

**Exploitation of Phenotypic Variations Among some Barley
(*Hordeum vulgare* L.) Genotypes for grain yield Under Irrigated
Conditions of Sudan**

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ABSTRACT

Barley in Sudan is grown in limited areas for grain and forage, although the barley is a well adapted crop to Sudan environment, it has a very small number of genotypes. Therefore, this study aims at the exploitation of phenotypic variations among the barley (*Hordeum vulgare* L.) genotypes in Sudan for possible utilization in breeding programmes and to identify the top yielding genotypes. A set of twenty barley genotypes were tested at three sites representing different environments of Sudan. The experiments were executed over two consecutive seasons (2010/2011 and 2011/2012) in a Randomized Complete Block Design (RCBD) with three replications. The results of the growth habit demonstrated that all the genotypes were resistant to lodging except the genotype 20 (local genotype) was susceptible to lodging. The results of the combined analysis showed very highly significant differences among the barley genotypes at three sites. Across the three sites, the common genotypes out-yielded the check were G3, G8 and G9. At Gezira, the genotypes G3, G8 and

G9 out yielding the check by 31, 24 and 40%, respectively, at Hudeiba high terrace soil by 34, 9 and 31%, respectively, while at Hudeiba karu soil by 61, 21 and 20%, respectively. According to the ASV (AMMI Stability Value) concept, the most stable genotype was the check Beladi having an ASV of 4.5 with the lowest mean seed yield (1970 kg/ha). In contrast, the most unstable genotype was G3 with an ASV of 37.7, however, it had the highest grain yield (2810 kg/ha). Among the six environments, when the genotypes were arranged according to AMMI estimate, genotype G3 ranked first in four environments (Gezira in season 2011, karu in two seasons and high terrace soil in season 2011), genotype G9 ranked first in one environment (Gezira in season 2010) and ranked third in the other five environments, while genotype G8 ranked second in the high terrace soil in season 2010 and fourth in two environments (Gezira in two seasons). The check Beladi did not appear in the first four ranking genotypes. Therefore, the genotypes G3, G8 and G9 could provide a good option for barley seed yield under Sudan conditions.

INTRODUCTION

Cultivated barley is a self-pollinating diploid species with seven paired chromosomes ($2n = 2x = 14$) (Briggs, 1978b), it is a winter and spring annual species (Forster *et al.*, 2000). Barley belongs to the family poaceae (syn. Gramineae) and the tribe triticeae (Briggs, 1978a). The genus *Hordeum* comprises over 32 species, including diploid and polyploid, perennial and annual types (Von Bothmer *et al.*, 1995). Worldwide, barley (*Hordeum vulgare* L. subsp. *vulgare*) is

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the fourth most important cereal after wheat, rice and maize (FAO Statistics, 2006). It is grown for different purposes, mainly for animal feed, human consumption, malting (Kling, 2004) and medical purposes (Ceccarelli and Grando, 1996). Vavilov (1951) suggested two centers of origin for barley, namely North Africa and East Asia.

Genetic diversity is one of the main resources sustaining human life, and one of the three pillars of biodiversity, diversity within species, between species and of ecosystems; and the crop shows adaptability to a wide range of agro-ecological environments ranging from 70°N in Norway to 46°S in Chile (Grando, and Helena, 2005) and it has a very good level of tolerance to high temperature compared to the other small grains (Barley”, Encyclopedia Britannica, 1998). Assessment of the extent of genetic variability within the cultivated crop has important consequences in plant breeding and conservation of genetic resources (Petersen *et al.*, 1994). On the contrary, reduction in genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes.

In Sudan, barley is produced mainly in limited areas in the northern states for grain and forage production and it is not widely spread because it has some limitations mainly the narrow gene pool. Farmers usually grow local genotype (Beladi 46), which has reasonable yield potentiality but susceptible to lodging. Accordingly, this study aims at the exploitation of phenotypic variations among the barley (*Hordeum vulgare* L.) genotypes in Sudan for possible

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utilization in breeding programmes and to identify the top yielding genotypes.

MATERIALS AND METHODS

The experiment was conducted for two consecutive seasons 2010/2011 and 2011/2012 in three sites. Hudeiba Research Station Farm (HRSF), Hudeiba Karu soil (HK) and Hudeiba High Terrace soil (HHT) which are located in Ed-Damer, River Nile State (Latitude 17° 34' N, Longitude 33° 56' E and Altitude 351m asl), while the third site is the Gezira Research Station Farm (GRSF), Wad Medani (latitude 14° 24' N, longitude 33° 29' E and Altitude 406.9 m asl).

The barley germplasm consisted of 19 genotypes introduced from ICARDA and Islamic Republic of Iran in addition to the local check Beladi 46. In each season, the experimental sites were dis plowed, harrowed and leveled. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications, with a plot size of 6 rows of 5 meter length and an inter-row spacing of 0.2 m using a seed rate of 40 kg/fed. The experimental seeds were drilled by hand after being treated with the insecticide Gausho (at the rate of 1.0g/1kg seeds) to avoid termites and aphids attacks. During both seasons the experiments were sown in the third week of November. Irrigation intervals ranged between 8-10 days in HHT site and 10-12 days in HK and GRSF. The crop was hand weeded twice before fertilizer application, as well as the use of a broad leaf herbicide (2,4-D) which was applied once at the tillering stage for the two sites in the River Nile State. Phosphorus fertilizer, in the form of

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triple super phosphate was applied at sowing in one site (HHT), while the nitrogen fertilizer in the form of urea was applied twice at the rate of 95 kg /ha in each time, the first time was at the 2nd irrigation and the second was at the 5th irrigation. The net harvested area was 3.2 m² from each plot. Basic agro-morphological characters were taken using standard descriptor lists developed by International Plant Genetic Resources Institute (IPGRI 1994) for barley crop, International Union for the Protection of New Varieties of Plants (UPOV) and objective description of variety of U.S. Department of Agriculture (USDA) (Table 1). The parameters measured were days to 50% heading, days to 90% maturity, plant height (cm), number of spikes per meter square, number of seeds per spike, thousand seed weight (g), biological yield (kg/ha) and grain yield (kg/ha)

Statistical analysis was done using GenStat software. The homogeneity test was done before running the combined analysis. The statistical procedures used for the stability analysis of genotypes was AMMI stability value (ASV) as described by Purchase (1997).

The equation of ASV as follows:

$$\text{ASV (i}^{\text{th}} \text{ genotype)} = \left(\left(\left(\text{SSPCA1/SSPCA2} \right) * \text{PCA1 score}_i \right)^2 + \left(\text{PCA2 score}_i \right)^2 \right)^{1/2}$$

RESULTS

Growth characteristics

The results of the growth habit demonstrated that there is a clear divergence among the genotypes i.e. the genotypes G3 and G8 were erect, G9 was intermediate, while the G20 was prostrate. In

consideration to vernalization requirement, the genotypes G3, G8 and G9 had spring growth class (seasonality) whereas; the G20 showed a moderate winter habit (facultative). Regarding plant waxiness, two classes were observed, G3 and G8 regarded as waxy and G9 and G20 with slight wax. The stem strength of the genotypes G3, G8 and G9 regarded as strong (resistant to lodging) and the genotype 20 (local genotype) had weak stem i.e. susceptible to lodging (Table 1).

Table 1: Characterization of the top yielding barley genotypes grown at Gezira (GRSF), Hudeiba High terrace (HHT) and Hudeiba karu (HK) sites for two seasons 2010/011 and 2011/012.

Characters	Barley Genotypes (G)			
	G 3	G 8	G 9	G20 (check)
Growth class (seasonality)	Spring	Spring	Spring	Facultative
Growth habit	Erect	Erect	Intermediate	Prostrate
Plant waxiness	Slightly waxy	Slightly waxy	Waxy	Waxy
Lodging	Resistant	Resistant	Resistant	susceptible

Biological yield (kg/ha)

In the three sites, a wide variation was observed between the seasons and genotypes (Table 2). Regarding the seasons, the performance of the second season was better than the first one. The biomass of twenty genotypes of barley ranged from 3281 to 17125 kg/ha at GRSF, from 5317 to 18278 kg/ha at HHT site and from 5000 to 8652 kg/ha at HK site (Table 2).

Table 2. The ranges for the biomass (kg/ha), grain yield (kg/ha), days to heading, days to maturity, plant height (cm), No. of spikes/m², No. of seeds/spike and 1000 seed weight (g) of the twenty barley genotypes grown at Gezira (GRSF), Hudeiba high terrace soil (HHT) and karu soil (HK) during winter seasons of 2010/2011 and 2011/2012.

Season	Biomass (kg/ha)	Grain yield (kg/ha)	Days to heading	Days to maturity	Plant height (cm)	Spike/m ²	Number of seeds/spike	Thousand seed weight (g)
<u>GRSF</u>								
2010/2011	10510-17125	148-2522	51 - 75	91 - 110	35-71	342-688	22-59	34-52
2011/2012	3281-7031	93-1657	-	-	41-61	183-618	14-52	24-50
<u>HHT</u>								
2010/2011	6833-18278	436-3616	54 - 91	83 - 117	51-90	384-789	5-39	26-40
2011/2012	5317-10240	392-4361	53 - 90	82 - 120	44-63	306-675	12-43	34-45
<u>HK</u>								
2010/2011	5000-8652	52-1876	56 - 102	86 - 122	38-72	238-572	8-43	25-38
2011/2012	5305-7838	2310-4982	56 - 87	85 - 114	67-102	193-664	15-41	25-46

At GRSF, among the top yielding genotypes, only G9 out yielded the check by 13% in the second season. On the other hand, at HHT the G3, G8 and G9 out yielded the check by 13, 11 and 50%, respectively in the second season, while at the HK site only the G3 and G9 out yielded the check by 30 and 15%, respectively in the first season, whereas only the genotype G3 out-yielded the check by 8% in the second season (Table 3).

Table 3. Biomass (kg/ha) of the top yielding genotypes of barley grown at Gezira (GRSF), High terrace (HHT) and karu (HK) sites for two seasons 2010/011 and 2011/012.

Genoty pes Numbe r.	GRSF		HHT		HK	
	2010/2 011	2011/2 012	2010/2 011	2011/2 012	2010/2 011	2011/2 012
3	5670	7917	5317	10500	7031	13677
8	6659	6860	8141	10333	5167	12543
9	6920	8542	7440	13924	6260	10865
20 (check)	7028	7542	9081	9299	5427	12635
SE±	462.8	363.6	416	1111.4	438.3	783.7
LSD	1330	1051.8	1200	3194.2	1258.4	2250.1
C.V. (%)	12.6	9.5	9.2	16.6	13.6	10.9

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Grain yield (kg/ha)

The seed yield of the twenty genotypes of barley ranged from 93 to 2522 kg/ha at GRSF, from 392 to 4361 at HHT site and from 52 to 4982 kg/ha at HK site (Table 2). The results of the combined analysis showed very highly significant differences among barley genotypes at all sites (Table 4). At GRSF, the highest yield was obtained by G3, G8 and G9 (1931, 1829 and 2061 kg/ha, respectively) and out-yielded the check by 31, 24 and 40%, respectively. In the HHT site, seven barley genotypes were superior to the check with G11, G3 and G9 as the top yielders having an increment over the check by 45, 34 and 31%, respectively. While in HK site the highest yield was achieved by ten genotypes and the foremost genotypes are G3, G4 and G2 which out-yielded the check by 61, 47 and 23%, respectively. Across the three sites, the common genotypes among the top yielding were G3, G8 and G9. At GRSF, the G3, G8 and G9 out-yielded the check by 31, 24 and 40%, respectively, by 34, 9 and 31% at HHT site and by 61, 21 and 20% at HK site (Table 4).

Table 4. Combined grain yield (kg/ha) of twenty genotypes of barley grown at Gezira (GRSF), High terrace (HHT) and karu (HK) sites for two seasons 2010/011 and 2011/012.

Genotypes Number.	GRSF		HHT		HK	
	Grain yield (kg/ha)	% of the check	Grain yield (kg/ha)	% of the check	Grain yield (kg/ha)	% of the check
1	1085	74	1933	82	2186	105
2	1594	108	2356	100	2568	123
3	1931	131	3145	134	3354	161
4	1465	99	2758	118	3060	147
5	1093	74	1171	50	2290	110
6	602	41	1387	59	1720	82
7	1417	96	1556	66	2518	121
8	1829	124	2562	109	2518	121
9	2061	140	3068	131	2498	120
10	1058	72	2471	105	2521	121
11	1360	92	3392	145	2537	122
12	146	10	536	23	1414	68
13	181	12	615	26	1181	57
14	628	43	1963	84	1614	77
15	157	11	1558	66	1877	90
16	1063	72	1983	84	1917	92
17	1268	86	2768	118	2426	116
18	334	23	574	24	1602	77
19	344	23	1210	52	1959	94
20 (check)	1476	100	2347	100	2087	100
SE±	47.4		209.4		115.2	
LSD	134.2		590.5		325.6	
Sig. level	***		***		***	
C.V. (%)	11		26.1		12.9	

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Additive main effects and multiplicative interaction (AMMI)

AMMI analysis of variance

Table 5 illustrates the contribution of genotype (G), environment (E), and GxE interaction according to the classical ANOVA in which the total sum of squares (SS) attributed to the environmental effect was the major contributing effect (57%) followed by genotype (31%) and the GxE interaction was the least. It means that there is a great environmental effect of total variance on genotypes and different genotypes reactions to environments. Results from analysis of multiplicative effects also showed that the first and the second interaction principal component axis (IPCA1) were significant and captured 37% and 27% of the total GxE interaction, respectively. The IPCA1 and IPCA2 contained 64 % of the total sums of squares, indicating that the AMMI model fits the data well (Table 5)

Table 5. Additive main effects and multiplicative interaction (AMMI) ANOVA for grain yield (kg/ha) of twenty genotypes of barley grown at six environments

Source of variation	DF	SS	MS	F	Percent explained
Total	359	486192811	1354298		
Treatments				29.54	
	119	449719395	3779155	***	
Genotypes (G)	19	137922301	7259068	56.74	31
Environment (E)	5	256649176	51329835	***	57
Block				8.01	
	12	12292325	1024360	***	
GE interaction	95	55147917	580504	4.54	12
IPC1				6.88	
	23	20238241	879924	***	37
IPC2				5.52	
	21	14841526	706739	***	27
Residuals				3.08	
	51	20068150	393493	***	
Error	189	24181090	127942		

The AMMI Stability Value (ASV)

The AMMI stability value (ASV) is based on the IPCA1 and IPCA2 scores. The genotypes with lowest ASV value would be considered as stable. According to the ASV concept, the most stable genotype was the check Beladi 46 (4.5) with the lowest mean seed

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Table 6. AMMI Stability Value (ASV) of the top yielding genotypes of barley grown at six environments

Genotypes	Grand					SPCA1/	
	mean	IPCA1	IPCA2	SSPCA1	SSPCA2	SPCA2	ASV
3	2810	-2.89987	-37.536	20238241	14841526	1.363623	37.7
8	2303	-7.12058	14.74885	20238241	14841526	1.363623	17.7
9	2542	-11.1616	1.68181	20238241	14841526	1.363623	15.3
20 (check)	1970	-1.96114	-3.63894	20238241	14841526	1.363623	4.5

Among the six environments, the genotypes were arranged according to AMMI estimate in table 7. The genotype G3 ranked first in four environments (GRSF in season 2011, HK in the two seasons and HHT in 2011) and ranked second in one environment (GRSF in season 2010) and the genotype G4 ranked second in three environments (GRSF in season 2011 and HK in the two seasons). The genotypes G9 ranked first in one environment (GRSF in season 2010) and ranked third in the other five environments, while the genotypes G8 ranked second in HHT in season 2010 and fourth in two environments (GRSF in the two seasons). The check Beladi 46 did not appear in the first four ranking genotypes (Table 7).

Table 7. The arrangement of barley genotypes (G) in each environment according to AMMI selections

Environment	Yield (t/ha)	1 st	2 nd	3 rd	4 th	5 th
Karu (HK) 2010	1036	G3	G4	G9	G7	G 8
Gezira (GRSF)						G 7
2011	781	G3	G4	G9	G8	
Karu (HK) 2011						G
	3348	G3	G4	G9	G2	17
Gezira (GRSF)						G 4
2010	1328	G9	G3	G11	G8	
High terrace (HHT) 2011	2009	G3	G11	G9	G17	G 4
High terrace (HHT) 2010	1926	G11	G8	G9	G17	G
						10

The GGE scattered biplot analysis showed that 85.98% of the variance was due to PC1 and PC2, of which 77.37% was due to PC1 and 8.61% was due to PC2. The six environments were divided into two mega environments. The first mega environment included GRSF(2010 and 2011), HK (2010 and 2011) and HHT2010. The second mega environment included only HHT2011. The genotype G3 was located at the first mega environment, while the G11 was located at the second mega environment (Fig. 1).

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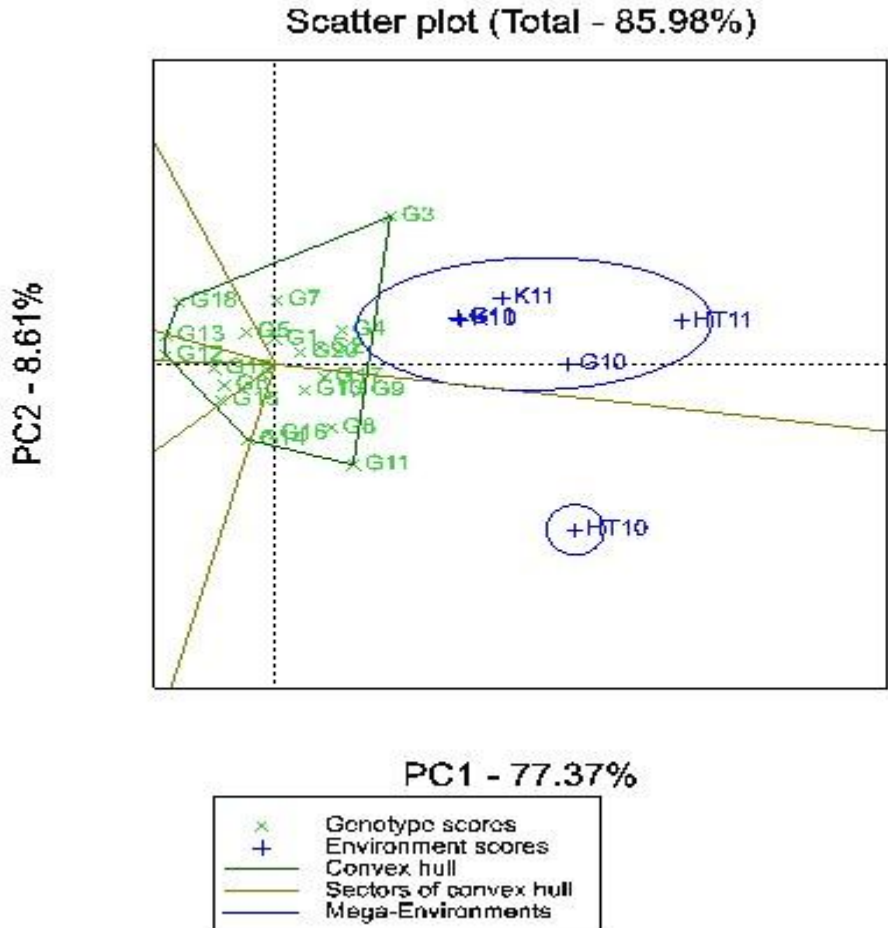


Figure 1. GGE scattered biplot for seed yield of twenty genotypes of barley at six environments.

Days to 50% heading

Considering the environment effect, the tested genotypes reached heading in a shorter duration in GRSF compared to HK (Table 2). As for the genotypic effect, the genotypes under test exhibited a highly significant variation in days to heading ranging from 51-75 days in GRSF, from 53-91 days in the HHT and 56-102 in the HK (Table 2). Among the top yielding genotypes, no significant differences were found on days to attaining 50% heading, except in HHT 2011/ 2012 and in HK 2010/2011, whereas the genotypes G3 and G8 headed earlier than the check (Baladi 46) (Table 8).

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Table 8. Days to heading and days to maturity of the top yielding genotypes of barley grown at Gezira (GRSF), High terrace (HHT) and karu (HK) sites for two seasons 2010/011 and 2011/012.

Genotypes	GRSF	HHT		HK	
	2010/201	2010/201	2011/201	2010/201	2011/201
Number.	1	1	2	1	2
<u>Days to heading</u>					
3	53	54	53	57	56
8	52	57	56	56	56
9	52	56	58	58	56
20					
(check)	53	56	60	60	57
SE±	0.814	0.675	0.646	0.729	0.568
LSD	2.358	1.943	1.871	2.094	1.631
C.V. (%)	2.4	1.8	1.6	1.8	1.5
<u>Days to maturity</u>					
3	91	83	84	89	93
8	91	85	83	87	87
9	91	86	84	96	92
20					
(check)	91	86	84	86	85
SE±	0.935	1.182	0.809	0.726	0.589
LSD	2.678	3.401	2.329	2.089	1.69
C.V. (%)	1.7	2.2	1.5	1.2	1

Days to 90% maturity

The variability on days to 90% maturity, ranged from 91 to 110 days at GRSF, from 82 to 120 days at HHT and from 85 to 122 days at HK (Table 2). Regarding the top yielding genotypes, no significant differences were found on days to attaining 90% maturity at GRSF and HHT, while at HK, significant differences were found on days to attaining 90% maturity and the G9 was the later than the check Baladi 46 (Table 8).

Plant height (cm)

A wide variation was observed among genotypes and environments for the plant height. Regarding the environments, the plant height in the first season at GRSF and HHT was greater than the second season, in contrast the plant height of the second season was greater than the first season at HK (Table 2). Regarding the genotypes, the plant height ranged from 35 to 71 cm at GRSF, from 44 to 90 cm at HHT and from 38 to 102 cm at HK (Table 2). Among the top yielding genotypes, in most environments, the check Beladi 46 was the tallest genotype, while the G9 was the shortest genotype. The plant height of G3 at Gezira in two seasons was stable (Table 9).

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Table 9. Plant height(cm) and number of spike/ m² of the top yielding genotypes of barley grown at Gezira (GRSF), High terrace (HHT) and karu (HK) sites for two seasons 2010/011 and 2011/012.

Genotypes	GRSF		HHT		HK	
Number.	2010/ 2011	2011/ 2012	2010/ 2011	2011/ 2012	2010/ 2011	2011/ 2012
	<u>Plant height</u>					
3	60	61	68	59	64	81
8	63	58	68	49	58	80
9	61	51	61	54	57	73
20						
(check)	71	59	76	62	63	85
SE±	2.1	1	3.1	2.7	2.2	1.3
LSD	5.9	2.9	9	7.7	6.2	3.8
C.V. (%)	6.1	3.4	8	8.3	6.3	2.8
	<u>Number of Spike/m²</u>					
3	511	407	348	444	374	455
8	475	293	447	423	359	362
9	484	386	409	510	427	463
20						
(check)	451	341	383	433	283	392
SE±	32.98	18.2	32.5	13.2	29.5	24
LSD	95.26	52.6	93	38.2	84.9	68.9
C.V. (%)	13.5	8.8	13	4.7	13.5	8.6

Number of spikes/m²

The highest number of spikes per meter square was observed in the first season compared to the second season in the three sites. Concerning the genotypes, the number of spikes per meter square ranged from 183 to 688 at GRSF, from 306 to 789 at HHT and from 193 to 664 at HK (Table 2). Wide variation was observed among the top yielding genotypes (Table 9). The highest number of spikes/m² was acquired by G3 at both seasons of GRSF (511 and 407, respectively) followed by G9 (484 and 386, respectively). Conversely, the highest number of spikes/m² was obtained by G9 in the second season of HHT and in the both seasons of HK (510, 427 and 463, respectively), followed by G3 (444, 374 and 455, respectively)(Table 9).

Number of seeds per spike

Number of seeds per spike showed a wide variation, which ranged from 14 to 59 at GRSF, from 5 to 43 at HHT and from 8 to 43 at HK (Table 2). Among the top yielding genotypes, the highest number of seeds per spike was achieved by the check Beladi 46 in the two seasons at GRSF(37 and 39, respectively) followed by G3 (35) in the first season and by G8 and G3 in the second season (38 and 37, respectively). In contrast, the highest number of seeds per spike was acquired by genotype G3 in the two seasons of HHT and the second season of HK (43,38 and 59, respectively) followed by the check in the first season of HHT (37) and the second season of HK (48). In the first season of HK the highest number of seed per spike was obtained by the check Beladi 46 (50) followed by the G3 (46) (Table 10).

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Table 10. Number of seeds/spike and thousand seed weight (g) of the top yielding genotypes of barley grown at Gezira (GRSF), High terrace (HHT) and karu (HK) sites for two seasons 2010/011 and 2011/012.

Genotypes	GRSF		HHT		HK	
	2010/2011	2011/2012	2010/2011	2011/2012	2010/2011	2011/2012
<u>Number of seeds/spike</u>						
3	35	37	43	38	46	59
8	33	38	30	29	41	40
9	33	32	32	37	41	43
20 (check)	37	39	37	34	50	48
SE±	2.823	2.2	1.1	2.5	1.5	1.9
LSD	8.096	6.2	3.2	7.2	4.4	5.5
C.V. (%)	17.4	13.3	7.3	17	7.1	7.9
<u>Thousand seed weight (g)</u>						
3	33	30	35	34	40	46
8	40	31	41	35	43	44
9	46	32	38	36	46	46
20 (check)	33	26	36	28	37	43
SE±	2.084	0.8	1.2	1.1	1.1	1
LSD	5.99	2.4	3.5	3.2	3.2	2.8
C.V. (%)	9.3	4.5	5.4	5.7	4.6	3.7

Thousand seed weight (g)

Wide variation was observed among the environments and genotypes on thousand seed weight. Concerning the environments, it was observed that the seed weight was heavier in the first season compared to the second season for both sites of GRSF and HHT. Conversely, at the HK site the heaviest seed weight was observed for the second season. Concerning the genotypes, the thousand seed weight ranged from 24 to 52 at GRSF, from 26 to 45 at HHT and from 25 to 46 at HK (Table 2). Regarding the top yielding genotypes, the G9 gained the heaviest seed weight for both seasons at GRSF and HK (46, 32, 46 and 46, respectively) and in the second season of HHT (36), followed by G8 (Table 10).

DISCUSSION

The progressive successes in wheat production in Sudan however, suggest that similar successes could be achieved in barley. Knowledge regarding the amount of genetic variation in germplasm arrays and genetic relationships between genotypes are important considerations for efficient conservation and utilization of germplasm resources (Manjunatha *et al.*, 2006). In the context of plant improvement, this information provides a basis for making decisions regarding selection of parental combinations that will maximize gain from selection and maintain genetic diversity. Information on the amount of genetic variation present, and the location of the genetic determinants of diversity may be useful for germplasm conservation and targeting gene discovery efforts (Hou *et al.*, 2005). Assessment of

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the extent of genetic variability within barley, is fundamental for barley breeding programs and the conservation of genetic resources, and is particularly useful as a general guide in the choice of parents for breeding hybrids.

The knowledge about the extent of fluctuations of yield and yield attributes over environments is very important to identify genotypes, which are widely adapted. Grain yield is quantitatively inherited character and there is considerable interaction between genotypes and environments. Some of the crop varieties are widely adapted, whereas others do not. Multi-location testing of genotypes provides an opportunity to the plant breeders to study the adaptability of genotypes to a particular environment and the stability of the genotype over different environments. The information on genotype x environment interaction is of major importance to the plant breeder in developing an improved stable variety.

Since, yield is a complex trait influenced by different yield contributing components, it is necessary to measure the nature of association among these components and their direct and indirect contributions to grain yield.

Analysis of variance of quantitative characters showed high significant differences among the genotypes. This indicated that, the genotypes under study exhibited sufficient variability. The results of the study showed that morphophysiological characters (Days to 50 % flowering, days to 90 % maturity, plant height number of tillers/meter square, number of seeds/spike, thousand seed weight, biological yield,

grain yield and harvest Index) were significantly affected by location, season and genotype. The high values obtained at Hudeiba-karu location may be attributed to the favorable environmental conditions, particularly, temperature in this location and also for soil properties. On the other hand, the significant difference among the tested genotypes in the morphophysiological characters that may reflect their differential responses to environment i.e. different studied genotypes have different growth classes, this accordance with Saxena and Sheldrake, 1980a, who stated that a single cultivar exhibits quite different growth and yield characteristics at different locations and seasons. Current study detected high morphological variation for location based on grain yield characters, which agreed with many studies in phenotypic characteristics in Ethiopian barley. (Kebebew *et al.*, 2001).

CONCLUSIONS

- A wide range of variability in performance was observed among the tested barley genotypes in this study.
- Amongst the twenty genotypes, the study illustrated the top-yielding genotypes (G3, G8 and G9) across the three sites for grain yield.
- At Gezira, the genotypes G3, G8 and G9 out-yielded the check by 31, 24 and 40%, respectively, at Hudeiba high terrace soil by 34, 9 and 31%, respectively, while at Hudeiba karu soil by 61, 21 and 20%, respectively

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- The results indicated the possibility of the development of barley varieties directly through further evaluation of those outstanding genotypes (G3, G8 and G9) or indirectly through a crop breeding programme.

RECOMMENDATION

- Based on the yield results, AMMI Selections per environment for seed yield as well as GGE biplot analysis, genotypes G3, G8 and G9 have been identified as better adapted to irrigated condition of Sudan.

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