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Evaluation of yield and yield components of advanced Kenyan barley (*Hordeum vulgare* L.) genotypes

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Abstract

Yield in barley is a complex trait that is dependent upon environmental, physiological and morphological factors of a genotype. The study aimed at evaluating yield and yield components of advanced barley lines. Field experiments were conducted under quarantine conditions at Kenya Agricultural and Livestock Research Organization-Njoro in the Central Rift Valley. Forty genotypes were sown in one meter twin rows arrange in a randomized complete block design with three replicates during the main season (March-August, 2015) and the off season (September 2015-January 2016). Data on plant height, spike length and grains per spike collected on ten randomly selected plants from each plot. Yield and biomass, thousand kernel weight for each plot were also collected followed by analyses using Statistical Analysis Software version 9.1. The analysis of variance revealed significant difference between seasons in all the parameters taken at $p \leq 0.01$. Genotypes were significant for all parameters ($p \leq 0.01$) while its interaction with season was significant for only the biomass and TKW ($p \leq 0.05$) and non-significant for the rest of the traits. There was significant ($p \leq 0.05$) difference for yield and yield components over seasons. The off season had higher values for plant height (7.9%), spike length (11.5%), grains per spike (5.7%), biomass (54.3%), yield (55.0%) and TKW (5.6%) than the Main season. However, harvest index was higher in Main season than in off season by 21.1%. Yield had a positive correlation with all the yield components but was significant only with biomass, harvest index and TKW ($p \leq 0.001$). Harvest index correlated negatively with all yield components ($p \leq 0.001$) except yield and thousand kernel weight. The number of grains per spike had a negative correlation with thousand kernel weight. Therefore, this study reveals that genetic variability for yield and yield components exists in barley genotypes and it can be used in barley improvement breeding programs.

Keywords: *Barley, yield, yield components, advanced barley lines*

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1. Introduction

Insuring the yield potential and stability of small-grain cereals, such as wheat (Triticum species), rice (Oryza sativa L.), and barley (Hordeum vulgare L.) is a priority for global food security (Zoltán *et al* 2020). Grain yield

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as the final end product of barley life cycle reflects metabolic functionality of plant organs in interaction with environmental factors. Overview of major yield determining genes in wheat and barley clearly shows complexity of developmental and physiological processes controlling plant and inflorescence architecture as well as seed characteristics (Nadolska-Orczyk *et al*., 2017). Yield in barley is a trait that is affected by an interaction of factors like environment, physiology and morphology of the genotype in question (Mousavi *et al*., 2012). The most basic components of yield are grain weight, plant height, number of grains per spike and grain / kernel weight (Madić *et al*., 2009). Grain yield is dependent on combined and well-balanced effects of these yield components (Turk *et al*., 2003). To be able to breed for a high yielding genotype, the relationship between yield and yield components and the correlation among yield components need to be well studied and understood (Dofing *et al*., 2003). Environmental factors like drought affect the yield components and consequently the grain yield of a genotype (Soleymani and Shahrajabian, 2013). The use of improved cultivars can help mitigate low productivity caused by low yielding genotypes around the world (Ehdaie and Waines, 1989).

Different genotypes respond differently to biotic and abiotic factors due to different genetic makeups and life processes that occur in them (Shah *et al*., 2002). Further studies on the relationship between physiological traits, yield and yield components are important in breeding programs (Mary and Gopalan, 2006). It has been postulated that negative effects on yield components affect grain yield of barley negatively (Pecio and Wach, 2015). Dwarf barley plants are reported to be susceptible to diseases and produce low quality malt when used for malting (Madić *et al*., 2009). The most important traits in barley plants are grain yield and quality of product, number of spikes per unit area, number of grains per spike and grain weight (Turk *et al*., 2003).

Successful breeding program in barley requires thorough understanding of existing genetic diversity and association to particular traits in relation to yield and yield components (Dofing *et al*., 1992). The values of yield components are usually controlled genetically but they are influenced significantly by the environment through genotype by environment phenomenon (Pecio and Wach, 2015). Various factors are considered responsible for better crop harvest but genotype is considered one of the most important factors in crop production (Shah *et al*., 2002). The difference in yield and Thousand Kernel Weight (TKW) of barley genotypes may be attributed to the difference in ability to accumulate assimilates and mobilize them during grain filling period (Megawer, 2011).

In an experiment by Bekele *et al*. (1992), cultivar differences were found to be significant on grain yield, biomass and harvest index. Plant height of barley is primarily dependent on genetic composition of the genotype while spike length is affected by breeding aimed at either increasing or decreasing plant height (Hellewell *et al*., 2000). Combined breeding, genetic and physiological approaches have demonstrated the importance of hormones in improving plant stature, adaptation and yield. A well-known example is the reduction in plant height during the Green Revolution in order to increase lodging resistance and consequently increase yield due to increased harvest-ability (Hedden, 2003). Grain per spike is significantly affected by the genotypes of barley (Shah *et al*., 2002). Genotypes have significant effect on plant height, grain yield, biological yield and harvest index (Maktoobian *et al*., 2014).

The expression of these traits represents a synthesis of individual traits and environmental conditions under which the plants develop (Madić *et al*., 2009). Finding sufficient amount of variability in which desired lines are to be selected from for further manipulations to achieve the target precedes the process of breeding (Al-Tabbal and Al-Fraihat, 2012). The variability that exists among genotypes should be studied and physiological traits properly characterized (Joshi *et al*., 1982). There is need to search for germplasm that can act as donor parents for specific genes that express given traits of agronomic importance (Ifftikhar *et al*., 2009). The objective of this study was to evaluate yield and its relationship to yield components in advanced Kenyan barley lines.

2. Materials and methods

2.1. Experimental site

The experiments were conducted at KALRO-FCR center-Njoro ($0^0$20'S; $35^0$56´E) quarantine fields located in the Central Rift Valley of Kenya for two seasons. The center lies at an elevation of 2,185 meters above sea level with *mollic phaeozem* being the predominant type of soil (Jaetzold and Schmidt, 2006). The area experiences an annual average precipitation of 998.79 ± 4.2 mm in a bimodal manner. The average maximum and minimum temperature of the area is about 23 ± 2^0C and 9 ± 2^0C, respectively (Kenya Meteorological Station Identification Number: 9035021).

2.2. Genotypes

Thirty-seven advanced barley lines were obtained from Kenya Malting Centre in Molo (Kenya). Three varieties (*Fanaka, Nguzo,* and *Cocktail*) were included in the experiments for comparison purpose (Table 1).

Table 1: Kenyan advanced barley lines and two varieties that was screened for resistance in the field and the green house

S. No.	Line	Category	Source
1	HBV 15-1	Two row	Malting Molo
2	HBV 15-2	Two row	Malting Molo
3	HBV 15-3	Two row	Malting Molo
4	HBV 15-4	Two row	Malting Molo
5	HBV 15-5	Two row	Malting Molo
6	HBV 15-6	Two row	Malting Molo
7	HBV 15-7	Two row	Malting Molo
8	HBV 15-8	Two row	Malting Molo
9	HBV 15-9	Two row	Malting Molo
10	HBV 15-10	Two row	Malting Molo
11	HBV 15-11	Two row	Malting Molo
12	HBV 15-12	Two row	Malting Molo
13	HBV 15-13	Two row	Malting Molo
14	HBV 15-14	Two row	Malting Molo
15	HBV 15-15	Two row	Malting Molo
16	HBV 15-16	Two row	Malting Molo
17	HBV 15-17	Two row	Malting Molo
18	HBV 15-18	Two row	Malting Molo
19	HBV 15-19	Two row	Malting Molo
20	HBV 15-20	Two row	Malting Molo
21	ULB 16-1	Two row	Malting Molo
22	ULB 16-2	Two row	Malting Molo
23	ULB 16-3	Two row	Malting Molo
24	ULB 16-4	Two row	Malting Molo
25	ULB 16-5	Two row	Malting Molo
26	ULB 16-6	Two row	Malting Molo
27	ULB 16-7	Two row	Malting Molo
28	ULB 16-8	Two row	Malting Molo

Table 1 (Cont.)

S. No.	Line	Category	Source
29	ULB 16-9	Two row	Malting Molo
30	ULB 16-10	Two row	Malting Molo
31	ULB 16-11	Two row	Malting Molo
32	ULB 16-12	Two row	Malting Molo
33	ULB 16-13	Two row	Malting Molo
34	ULB 16-14	Two row	Malting Molo
35	ULB 16-15	Two row	Malting Molo
36	ULB 16-16	Two row	Malting Molo
37	ULB 16-17	Two row	Malting Molo
38	FANAKA	Two row	Malting Molo
39	NGUZO	Two row	Malting molo
40	COCKTAIL	Two row	Malting Molo

2.3. Field experimental procedure

Primary ploughing was done using a disc plough before the onset of rain to allow for the weeds to dry. Secondary ploughing was done twice by harrowing to obtain a fine tilth which is suitable for planting of small cereals like barley. The genotypes were sown at a depth of about five centimeters in double rows (plot) of one meter in length at a rate of 108.33 kg / ha and a spacing of 20 cm between the rows. Paths of 30 cm and 50 cm were used to separate two plots within a replicate and replicates, respectively. Diammonium phosphate fertilizer was applied during planting at a rate of 125 Kg / ha to supply nitrogen at 22.5 KgN / ha and phosphorous at 57.5 KgP / ha. Top dressing was done at stem elongation stage (GS29 according to Zadoks *et al.*, 1974) using Calcium Ammonium Nitrate (CAN) at a rate of 100 kg / ha to supply nitrogen at 33 kg / ha. The experiment was conducted in a Randomized Complete Block Design (RCBD) with three replicates for two seasons.

Pre-emergent herbicide Stomp 455 CS (pendimethalin) was applied to control grass weeds a day after sowing at a rate of 1365 g pendimethalin / ha. At growth stage GS28, Buctril MC (bromoxynil ectanoate 225 g / l + MCPA ethyl hexyl ester 255 g / l) was applied at a rate of 281.25 g bromoxynil ectanoate / ha and 281.25 g MCPA ethyl hexyl ester / ha to control broad leaved weeds. Cereal aphids were controlled by applying a systemic insecticide Thunder OD (Imidacloprid + Beta-cyfluthrin) applied at a rate of 30 g Imidacloprid / ha and 15 g Beta-cyfluthrin / ha at GS 20 and GS29.

3. Data collection

Data on plant height, spike length, number of grains per spike were collected from ten randomly selected plants. Plant height was measured from the base of the plant to the tip of the spike (excluding the awns) at physiological maturity. Spike length was measured from the first node where the lowest spikelet emerges to the tip of the spike (excluding the awns) at physiological maturity. Grains per spike were manually counted and the total biomass of the genotypes weighed using a weighing balance. A TKW was determined by counting one thousand grains using an electric counter and weighed on an electric weighing balance with a precision of 0.00 g in the laboratory. Harvest index calculated using the following formula:

$$Harvest\ index = \frac{Grain\ yield\ (g)}{Total\ biomass\ (g)}$$

The data collected was analyzed using Statistical Analysis Software (SAS) program version 9.1 (SAS Institute Inc. Cary North California) to obtain Analysis of variance (ANOVA) and correlations among the

parameters. Duncan Multiple Range Test (DMRT) (Gomez and Gomez, 1984) was used to separate means at 5% level of significance. The ANOVA of the data followed the following statistical formula:

$$Y_{ijkl}=\mu+S_i+R_j+G_k+SG_{ik}+\varepsilon_{ijkl}$$

where Y_{ijkl} is the observation; μ is the overall mean; S_i is the effect due to the i^{th} season; R_j is the effect due to the j^{th} replicate; G_k is the effect due to the k^{th} genotype; SG_{ik} is the interaction effect due to season and genotypes and ε_{ijkl} is the random error component. This was a mixed model with the season, replicates and the interaction between season and genotype being random and the genotypes fixed.

4. Results

There was significant ($p \leq 0.05$) difference for the means of yield and all yield components between seasons. The February-July 2016 season had higher values for plant height (7.9%), spike length (11.5%), grains per spike (5.7%), biomass (54.3%), yield (55.0%) and TKW (5.6%) than the July-December 2015 season. Harvest index was however higher in July-December 2015 season than in February-July season by 21.1% (Table 2).

Table 2: Summary of means of agronomic data of the barley genotypes used in the experiment for the two seasons at KALRO-FCRC-Njoro in the year 2015 and 2016

Season	Plant height (cm)	Spike length (cm)	Grains per spike	Biomass (tonsha^{-1})	Yield (tonsha^{-1})	Harvest index	Thousand kernel weight (g)
Main season	76.737b	8.714b	25.861b	17.8581b	3.2622b	0.17479a	33.0220b
Off season	83.313a	9.468a	27.436a	39.1110a	7.2473a	0.13794b	34.9950a

Note: Figures followed by similar letters are not significantly different at $p \leq 0.05$ by DMRT.

In this experiment, analyses of variance over season showed significance ($p \leq 0.05$) for yield and all the yield components. Replication in this experiment had no significant effect on most of the yield components. It however had significant ($p \leq 0.05$) effects on the grain yield of barley and the harvest index. On the other hand, genotypes were highly significant for all the parameters taken ($p \leq 0.001$) except spike length where it was slightly significant ($p \leq 0.01$). The interaction between season and genotypes was not significant for the yield and most of the yield components except biomass and TKW which were significant at P≤0.01 and P≤0.05 respectively (Table 3).

Table 3: Mean squares for combined analyses for plant height, spike length, grains per spike, biomass, yield, harvest index and thousand kernel weight for two seasons at KALRO-FCRC-Njoro in 2015 and 2016

Source	DF	Plant height (cm)	Spike length (cm)	Grains per spike	Biomass (tonsha^{-1})	Yield (tonsha^{-1})	Harvest index	Thousand kernel weight (g)
Seasons	1	2466.363***	31.211**	152.912***	10478139.50***	139347.2183***	0.081758***	173.740**
Rep	2	112.073	2.224	0.506	227348.96	8532.6012*	0.017002*	44.328
Genotypes	39	245.452***	5.860**	32.834***	181411.18***	11333.3175***	0.024596***	193.888***
Season genotype	38	72.637	3.574	6.671	75722.36**	2231.3397	0.003050	29.935*
Error	156	48.478	3.248	4.557	42477.45	2533.2250	0.715785	19.860
CV		8.70	19.83	8.01	36.31	55.99	43.70	13.10
R^2		0.79	0.44	0.70	0.76	0.63	0.63	0.75

Note: ***, ** and * are significant at $p < 0.001$, $p < 0.01$ and $p < 0.05$ respectively by DMRT.

The tallest plants were among genotype HA17 with a mean of 88.45 cm which was 22.2% taller than the shortest check (*Cocktail*) while the shortest genotypes was HA2 with a mean height of 65.39 cm which was 5% shorter than the shortest check (*Cocktail*). The shortest and longest spike lengths were observed on genotypes HA14 and HA15 with a 39.6% difference (Table 4). The highest number of grains per spike was observed on genotype UO9 with a mean of 38.88 grains while the lowest mean number of grains per spike was observed on genotype HA5 with a mean number of 21.95 grains. The highest mean biomass was observed on genotype HA19 as 997.0g and also had the highest mean yield of 197.37 g, it was followed by genotype UO5 on biomass and HA8 on yield. Genotype HA20 had the lowest biomass, yield and harvest index of 217.70 g, 11.80 g 0.04180 respectively. The highest harvest index of 0.32273 was observe on genotype HA2 followed by 0.28811 on genotype HA8. Maximum TKW of 47.13 g was observed on genotype HA15 as opposed to check varieties *Fanaka* and *Cocktail* that had the lowest TKW of 23.61 g and 23.27 g respectively (Table 4).

Table 4: **Mean comparisons for plant height, spike length, biomass, plot yield, harvest index and thousand kernel weight of the genotypes tested in 2015 and 2016 at KALRO-FCRC-Njoro.**

Genotypes	Plant height (cm)	Spike length (cm)	Grains per spike	Biomass (g)	Yield (g)	Harvest index	Thousand kernel weight (g)
HA1	76.58e-m	9.655a-e	28.165a-i	245.9kl	31.41kl	0.11930c-g	29.902k-p
HA2	65.39n	7.500de	23.110m-p	514.1c-l	156.67a-d	0.32273a	42.257a-c
HA3	78.92a-k	8.783b-e	25.333h-m	767.4a-d	115.78c-i	0.16943b-g	42.447a-c
HA4	82.70a-i	8.868b-e	25.388a-f	534.0c-k	54.72g-l	0.09153e-g	35.383d-k
HA5	71.69j-n	8.235c-e	21.945p	309.4i-l	66.78f-l	0.18341b-g	39.633c-f
HA6	83.20a-i	9.588a-e	28.110a-i	481.0c-l	109.32c-j	0.23123b-e	46.680ab
HA7	84.88a-f	8.143c-e	26.000c-m	797.9a-c	123.55c-h	0.16885b-g	38.523c-g
HA8	68.95l-n	7.445de	24.000k-p	684.0b-g	192.17ab	0.28811a-c	37.810c-g
HA9	68.01mn	8.917c-e	25.612g-m	325.9i-l	71.08f-l	0.13758e-o	27.530n-q
HA10	70.33k-n	8.628b-e	25.227h-m	355.4h-l	69.88f-l	0.20801b-g	32.727g-n
HA11	71.39j-n	7.972c-e	24.333k-p	424.3g-l	96.68d-k	0.23776a-e	36.323c-k
HA12	80.47a-j	9.340b-e	23.777op	377.4g-l	38.78j-l	0.08961b-g	30.862j-p
HA13	87.80a-c	9.095b-e	22.278op	512.1c-l	52.03h-l	0.10896d-g	34.212e-m
HA14	84.42a-h	7.255e	29.167a-d	764.4a-c	112.86c-j	0.16240b-g	31.197h-p
HA15	76.06f-m	12.005a	22.778n-p	587.2b-j	148.18a-e	0.27106a-d	47.133a
HA16	80.78a-j	8.550b-e	24.333k-p	608.6b-i	69.75f-l	0.11600c-g	34.327e-m
HA17	88.45a	9.622a-e	27.665b-j	774.7a-d	60.40f-l	0.07038c-g	34.873e-l
HA18	83.20a-i	8.355b-e	25.775f-m	540.5c-k	116.95c-i	0.22609b-f	41.248b-d
HA19	77.61d-m	8.822b-e	27.668b-j	977.0a	197.37a	0.21889b-g	30.897i-p
HA20	74.55h-n	7.402de	25.580g-m	217.7l	11.80l	0.04180g	22.580q
UO1	86.92a-d	9.643a-e	29.277a-d	729.3a-f	127.06b-f	0.17968b-g	37.138c-j
UO2	80.22a-j	9.077b-e	24.945k-o	424.4f-l	52.91g-l	0.10381d-g	28.023m-q

Table 4 (Cont.)

Genotypes	Plant height (cm)	Spike length (cm)	Grains per spike	Biomass (g)	Yield (g)	Harvest index	Thousand kernel weight (g)
UO3	75.56g-m	8.005c-e	23.500m-p	511.8c-l	111.14c-j	0.21486b-g	40.093c-e
UO4	78.03b-l	9.155b-e	26.612d-l	424.3g-l	47.58i-l	0.14714c-g	33.537f-n
UO5	87.17a-d	9.983a-d	27.833b-j	867.5ab	171.28a-c	0.19660b-g	37.547c-h
UO6	86.67a-e	8.967b-e	30.222a-c	679.6b-g	123.03c-h	0.17292b-g	33.938e-m
UO7	82.44a-i	9.972a-e	29.223a-d	745.7a-e	130.44a-f	0.19281b-g	37.547c-h
UO8	88.75a	10.957ab	30.667ab	554.1c-j	69.99f-l	0.12356c-g	33.070g-n
UO9	88.14ab	9.848a-e	30.888a	732.2a-e	108.46c-j	0.14911c-g	35.107d-k
UO10	85.89a-f	10.233a-c	28.890a-e	638.2b-h	68.01f-l	0.09809d-g	28.650l-q
UO11	77.81c-m	9.522a-e	27.778b-j	450.7e-l	64.46f-l	0.11757c-g	26.355o-q
UO12	87.11a-d	10.360a-c	28.777a-f	542.3c-k	82.17e-l	0.14714c-g	33.550f-n
UO13	87.22a-d	9.523a-e	28.443a-g	671.2b-g	58.43f-l	0.08907e-g	33.813e-n
UO14	80.47a-j	8.883b-e	25.167i-o	613.9b-i	80.35e-l	0.18342b-g	32.327g-o
UO15	82.11a-i	9.865a-e	28.223a-h	648.7b-h	27.29kl	0.05109fg	28.254m-q
UO16	80.31a-j	9.345b-e	27.943a-j	777.3a-d	95.83d-k	0.11641c-g	33.553f-n
UO17	84.39a-h	9.317b-e	26.777d-k	497.6c-l	59.97f-l	0.09157e-g	25.215pq
FAN	73.44i-n	7.790c-e	27.447c-j	302.2j-l	24.93kl	0.08047e-g	23.613q
NGU	75.25a-k	9.578a-e	27.500c-j	426.5f-l	92.29d-k	0.18480b-g	34.310e-m
COC	68.81l-n	9.432b-e	26.553d-l	545.6c-k	64.71f-l	0.10381d-g	23.270q

Means within each column followed by same letters are not significantly different at $p \leq 0.05$ by DMRT.

A TKW correlated positively with all parameters but non-significantly with grains per spike ($r = –0.14$) plant height ($r = 0.08$) and spike length ($r = 0.08$). However, it had a positive and significant correlation with biomass ($r = 0.31$), yield ($r = 0.55$) and harvest index ($r = 0.41$). A TKW had a negative but non-significant relationship with grains per spike ($r = –0.14$). Harvest index correlated negatively with all the parameters measured except yield and TKW. It correlated negatively and significantly with plant height ($r = –0.42$), spike length ($r = –0.29$) and grains per spike ($r = –0.29$). It also correlated negatively but non-significantly with biomass ($r = –0.11$) and positively and significantly with yield ($r = 0.43$) and TKW ($r = 0.41$). Yield correlated positively with all the yield components measured. It had positive but non-significant correlation with plant height ($r = 0.21$), spike length ($r = 0.10$) and grains per spike ($r = 0.17$) but significantly correlated to biomass ($r = 0.72$). Biomass correlated positively with all the parameters except harvest index. It had a strong significant correlation with plant height ($r = 0.60$) and weak significant correlation with spike length ($r = 0.29$) and grains per spike ($r = 0.45$). Grains per spike had a positive correlation with all parameters except harvest index and TKW. It strongly correlated positively and significantly with plant height ($r = 0.64$) and weakly with spike length ($r = 0.36$). The correlation between grains per spike and harvest index and TKW was –0.29. Spike length correlated positively with plant height ($r = 0.45$) (Table 5).

Table 5: Correlation analyses for plant height, spike length, grains per spike, biomass plot yield harvest index and thousand kernel weight for the barley genotypes used in the experiment carried out at KALRO-FCRC-Njoro in 2015-2016

	Plant height (cm)	Spike length (cm)	Grains per spike	Biomass (g)	Yield (g)	Harvest index	Thousand kernel weight (g)
Plant height (cm)	1.00000	0.44655***	0.64013***	0.59983***	0.20886	-0.42480***	0.08486
Spike length (cm)		1.00000	0.36404***	0.29103**	0.10035	-0.28564*	0.08180
Grains per spike			1.00000	0.45276***	0.16971	-0.29467**	–0.14175
Biomass (g)				1.00000	0.72487***	-0.11465	0.30634**
Yield (g)					1.00000	0.43456***	0.54642***
Harvest index						1.00000	0.41102***
TKW (g)							1.00000

Note: ***,** and * are significant at $p < 0.001$, $p < 0.01$ and $p < 0.05$ respectively by DMRT.

5. Discussion

The genotypes in this experiment were evaluated in two seasons during long rains (March-August) and short rains (September-January). This was important due to the differences in the environmental conditions which play an important role in days to maturity in barley plants and consequently impact on the yield and yield components (Safavi *et al.*, 2012). The significance of season to most of the parameters suggests seasonal variations between the two seasons when the experiment was conducted. This significant variation could be attributed to variability in availability of moisture, temperature and other environmental variation. This finding is similar to an experiment by Maktoobian *et al.* (2014) who found drought stress to affect plant height, grain yield, harvest index and TKW significantly. Season was also significant for the number of grains per spike in an experiment by Madić *et al*. (2009). The significant effect of season and genotype on plant height suggests that plant height is controlled by genetic make-up of a genotype but environment has a significant effect to it. This is in tandem with the findings of Shah *et al*. (2002) who concluded that plant height in barley is dependent on genetic composition of a plant and climatic conditions. Seasons were also found to be significant on plant height and grain yield (Madić *et al.*, 2009).

Significant effect due to genotypes that was observed on all the parameters implies that the parameters taken are affected by the genetic make-up of a given genotype either directly or indirectly. The significant effect of genotype on plant height, TKW, biomass and grain yield was consistent with the findings of Shah *et al*. (2002) and Maktoobian *et al*. (2014). Genotypes were found to be significant for number of grains per spike (Madić *et al.*, 2009). This suggests variability which can be exploited for further breeding work among the genotypes used in this experiment. Improvement of the available genotypes through selection and crossing using the traits studied in this work can be effective.

Non-significant effect for the interaction between season and genotype for all the parameters except biomass and TKW is an indication that the genotypes used in the experiment were stable genetically and that there was minimal influence of the environment to the genotype for given specific traits. This observation was similar to what Al-Tabaal and Al-Fraihat (2012) found. It however, partially contrasted with those of Madić *et al*. (2009), who found that the interaction between season and genotype had significant effect on plant height and grain yield. Considering all the yield components studied in this experiment, there was no importance in replication due to non-significance observed for all the traits. It shows that experimental plots were in a quite homogenous environment and were affected similarly by the environmental factors. Miseda *et al*. (2016) working on wheat, found that replication in an experiment had significant effect on biomass and not significant for other yield and yield components.

Genotype HA19 had the highest biomass and yield. Low values for biomass and yield in genotype HA20 consequently led to the lowest value of harvest index due to the interrelationship that the components have in the equation for calculating harvest index. Harvest index, being the ratio of the grain yield to biological yield of barley plants, HA2 was found to be efficient in mobilizing assimilate to the grains better than all the other genotypes used in this experiment (Nejad *et al.,* 2014). The same genotype was observed to be having the lowest average plant height too. Its short stature gives it the potential to be used in breeding programs when targeting reduction in barley plant height. The rest of the genotypes had varied traits in between the lowest and the highest values indicating variability among the genotypes.

The positive correlation between grain yield and all the yield components is an indication that all the yield components contribute towards yield as much as some of the yield components were observed to be non-significant in their contribution. This was consistent with the work by Madić *et al*. (2009), who postulated that yield difference is attributed to difference in yield components such as TKW, number of kernels per spike, increase in total biomass or improved harvest index. Positive and significant relationship between grains per spike and spike length indicates and confirms the findings that grains per spike are dependent on spike length (Madić *et al.,* 2009). Increase in the number of grains per spike however, was found to be decreasing grain weight. This consequently affected the relationship between number of grains per spike and harvest index making it negative. All the parameters had a positive correlation with TKW except grains per spike which had a negative correlation. Increasing the number of grains per spike increases the sinks to which assimilates are to be mobilized to and hence lead to lower accumulation per seed and consequently reduced grain weight. Positive correlation of harvest index to yield was consistent with the work by Nasri *et al*. (2014) where a positive significant correlation was observed. This shows that the plants were generally efficient in translocating assimilates from the sources to the most important sink which is the grains (Sokoto *et al.,* 2012). Yield correlated positively with all the yield components and biomass had a strong correlation with yield. For every unit increase in biomass, there is a 0.72 unit increase in yield. Harvest index increased as yield increase but it decreased as biomass increased. This was partially in contrast with the work by Nejad *et al*. (2014) where harvest index increased with the increase in biomass.

6. Conclusion

There was genetic variation among the Kenyan Advanced Barley Lines and varieties evaluated during the study as observed in the analyses of variance. This can be utilized for improvement of the crop through careful and purposeful selection. A suitable breeding strategy is therefore required to combine most, if not all, of the desired traits into a single genotype in order to come up with a superior genotype. Yield is affected by all the yield components tested with an increase in the components showing an increase in the yield.

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