from the mass of water lost on drying to the original milled sample and kernel protein content was also determined using Kjeldahl method.

Statistical analysis

Analyses of variance were performed on all traits. Thereafter, combined analyses of variance were performed using fixed linear model where both genotypes and environments were fixed. Mean separation was carried out using least significant (LSD) at 5% level of significant. The G x E interaction was further partitioned using additive main effects and multiplicative interaction (AMMI) statistical model. The AMMI analysis of variance summarizes most of the magnitude of genotype x environment interaction into one or few interaction principal component analysis (Zobel et al., 1988; Guach, 1988). The larger the IPCA scores, either negative or positive, the more specifically adapted a genotype is to a certain environments; the smaller the IPCA scores, the more stable the genotype is over all environments studied. AMMI analysis was performed for grain yield. The method of Eberhart and Russell (1966) was used to calculate the regression coefficient (b_i), deviation from regression (Sd_i^2) and coefficient of determination (R_i^2). It was calculated by regressing mean grain yield of individual genotypes on environmental index. Shukula stability variance (σi^2) and Ecovalence (Wi^2) suggested by Wricke (1962) were also computed, where stability values with minimum values are considered stable.

Variability of genotypes for protein content and seed size across environments were also measured by coefficient of variation (CV_i) (Francis and Kannenberg, 1978) and genotypic variance across environmental (Si^2).

RESULTS

Phenotyping

Grain yield

Mean grain yield of locations averaged over genotypes was between 3376.0 and 831.0 $kgha^{-1}$ at E5 and E11, respectively (Table 2). The mean grain yield over all the genotypes and locations was 2178.7 $kgha^{-1}$. Moreover, performances of genotypes were not consistent across locations. G1, G12 and G13 won all the genotypes at all most all environments except E4, E5 and E6. At E4, G12 with grain yield of 4427.0 $kgha^{-1}$ and at E5, G5 with 4614.7 $kgha^{-1}$ were the top performing genotypes. G17 produced the least when genotypes are ranked according to their grain yield performance. When environments were compared, the highest mean grain yield (3376.0 $kgha^{-1}$) was obtained at E5, while E11 (831.0 $Kgha^{-1}$) and E12 (1791.50 $Kgha^{-1}$) were relatively low yielding environments. The low grain yield at these environments that represent Dabat could be because of the water logging of the trial site. Moreover, relatively small amount of annual rainfall coupled with high disease pressure resulted in poor stand and low grain yield (Table 1).

Malting quality traits

Highest mean thousand kernel weight was recorded at Adet (40.85 g) and lowest mean at Dabat (37.42 g). Genotypes G13 (46.1 g), G11(45.9 g), G3 (43.37) and G1(42.49 g) provided the highest thousand kernel weight but genotype G2, G16 and G17 had low mean thousand kernel weight over locations with corresponding values of

Table 1. Total annual rainfall, soil type and altitude of the locations.

Location	Altitude (m.a.s.l)	Total annual rainfall (mm)	Soil type
Adet	2240	1331.8	Nitosol
Debretabor	2630	1378.6	Luvisol
Dabat	2620	963.4	Cambisol
Laygaint	2500	950.4	NA

Sources: NMSA, BBO, Tsige (2002) and Yihenew (2004), NA: not Available.

33.1, 35.1 and 34.4 g. G15 also produced highest hectoliter weight 60.56 $kghl^{-1}$ and G2 with 56.66 $kghl^{-1}$ gave the lowest. The standards set for thousand kernel weight and hectoliter weight by National Standard Authority ranged from 35 to 45 g and 60 to 65 $Kghl^{-1}$, respectively. The mean thousand kernel weight of most genotypes, but G2 and G17 fulfill the requirement; however, hectoliter weight of genotypes averaged over all locations except G7, G10, G14 and G15 did not meet the standards. Kernel protein content of genotypes averaged from all locations was between 9.25% for G19 and G20 and 11.0% for G2 (Table 3). Protein content for G2, G4 and G5 was high with 11.0, 10.5 and 10.5%, respectively. All genotypes gave acceptable mean kernel protein and met the standards set by the National Standard Authority for malting barley that should be between 9 and 11.5. Kernel protein content that exceeds recommended levels is undesirable for malting because it increase steep times and cause uneven water uptake during steeping, uneven germination during malting, increased malt loss due to abnormal growth, excessive enzymatic activity, low extract yield, excessive nitrogenous compounds in the wort during brewing, and chill haze formation in beer (Burger et al., 1979). Table 4 reveals that Adet (11.49) and Debretabor (10.45) were the locations where high protein content was recorded while the mean kernel protein contents obtained from Dabat and Laygaint was 8.35 and 8.82, respectively and the standard set by Ethiopian National Standard Authority was not achieved at these locations. This might be due to low fertility and low temperature.

G1, G11 and G19 had the large mean percentage of kernels trapped by 2.8, 2.5 and 2.8 + 2.5 mm size sieves (Table 3). From the tested genotypes, only G1 and G11 fulfills the standard greater than 80% of the kernel that passed through 2.5 + 2.8 mm size sieve. Genotype that had high percent of screen loss was G2. These genotypes had small kernel size much below the standard as observed in the test using 2.2 and <2.2 mm size sieve. Other genotypes provided kernel sizes in between these two ranges. Highest percentage of acceptable kernel size (92.5%) was recorded at Laygaint. Adet was the locations where higher kernel sizes were recorded next to Laygaint (Table 4). From the result it can be deduced that genotypes grown at these location meet the standard. It can be seen from Table 3 that G4 obtained germination energy of 99.75% followed by G1 (99.42%). The least germination energy was obtained from G9 and G3 (97%). All genotypes showed germination energy that meets the standard (> 95% in 120 h). The highest germination energy (99.55%) was observed from seeds harvested at Dabat because of early harvesting (Table 4). All genotypes had germination capacity above 97% that is the minimum requirement set by National Standard Authority. G4 was the top in germination capacity with 100% seeds germinated.

Genotype by environment interaction components

The combined analysis of variance revealed a highly significant ($p<0.01$) variation for the genotype, environment and genotype by environment interaction effects for grain yield, thousand grain weight and hectoliter weight (Table 5). This indicated genotype, environment and their interaction are important in governing the expression of these traits. It agrees with the finding that yield and quality traits are influenced by genotype (G), environment factors (E) and their interaction (Uhlen et al., 1998). The presence of variation between environments point out the presence of dissimilarity and provide a baseline information to categorize potential, low potential and intermediate yielding agro ecologies. The genotype effect depicted clear variation among tested genotypes thus wide and specific adaptation of genotypes is crucial for vertical increase of production. The significant GxE interaction indicated the differential genotypic performance across environments. It reduces the association between phenotypic and genotypic values, and thus, genotypes that perform well in one environment may perform poorly in another (Fox et al., 1996).

Generally, larger interaction component cause difficulties in selection of widely adapted, high yielding genotypes under diverse environments. The presence of significant G x E interaction and environment effects on yield traits were reported by Finlay and Wilkinson (1963) and Tesfaye et al. (1998) in barley.

Additive main effects and multiplicative interaction analysis for grain yield

Additive main effects and multiplicative interaction

Table 2. Mean grain yield (Kgha^{-1}) of twenty malting barley genotypes evaluated at four testing sites in the 2004, 2005 and 2007 main rain cropping season.

Genotype	Environment												Mean ($\bar{x}$)
	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	
G1	4225.0	3548.3	3763.7	4164.0	3552.0	2889.7	1774.0	1805.7	1949.0	2869.7	885.5	2120.3	2795.5
G2	2592.0	1930.0	2138.0	1356.3	1881.3	2511.0	904.8	767.7	1223.5	1743.7	772.7	1309.3	1594.2
G3	3520.0	3296.0	3285.0	3370.0	3878.7	2830.3	1364.7	712.1	1413.0	1997.7	1663.7	1318.3	2387.3
G4	2460.0	2465.7	2340.0	3345.3	2395.3	2598.7	1377.0	997.3	1295.7	1964.7	1029.3	806.7	1923.0
G5	2785.7	2415.0	2477.0	3964.7	4614.7	2905.0	1562.3	735.8	805.2	1905.7	841.2	1857.7	2239.1
G6	3414.0	2829.3	2998.3	4061.0	3701.7	3942.0	406.3	834.3	1970.7	2052.3	175.3	1619.7	2333.7
G7	3395.7	2617.0	2883.3	2362.0	2190.3	2063.0	1235.3	1564.0	920.2	1488.7	622.3	522.0	1821.9
G8	3639.7	3279.0	3336.0	3436.7	3693.7	2625.3	863.5	1159.7	1794.7	2142.0	920.8	1257.0	2345.6
G9	3580.3	3213.7	3273.7	3085.7	3616.7	2801.0	716.2	771.8	1073.2	2236.0	1271.5	1218.0	2238.1
G10	3633.7	2808.7	3098.3	3851.3	3812.3	3308.3	1116.2	607.7	894.4	2360.7	1091.9	497.3	2256.8
G11	3732.7	3190.0	3338.3	3589.0	3887.0	3386.0	769.2	1165.2	1078.0	1895.0	987.8	1181.3	2349.9
G12	4103.7	3806.0	3832.0	4427.3	3113.3	3460.3	822.3	1505.3	1529.7	1685.7	660.8	1127.3	2506.2
G13	3933.0	3962.7	3824.7	3918.7	4038.7	2645.3	1289.7	1678.0	1611.0	2196.0	1068.8	1785.3	2662.6
G14	3527.7	3221.3	3251.0	3563.0	3629.0	3135.3	1429.0	2154.3	1340.5	1905.0	840.0	1117.7	2426.0
G15	3583.3	3248.7	3293.0	3820.3	3654.3	2948.0	1344.0	1241.7	1823.7	1965.3	600.2	247.7	2314.2
G16	2590.3	1925.0	2134.7	2861.7	3426.7	2348.0	1177.7	905.2	1388.5	2480.0	1055.6	687.5	1915.0
G17	2066.0	1417.0	1618.7	1545.0	1865.0	1446.7	1481.3	529.9	963.1	2799.7	212.5	539.6	1373.7
G18	2593.0	2457.0	2402.0	4377.7	3803.0	3251.7	1022.8	1386.0	1376.2	1886.7	607.8	1231.0	2199.6
G19	3620.7	2983.3	3179.0	2777.3	3112.0	1683.3	1420.3	1198.7	1408.7	1392.3	435.7	623.2	1986.11
G20	2608.7	3031.0	2696.7	1838.0	3657.0	2515.7	465.6	1350.7	995.1	1727.7	879.0	1088.9	1904.45
Mean ($\bar{x}$)	3280.0	2882.0	2958.0	3286.0	3376.0	2765.0	1127.0	1153.0	1343.0	2035.0	831.0	1108.0	2178.7
SE ±	220.0	236.1	164.8	220.9	266.7	137.6	58.09	58.9	42.13	146.1	101.4	44.30	65.2
LSD (5%)	629.72	675.8	471.9	632.5	763.5	394.0	166.3	168.7	120.6	418.4	290.4	126.8	181.2
C.V (%)	11.61	14.18	10.0	12.0	14.0	9.0	9.0	9.0	5.0	12.0	21.0	7.0	18.0

Table 3. Mean grain protein content and other quality traits of twenty malting barley entries, tested at Adet, Debretabour, Laygaint and Dabat (2005).

Genotype	Germination		Protein (%)	HLW (kgha^{-1})	TGW (g)	Sieving test (%)				
	GE (%)	GC (%)				2.8 mm	2.5 mm	2.8+2.5 mm	2.2 mm	<2.2 mm
G1	99.42	99.67	9.90	59.66	42.49	56.05	30.83	86.93	9.08	3.98
G2	97.58	98.75	10.85	56.77	33.10	1.30	10.43	11.73	33.81	54.43
G3	97.67	97.83	9.78	58.03	43.37	33.91	44.28	78.18	16.41	5.33
G4	99.75	100.00	10.55	59.66	37.46	7.21	48.38	55.59	31.58	12.72
G5	99.17	99.92	10.47	58.93	42.37	39.63	37.23	76.86	14.50	8.48

Table 3. Cont.

G6	97.75	99.50	9.65	59.02	39.16	18.62	39.13	57.75	24.64	17.47
G7	98.83	99.25	9.51	60.01	37.70	32.89	41.93	75.18	17.79	7.18
G8	97.25	98.67	9.82	57.31	42.98	28.23	44.38	72.60	20.85	6.42
G9	96.42	97.50	9.98	57.84	42.89	28.84	41.97	70.81	21.49	7.57
G10	98.67	99.42	9.25	60.03	37.24	3.52	36.57	40.08	36.93	22.91
G11	98.67	99.58	9.80	59.53	45.90	37.48	46.48	83.95	12.46	3.53
G12	98.42	99.67	9.49	58.85	38.76	18.83	46.18	65.02	22.89	11.99
G13	99.33	99.42	10.32	59.73	46.06	28.00	47.98	75.98	14.82	9.14
G14	97.58	98.25	9.81	60.37	39.87	37.54	40.56	78.11	13.50	8.32
G15	99.00	99.92	9.73	60.56	41.37	18.49	45.13	63.62	23.30	12.98
G16	98.00	98.08	9.41	57.20	35.11	20.08	37.46	57.54	25.62	16.76
G17	97.50	97.83	9.51	57.95	34.37	12.42	29.80	42.19	29.48	28.70
G18	98.42	98.50	9.35	58.39	41.59	32.26	38.28	70.54	20.77	8.60
G19	98.00	98.50	9.07	58.65	38.80	35.29	43.45	78.78	14.74	6.37
G20	98.00	99.25	9.28	59.33	37.68	8.89	51.58	60.47	28.97	10.47
Mean ($\bar{x}$)	98.3	98.9	9.8	58.89	39.91	24.9	40.1	65.1	21.7	13.2
SE ±	1.48	1.27	0.36	0.75	0.56	8.03	5.92	9.06	5.31	5.04
LSD (5%)	2.48	2.13	0.60	2.09	1.55	13.44	9.89	15.15	8.87	8.42
C.V (%)	2.13	1.82	5.2	7.6	8.4	45.36	20.82	19.67	34.56	54.18

TSW = Thousand seed weight, PC = protein content, GE = germination energy, GC = germination capacity.

Table 4. Mean values of malting quality traits of malting barley genotypes grown at four representative locations in the 2004 main cropping season.

No.	Location	TSW (g)	PC (%)	GE (%)	GC (%)	Kernel size test using sieve sizes of (mm)				
						2.8	2.5	2.5+2.8	2.2	<2.2
1	Adet	40.85	11.49	96.51	97.55	28.05	41.39	69.45	20.08	10.34
2	Debretabor	41.14	10.45	98.83	99.70	33.86	42.73	76.65	16.19	7.11
3	Dabat	37.42	8.35	99.55	99.9	23.65	43.18	66.82	20.92	12.32
4	Laygaint	39.16	8.82	98.35	98.75	14.34	33.11	47.47	29.55	22.91
Mean ($\bar{x}$)		9.8	98.9	39.91	98.3	24.9	40.1	65.1	21.7	13.2
SE ±		0.36	1.27	0.56	1.48	8.03	5.92	9.06	5.31	5.04
LSD (5%)		0.60	2.13	1.55	2.48	13.44	9.89	15.15	8.87	8.42
C.V (%)		5.2	1.82	8.4	2.13	45.36	20.82	19.67	34.56	54.18

TSW = Thousand seed weight, PC = protein content, GE = germination energy, GC = germination capacity.

Table 5. Combined analysis of variance for twenty genotypes for yield and quality traits grown in 2004, 2005 and 2007 main rain cropping season.

Yield and quality traits	Mean squares (MS)		
	Environments (E)	Genotypes (G)	G x E
GY	200582000**	4365559.1**	60865505.0**
TKW	322.97**	469.51**	154.50**
HLW	403.39**	43.48**	51.6**
KPC	42.31**	0.88**	0.17 ns
GE	34.42**	2.53 ns	4.43 ns
GC	23.01**	2.45ns	3.30ns
SS	1356.32**	784.94**	128.76 ns
ST	446.30**	320.68**	69.66 ns
SY	3108.22**	1275.69**	164.17 ns
SL	634.47**	236.21**	56.39 ns

ns = non significant, * = significant (P<0.05) and ** = highly significant (P<0.01).

Table 6. Additive main effects and multiplicative interactions (AMMI) analysis of variance for grain yield of 20 genotypes of malting barley across 12 environments.

Source	Degree of freedom	Mean square	Variance explained (%)
Total	719	-	-
Treatment	230	3868773.39	92.39
Blocks	24	60865505.0	3.91
Environment	11	60865505.0**	75.24
Genotypes	19	4365559.1**	9.32
Interactions	209	657185.2 **	15.44
IPCA 1	29	1695438.4**	35.80
IPCA 2	27	1123189.2**	22.08
IPCA 3	25	637724.8**	11.61
IPCA 4	23	554398.6**	9.28
IPCA 5	21	439107.1**	6.71
Error	456	78097.8	3.70

** P< 0.01, ** Highly significant at the 0.01 probability level, *Significant at the 0.05 probability level, IPCA- Principal component axis for interaction.

(AMMI) analysis proved significant (P<0.05) main effects and interaction effects for grain yield (Table 8). It showed that 75.24% of the total sum of squares was attributable to environmental effects, 9.32% of genotypic effects and 15.44% to GxE effects (Table 7). A large sum of squares for environments indicated that the environments were diverse; with large differences among environmental means causing most of the variation in grain yield. The magnitude of the G x E sum of squares was highly significant (p<0.01) indicating that there were large differences in genotypic response across locations. Results from AMMI analysis also showed that the first principal component axis (IPCA1) of the interaction captures 35.80% of the interaction sum of squares at 29 of the degrees of freedom (Table 6). Similarly, Purchase et al. (2001) and Romagosa et al. (1996) reported 41 and 72% of the G x E interaction explained by the first IPCA in wheat and barley. The second interaction principal component axis explained a further 22.08% of the GxE sum of squares and only 11.6% by the third IPCA axis. The mean squares for the IPCA1, IPCA2 and IPCA3 were significant at P = 0.01 and cumulatively contributed to 69.5% of the total GxE. F-test at P = 0.01 revealed that the first four principal component axes of the interaction were significant for the model. However, the prediction assessment indicated that AMMI 2 with only two interaction principal component axes was the best predictive model (Zobel et al., 1988). Further interaction principal component axes captured mostly noise and therefore did not help to predict validation observations. Thus, the interaction of the twenty genotypes with twelve environments was best predicted by the first two principal components of genotypes and environments and genotypes and environments with similar signs of their

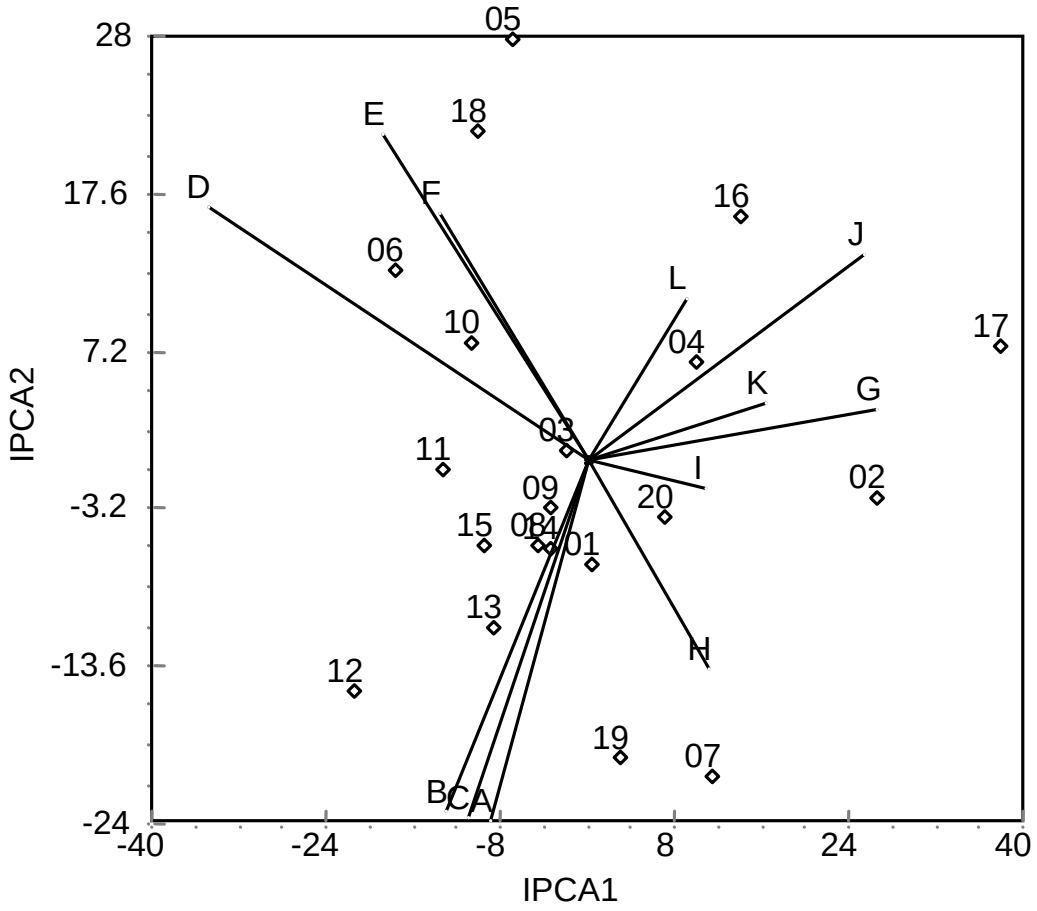

Figure 1. Biplot of principal component analysis axis (PCA) 1 against principal component analysis axis (PCA) 2 of twenty genotypes grown at twelve environments. 01 = G1, 02 = G2, 03 = G3, 04 = G4, 05 = G5, 06 = G6, 07 = G7, 08 = G8, 09 = G9, 10 = G10, 11 = G11, 12 = G12, 13 = G13, 14 = G15, 16 = G16, 17 = G17, 18 = G18, 19 = G19, 20 = G20. A = Adet-2004, B = Adet-2005, C = Adet-2007, D = Debretabor-2004, E = Debretabor 2005, F = Debretabor-2007, G = Dabat-2004, H = Dabat-2005, I = Adet-2007, J = Laygaint-2004, K = Laygaint-2005, L = Laygaint-2007.

IPCA scores interact positively for that trait.

AMMI 2 biplot as shown in Figure 1 has four sections: genotype G12, G19 and G13 were good for locations Adet: genotype G6, G18 and G10 were good for location Debretabor G2 and was good for Laygaint; and for Dabat genotypes G16 was good. Genotypes G1, G3, G9 and G4 located near the plot origin have low GxE interaction than the vertex genotypes and thus stable. Genotypes G5, G17 and G7 located far from the vertex were unstable over locations.

Stability analysis

Stability in performance of genotypes across environments using Eberhart and Russell's regression coefficient, deviation from regression, Wricke ecovalence and Shukula stability variance were performed for grain yield. According to Eberhart and Russell's model, genotypes performance across environments is generally expressed in terms of three parameters, mean yield, the regression coefficient (β_i) and the deviations from regression (s^2d_i). A stable genotype should have a high mean yield, unit regression coefficient and deviation from regression nearly equals to zero (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966). Accordingly, genotype G1 was the most stable because it had high grain yield, its regression coefficient was almost equal to unity and it had none significantly the least deviation from regression. In contrast, G6, G10 and G11 had Sd_i^2 values significantly different from zero and β_i greater than one that is, and below average stability, so were regarded as sensitive to environmental changes. Genotypes G2 and G17 had regression coefficients less than unity (βi <1.0) that is, above average stability and significantly different deviation from regression. These genotypes are therefore, insensitive to environmental changes and have specifically adapted to low potential environments.

Table 7. Mean grain yield and genotypic stability parameters for 20 malting barley genotypes grown over 12 environments.

Genotype	Mean	W_i^2 %	b_i	S^2d_i	σ_i^2
G1	2795.53	2.56	1.02	65798.92	359720.73
G2	1594.16	9.43	0.51	108814.66	503106.53
G3	2387.33	2.34	1.03	55164.67	324273.23
G4	1922.96	3.63	0.74	40716.72	276113.39
G5	2239.09	8.51	1.06	334503.28	1255401.92
G6	2333.73	7.72	1.27	223435.63	885176.43
G7	1821.91	5.15	0.81	142847.81	616550.35
G8	2345.64	1.21	1.09	-5105.23	123373.56
G9	2238.10	2.16	1.11	35010.17	257091.55
G10	2256.75	4.21	1.28	54990.73	323693.41
G11	2349.88	2.36	1.24	-5447.04	122234.18
G12	2506.15	7.14	1.33	155931.46	660162.52
G13	2662.63	2.84	1.14	57028.42	330485.73
G14	2426.04	2.00	1.02	40127.77	274150.21
G15	2314.17	3.49	1.22	56997.44	330382.46
G16	1915.03	4.55	0.78	102283.13	481334.76
G17	1373.73	14.50	0.46	289886.81	1106680.35
G18	2199.57	5.94	1.05	218517.97	868784.21
G19	1986.11	4.64	0.99	161276.34	677978.77
G20	1904.45	5.61	0.87	186810.96	763094.18

GY = Grain yield, bi = slopes of regressions, S2di = deviations from regression, Wi = Wricke ecovalence, = Sukula stability variance.

The result of Wricke's ecovalence (W_i) and Shukula's stability variance (σi^2) showed that G8, G14 and G19 were comparatively stable as their contribution to the GxE interaction sum of squares was least and with minimum stability variance (σi^2). On the other hand, G17 and G2 were unstable in grain yield performance because these genotypes had relatively higher ecovalence (Wi) and stability variance (σi^2) (Table 7). Kernel protein content and seed size variability of genotypes across environments using Francis and Kannenberg (1978) conventional coefficient of variation (CV_i) and variance of genotypes across environments (Si^2) was performed as indicated in Table 8. The model identified G15, G19 and G12 in kernel protein content and G4, G1 and G3 in seed size respectively showing relatively consistent performance across locations. Kernel protein content and seed size of these genotypes might have a relatively small variation on varied locations while grain protein content of G3, G9 and G11 and seed size of G1, G11 and G19 show considerable variation across environments.

DISCUSSION

Despite its potential and market demand, production of barley for malt is not expanded in northwestern Ethiopia. These could be attributed to the lack of information on the effect of genotype, predictable and unpredictable environmental variations and their interaction on yield and quality attributes of the crop. Thus, twenty genotypes were tested at four locations under rain-fed conditions in 2004, 2005 and 2007 main cropping seasons to assess phenotypic performance, determine the effect of genotype, environment, and their interaction and to identify stable ones in yield, consistent performance in protein content and seed size. Data were collected on grain yield and quality traits and analysis of variance (ANOVA), additive main effects and multiplicative interactions analysis (AMMI) and stability analysis were undertaken. The combined analysis of variance over locations has shown highly significant difference among genotypes, environments and genotype by environment interaction on grain yield. The effect of environment on this trait was greater than genotypes and genotype by environment interaction. Even though genotypes' performance ranking was not consistent across environments, most genotypes performed well in grain yield at Debretabor and Adet locations. Kernel protein content, thousand kernel weight and hectoliter weight of genotypes were promising at Debretabor and Adet.

Additive main effects and multiplicative interactions (AMMI) model analysis was used to partition the GxE interaction of grain yield. The first two principal component

Table 8. Estimates of variability in performance for protein content and seed size for twenty malting barley genotypes at four environments.

No.	Genotype	Protein (%)	Protein content variability		seed size	Seed size Variability	
			Si^2	CV_i	(2.8+2.5 mm)	Si^2	CV_i
1	G1	9.90	1.43	14.6	86.93	21.53	13.0
2	G2	10.85	1.42	12.9	11.73	21.33	40.7
3	G3	9.78	1.36	11.5	78.18	21.65	17.8
4	G4	10.55	1.36	16.5	55.59	21.47	15.9
5	G5	10.47	1.33	12.3	76.86	21.23	30.1
6	G6	9.65	1.30	17.5	57.75	21.38	38.4
7	G7	9.51	1.30	15.4	75.18	21.85	18.6
8	G8	9.82	1.30	14.1	72.60	21.82	31.0
9	G9	9.98	1.29	11.5	70.81	21.89	26.9
10	G10	9.25	1.28	16.2	40.08	21.83	48.8
11	G11	9.80	1.28	11.5	83.95	22.67	9.5
12	G12	9.49	1.27	13.6	65.02	22.61	32.1
13	G13	10.32	1.25	16.7	75.98	22.95	34.6
14	G14	9.81	1.20	12.9	78.11	23.06	35.3
15	G15	9.73	1.17	17.5	63.62	23.03	37.2
16	G16	9.41	1.15	20.2	57.54	23.46	24.3
17	G17	9.51	1.11	18.2	42.19	23.58	25.1
18	G18	9.35	1.10	16.2	70.54	23.58	22.7
19	G19	9.07	1.09	16.2	78.78	23.54	9.4
20	G20	9.28	1.08	16.2	60.47	23.44	20.9

GP = Kernel protein content, Si^2 = variance of genotypes acrose environments; CV_i = Francis and Kannenberg (1978) conventional coefficient of variation.

axes for interaction alone captured most of the interaction sum of squares. The sign and magnitude of IPCA scores revealed the relative contribution of each genotype and environment for the genotype and environment interactions and the biplot graph of AMMI scattered genotypes and environments based on their interaction (Zobel et al., 1988; Guach, 1988). It helped to summarize the pattern and magnitude of GxE interaction and main effects that reveal clear insight into the adaptation of genotypes to environments and helped enhanced understanding of GxE interactions. Stability analysis using Eberharts and Russell's coefficient of regression (β_i) (1966), deviation from regression (s^2d_i), Wricke's (1962) ecovalence (W_i) and Shukula's (1972) stability variance (σi^2) on genotypes performance across environments have shown similar results in identifying the stable genotypes. Relatively, G1 had better grain yield stability. G13 and G12 showed specificity in environments; however, a potential high yielder averaged over locations. G3, G11 had better consistent performance across environments in protein content and G1, G11 in seed size. Therefore, G1 could be used for production and further malting barley improvement programs in the sub-region.

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