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**Research Article**

# EVALUATION OF MALT BARLEY (*Hrdeum Vulgare* L.) GERMPLASM FROM LOCAL CROSSES AND INTRODUCTIONS FOR YIELD AND RELATED TRAITS, SOUTH EAST AND CENTRAL HIGH LANDS OF ETHIOPIA

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## Abstract

This study was conducted to find out variability of some yield, quality and related traits from local crosses and US Davis genotypes. Ten crosses and US Davis genotypes with standard check were tested at Bekoji, Holetta and Koffele with RCBD in 2013 cropping season. Highest grain yield was recorded for KARC-C001/08-KU-11 (51.1 q/ha), Msel/Ocra-E (48.7 q/ha), KARC-C001/08-KU-06 (48.3) ranked first, second and third respectively while the lowest yield was recorded for KARC-C001/08-KU-11 (31 q/ha) at Bekoji and Highest yield was recorded for Msel/Ocra-C (35.6 q/ha), Msel/Ocra-M (34.6 q/ha) and Msel/Ocra-E (34 q/ha) ranked first second and third respectively while the lowest yield was recorded for KARC-C001/Ku-20 (18.1 q/ha) at Koffele. The evaluated genotypes met the quality standard of malt barley grain in hectoliter weight and thousand kernel weights. This study revealed that greater yield response with better malt quality traits could be obtained through selection. Crossing and evaluation with appropriate selection procedure is crucial to recommend elite varieties under different barley growing environment.

**Keywords:** National Variety, Trial, Yield, Kernel weight

## Introduction

Traditional approaches to breeding for improved barley production and quality for the past hundred years include conventional breeding, mutagenic procedures, haploid production, inter specific and inter generic crosses, and molecular marker-assisted selection breeding. Methods and advancements in traditional methods of barley breeding have been presented in numerous scientific essays, book chapters, and professional journals (Briggs 1978; Wiebe 1978; Starling 1980; Anderson and Reinbergs 1985; Swanston and Ellis 2002; Thomas 2003; Ulrich 2002).

In breeding barley, scientists are faced with deciding on the choice of parent barleys and later, with choosing the resulting segregates to save for future generations. In addition to determining the value or effect of a particular allele, the scientists must select the most appropriate available breeding method. Crossing cultivars of different genetic backgrounds is perhaps the most basic method in barley breeding. As barley is a self-fertilizing plant, artificial crosses are required to produce recombinant plants (Wiebe 1978). Controlled crossing requires basic knowledge of

plant morphology and the ability to recognize the progression of events from early floral development through pollination. Intercrossing plants with a restricted range of parental lines can reduce the number of gene pairs segregated, thus preserving previous genetic advances while providing a reasonable chance of improving specific traits (Eslick and Hockett 1979). The disadvantage of this approach to improving various traits is that it leads to a restricted gene pool (Anderson and Reinbergs 1985). Despite such theoretical and demonstrated losses in genetic diversity that are the consequence of limited parental selection, decades of selection and restriction have nevertheless not prevented continued gains from selection (Rasmusson and Phillips 1997; Condon et al. 2008).

The bulk breeding system is adapted to mass selection and is useful in identifying numerous phenotypic characteristics. Composite crossing is a type of bulk breeding where a number of single crosses are combined into a composite mixture, providing an efficient selection method. When using the composite crossing technique, projected objectives are generally long term in nature, allowing for recombination of many genes from a broad-based germplasm (Anderson and Reinbergs 1985). Several widely used methods that may be considered as conventional barley breeding programs include single-seed descent breeding (SSD) and pedigree breeding (Tourte 2005). The *SSD breeding method* was proposed as a way to maintain maximum genetic variation in self-pollinating species while obtaining a high level of homozygosity. This method may be used for parental evaluation, which is accomplished by evaluating an array of homozygous lines from several crosses and identifying those crosses that have the highest proportion of superior progeny. *Pedigree breeding* is best applied where genetic characters are highly heritable and can be identified in early segregating populations but not for characters with low heritability. Pedigree breeding is the most common method employed for characters with complex inheritance, such as malting quality. Breeders working within narrow germplasm pools regularly use pedigree breeding–based methods, frequently in combination with the SSD method to get many lines into advanced states of homozygosity without losing genetic variability. A strong point of the pedigree system is the ease with which the planned breeding can be modified at any stage of selection (Lupton and Whitehouse 1957). Modification of the pedigree system as proposed by these authors provides for yield estimates at the same time as line generations are being advanced. General Objective of the study is to develop new varieties having high yielding and good malt quality traits through crossing, evaluation and selection.

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pool (Anderson and Reinbergs 1985). Despite such theoretical and demonstrated losses in genetic diversity that are the consequence of limited parental selection, decades of selection and restriction have nevertheless not prevented continued gains from selection (Rasmusson and Phillips 1997; Condon et al. 2008).

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## 2. Materials and Methods

### Description of the study area

The study was conducted at Bekoji and Koffele PVT in 2012 and NVT in 2013 cropping season. The experimental sites are sub-stations of Kulumsa Agricultural Research Center located in Arsi and West Arsi Zone, in south east Ethiopia. The site receives an annual average rainfall of 1020 and 1211 mm at Bekoji and Koffele respectively in the main crop growing season. The station is situated at an altitude of 2,780 and 2,660 m.a.s.l. with an annual average temperature ranges from $8^0$C to 18.6 and 7.1 to 18 $^0$C at Bekoji and Koffele respectively.

### Materials Used and Experimental Design

The field experiment was carried out with ten advanced (promising) malting barley genotypes that are developed through crossing from Kulumsa Agricultural Research center with five released varieties as a check in RCBD, with three replications in the 2012 main cropping season. Genotypes were planted at the seed rate of 75 kg $ha^{-1}$ hand drilling in plots of 3 $m^2$ (1.2x2.5 m) with six rows measuring 0.2 m within row spacing. Fertilizer rates of 41 kg N $ha^{-1}$ and 46 kg $P_2O_5$ $ha^{-1}$ were applied.

Table 1. List of Genotypes used for evaluation

| Germplasm | Source | Germplasm | Source |
|---|---|---|---|
| KARC-C001/Ku-06 | Kulumsa Cross | Msel/Ocra-M | USDAVIS |
| KARC-C001/08-Ku-11 | Kulumsa Cross | 29 IB 20/Ocra-J | USDAVIS |
| KARCC001Ku-12 | Kulumsa Cross | Beka | Check |
| KARC-C001/08-Ku-15 | Kulumsa Cross | Mscal-21 | Check |
| KARC-C001/08-Ku-19 | Kulumsa Cross | Bekoji I | Check |
| KARC-C001/Ku-20 | Kulumsa Cross | EH 1847 | Check |
| Msel/Ocra-C | USDAVIS | HOLKR | Check |
| Msel/Ocra-E | USDAVIS | | |

## Data to be collected

Grain yield data was measured from the central four rows at maturity. Days to maturity, days to heading, plant height, crop stand, hectoliter weight and thousand kernel weight data were collected.

## Data Analysis

To reveal the total variability present within the tested genotypes in randomized complete block design, the data were computed for all the characters evaluated as per Gomez and Gomez, 1984. The data was subjected to analysis of variance by using SAS soft ware version 8 (SAS, 1999). Variance components and genetic parameters were computed. ANOVA of randomized complete block design was computed using the following mathematical model: Let $Y_{ij}$ was the observation for the $i^{th}$ treatment, which was supposed within the $j^{th}$ replication.

The linear model is:

$$* Yij = « + rj + gi + £ig$$

Where: Yij= the observed value of the trait Y for the $i^{th}$ genotype in $j^{th}$ replication

μ= the general mean of trait Y

rj= the effect of $j^{th}$ replication

gi= the effect of $i^{th}$ genotypes and

εij= the experimental error associated with the trait y for the $i^{th}$ genotype in $j^{th}$ replication.

**Table 2**. Analysis of Variance (ANOVA**)**

| Source of variation | Df | Mean squares | Expected Mean Squares | F ratio |
|---|---|---|---|---|
| Replication | (r-1) | $MS_r$ | $\sigma^2_e + g\sigma^2_r$ | |
| Genotype | (g-1) | $MS_g$ | $\sigma^2_e + r\sigma^2_g$ | $MS_g/MS_e$ |
| Error | (r-1) (g-1) | $MS_e$ | $\sigma^2_e$ | |
| Total | rg-1 | | | |

Where: r=number of replications, g = number of genotypes, DF = degree of freedom, $MS_r$ = mean Square due to replications, $MS_g$ = mean square due to genotypes, and $MS_e$ = mean square due to environment, $\sigma^2_e$=Environmental variance and $\sigma^2_g$=Genotypic variance.

## 3. Results and Discussion

The analysis result indicated that there is a highly significant difference between genotypes (Table 3). The genotypes showed grain yield potential ranging from 18.1 to 35.6 q/ha at Koffele. Highest yield was recorded for Msel/Ocra-C (35.6 q/ha), Msel/Ocra-M (34.6 q/ha) and Msel/Ocra-E (34 q/ha) ranked first second and third respectively while the lowest yield was recorded for KARC-C001/Ku-20 (Fig. 3). The evaluated genotype showed better performance than the standard checks in grain yield. The analysis result revealed that there is a highly significant difference between genotypes in HLW (Table 3). Mean value of the genotypes in HLW ranging from 55.3 to 62.8 at Bekoji. The highest hectoliter weight was recorded for Msel/Ocra-C while the lowest was recorded for Msel/Ocra-E. Even though there is a difference between genotypes, the whole genotypes met the national quality standards requirement based on Ethiopian Quality Standard Authority standards range from 48 to 62 kg/HL (EQSA, 2006).

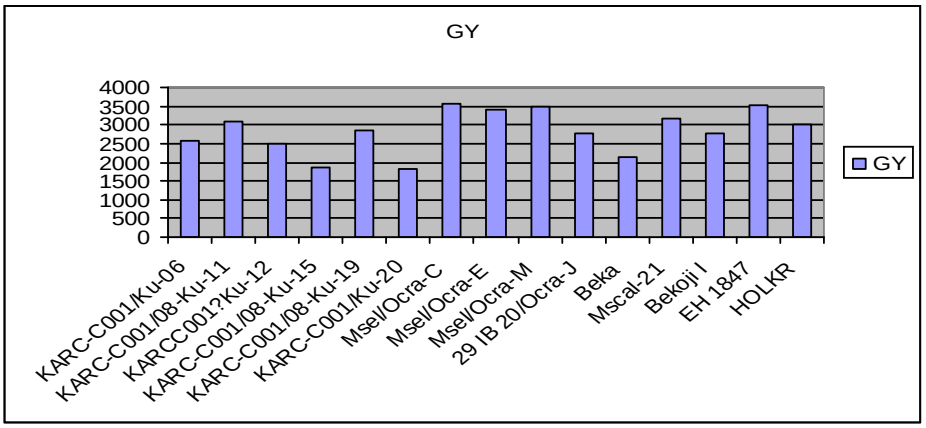



Fig. 3. Yield difference between genotypes at Kofele

In preliminary variety trial the analysis result in grain yield showed highly significant difference between genotypes (Table 5). The genotypes grain yield potential ranged from 23.8q to 57.4q. The highest grain yield was recorded for KARC-C001/08-KU15 (57.4q), KARC –C001/08-KU06 (56.2), Miscal 21 (55.8) and Msel/Orca E (52.31) first, second third and fourth respectively. The evaluated genotypes did not perform better than the standard checks at Holetta (Table 4). The genotypes yield potential is influenced by both genetic and environmental factors.

Table 3. Malt Barley National Variety Trial III location Koffele

| TRT | DH | DM | PH | STD | HLW | TKW | GY |
|---|---|---|---|---|---|---|---|
| KARC-C001/Ku-06 | 95.3A | 150.000A | 122.0A | 61.6EDC | 60.2BAC | 37.8EDF | 2593.3EBDFC |
| KARC-C001/08-Ku-11 | 91.3BAC | 145.3EBDAC | 117.0BA | 56.6E | 59.0BDC | 36.2F | 3105.0BAC |
| KARCC001Ku-12 | 91.3BAC | 145.0EBDAC | 112.6BAC | 55.0E | 60.8BA | 31.3G | 2488.2EDFC |
| KARC-C001/08-Ku-15 | 97.3A | 147.3BAC | 105.6BC | 60.0ED | 57.8BDEC | 39.4EDF | 1844.3EF |
| KARC-C001/08-Ku-19 | 79.3EDF | 143.0EDC | 106.6BC | 63.3BEDC | 58.2BDEC | 37.6EF | 2846.8BDAC |
| KARC-C001/Ku-20 | 83.3EDC | 149.3BA | 112.0BAC | 58.3ED | 60.3BAC | 40.8EDC | 1813.3F |
| Msel/Ocra-C | 72.6F | 140.3E | 118.0BA | 71.6BA | 62.8A | 47.4A | 3566.0A |
| Msel/Ocra-E | 74.0F | 141.3ED | 107.3BC | 76.6A | 55.3E | 36.8F | 3401.0BAC |
| Msel/Ocra-M | 76.6EF | 146.0BDAC | 123.0A | 78.3A | 57.3BDEC | 38.1EDF | 3469.2BA |
| 29 IB 20/Ocra-J | 77.3EDF | 143.3EDC | 106.0BC | 76.6A | 57.0DEC | 41.4BDC | 2776.8EBDAC |
| Beka | 96.0A | 150.0A | 105.0BDC | 60.0ED | 59.6BDAC | 39.2EDF | 2123.8EDF |
| Mscal-21 | 86.0BDC | 145.3EBDAC | 103.3DC | 66.6BDC | 58.7BDEC | 45.6A | 3159.3BAC |
| Bekoji I | 92.6BA | 146.6BAC | 102.3DC | 55.0E | 60.6BAC | 45.1BA | 2779.3EBDAC |
| EH 1847 | 78.6EDF | 144.6EBDC | 91.6ED | 70.0BAC | 56.5DE | 38.6EDF | 3510.7BA |
| HOLKR | 90.6BAC | 144.3EBDC | 88.3E | 63.3BEDC | 59.3BDAC | 44.2BAC | 3022.7BDAC |
| Mean | 85.5 | 145.46 | 108 | 64.8 | 58.9 | 39.9 | 2833.3 |
| CV | 6.35 | 2.1 | 7.5 | 8.3 | 3.6 | 5.5 | 20 |
| LSD | 9.5 | 5.13 | 13.5 | 9 | 3.5 | 3.6 | 949.5 |

*RT= Treatment, DH= Days to heading, DM= Days to maturity, PH= Plant height, STD= Crop stand, HLW= Hectoliter weight, TKW= Thousand kernel weight, GY= Grain yield in kg CV=coefficient of variation, LSD=Least Significant difference*

Table 4. Malt Barley National Variety Trial III location Holetta

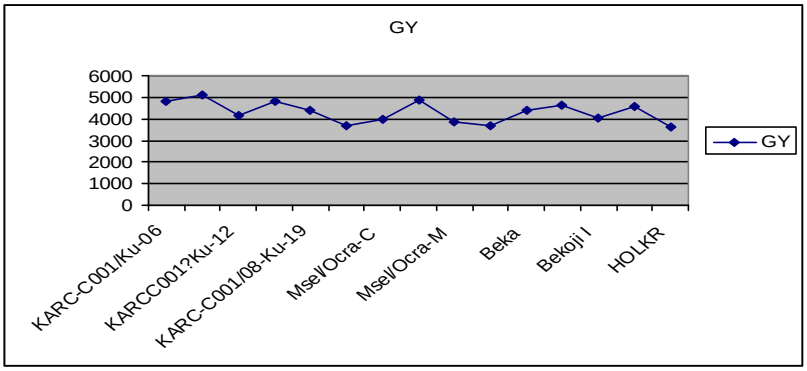
| Trt | GY | TKW | STD | NB | SC | PH | DM | DH |
|---|---|---|---|---|---|---|---|---|
| KARC-C001/08-Ku-06 | 1395.5DGEF | 32.9G | 81.6FDEC | 5.0DEC | 8.3BA | 93.0EDC | 128.0BDC | 86.0A |
| KARC-C001/08-Ku-11 | 1637.8DE | 34.4FG | 88.3BDAC | 6.6BDAC | 8.3BA | 100.6BDC | 125.3DC | 80.0BC |
| KARC-C001/08-Ku-12 | 1876.2DC | 32.5G | 80.0FDE | 5.6BDEC | 8.6BA | 91.6ED | 126.6BDC | 83.6BA |
| KARC-C001/08-Ku-15 | 2436.3BC | 40.6CD | 91.0BAC | 5.0DEC | 8.3BA | 103.0BAC | 129.6BDC | 83.0BA |
| KARC-C001/08-Ku-19 | 1478.0DEF | 36.4F | 85.0BDEC | 4.0E | 8.6BA | 85.6EFG | 125.3DC | 78.6BCD |
| KARC-C001/08-Ku-20 | 917.2GF | 36.8FE | 75.0FG | 4.3DE | 8.6BA | 79.6HFG | 123.3D | 78.3BCD |
| Msel/Ocra-C | 1190.0GEF | 36.2F | 75.0FG | 5.0DEC | 9.0A | 68.0I | 124.3D | 73.6ED |
| Msel/Ocra-E | 1393.5DGEF | 36.0F | 76.6FEG | 4.3DE | 9.0A | 77.6HIG | 123.6D | 70.0E |
| Msel/Ocra-M | 743.2G | 39.4ED | 68.3G | 8.3A | 7.3B | 75.3HI | 135.0BA | 85.6A |
| 29 IB 20/Ocra-J | 1014.7GEF | 41.2BCD | 76.6FEG | 7.0BAC | 9.0A | 77.3HIG | 138.6A | 88.3A |
| Beka | 2486.0BC | 42.8BC | 91.0BAC | 5.6BDEC | 8.0BA | 109.3BA | 140.6A | 83.6BA |
| Misccal-21 | 2889.3BA | 44.1BA | 93.3BA | 7.6BA | 9.0A | 91.3ED | 123.6D | 72.6E |
| Bekoji-1 | 3499.7A | 46.9A | 95.0A | 7.0BAC | 5.6C | 112.0A | 133.3BAC | 85.6A |
| EH 1847 | 2937.7BA | 42.2BCD | 90.0BAC | 7.6BA | 8.3BA | 93.3EDC | 124.3D | 74.6ECD |
| Holkr | 1970.2DC | 40.0CD | 91.6BA | 6.6BDAC | 8.6BA | 89.0EF | 128.3BDC | 86.0A |
| Mean | 1857.6 | 38.8 | 83.9 | 6 | 8.3 | 89.8 | 128.6 | 80.6 |
| CV | 21.8 | 4.6 | 6.8 | 23.7 | 10.1 | 6.6 | 3.9 | 4.1 |
| LSD | 677.4 | 3 | 9.6 | 2.3 | 1.4 | 10 | 8.5 | 5.5 |

Table 5. Malt barley Preliminary variety Trial Evaluation of Local crosses and USDAVIS 2012

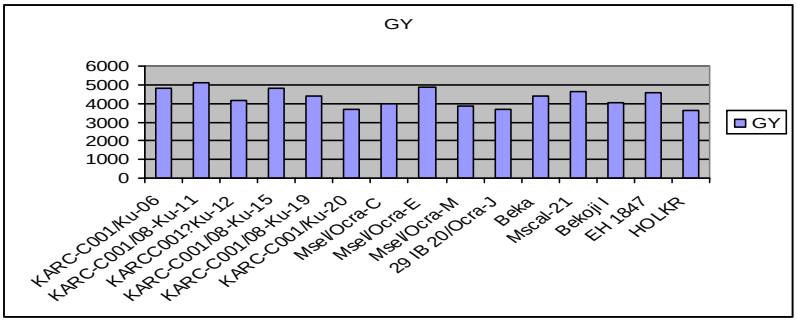
| Trt | GY | TKW | HLW | DH | DM | SC | PH | STD |
|---|---|---|---|---|---|---|---|---|
| KARC-C001/08-KU06 | 5629.7BA | 47.4FDEG | 67.6EDHGF | 90.6FECD | 152.0A | 6.0ED | 124.6A | 94.3BAC |
| KARC-C001/08-KU08 | 3906.3EDFC | 42.2JHIK | 68.2EBDHGCF | 91.6BC | 150.6BAC | 6.3EDC | 110.6BDAC | 96.0BA |
| KARC-C001/08-KU10 | 3060.7EGF | 40.6JK | 68.1EDHGCF | 94.3BA | 151.0BAC | 8.3A | 109.6BDAC | 90.0BDAC |
| KARC-C001/08-KU11 | 5014.7BDAC | 44.4JHIG | 70.1BDAC | 91.3BCD | 146.0 ED | 6.3EDC | 121.3BA | 96.0BA |
| KARC-C001/08-KU12 | 4736.7BDAC | 40.2JK | 70.8BA | 92.3BC | 148.0EBDC | 6.0ED | 121.0BA | 91.6BDAC |
| KARC-C001/08-KU15 | 5749.7A | 50.8BDEC | 69.2EBDAC | 92.3BC | 149.6BDAC | 5.6 ED | 86.0DE | 98.0A |
| KARC-C001/08-KU16 | 4205.3EBDFC | 45.5FHIG | 70.3BAC | 91.0BECD | 147.6EDC | 6.3EDC | 115.3BAC | 95.0BAC |
| KARC-C002/08-KU19 | 4584.3BDAC | 46.5FHEG | 70.3BAC | 87.3FG | 149.0EBDAC | 7.3BAC | 117.0BAC | 96.0BA |
| KARC-C002/08-KU20 | 4999.3BDAC | 48.0FDEG | 68.2EBDHGCF | 88.0FEGD | 152.6A | 6.6BDC | 115.3BAC | 88.3BDEC |
| Beka | 2878.7GF | 39.8K | 66.0HG | 96.3A | 152.6A | 6.3EDC | 95.0BDC | 73.3 G |
| Msel/Orca C | 4694.7BDAC | 47.4FDEG | 69.7EBDAC | 77.3I | 150.6BAC | 7.6BA | 91.0DEC | 92.6BDAC |
| Z11801210/CIMMYT7862E | 3981.3EDFC | 46.0FHG | 70.9A | 92.3BC | 149.0EBDAC | 6.0ED | 92.0DEC | 88.3BDEC |
| Msel/Orca E | 5231.0BAC | 46.9FEG | 66.5HGF | 77.3I | 146.3ED | 6.6BDC | 91.6DEC | 93.3BDAC |
| Msel/Orca K | 3826.3EGDFC | 48.8FDEC | 69.0EBDACF | 78.3I | 145.6 E | 7.3BAC | 93.6BDC | 86.6DEC |
| Msel/Orca M | 4518.0EBDAC | 51.6BDAC | 67.7EDHGCF | 83.0H | 149.6BDAC | 6.6BDC | 93.3BDEC | 85.0FDE |
| 29IB20/Orca G | 2387.7G | 52.5BAC | 68.6EBDAGCF | 86.0HG | 149.6BDAC | 8.3A | 94.0BDC | 76.6FG |
| 29IB20/Orca J | 4140.3EBDFC | 53.4BA | 67.1EHGF | 84.6HG | 151.6BA | 7.3BAC | 108.6BDAC | 90.0BDAC |
| Msel/Conrad D | 2869.0GF | 39.1K | 65.7H | 90.3FECD | 149.6BDAC | 8.3A | 84.0DE | 80.0FEG |
| Z05500120/CIMMYT7862H | 3694.7EGDF | 41.2JIK | 69.3EBDAC | 90.3FECD | 150.3BAC | 8.0A | 64.6E | 86.6DEC |
| Miscal-21 | 5584.7BA | 55.4A | 68.4EBDAGCF | 87.6FEG | 147.3EDC | 5.3 E | 112.0BDAC | 94.3BAC |
| mean | 4284.6 | 46.4 | 68.6 | 88.1 | 149.4 | 6.8 | 102.1 | 89.6 |
| LSD | 1492.8 | 4.3 | 2.6 | 3.5 | 3.7 | 1.2 | 28.8 | 9.1 |
| CV | 21.1 | 5.7 | 2.3 | 2.4 | 1.5 | 11.3 | 17.1 | 6.2 |

The evaluated genotypes yield potential ranged from 18.1 to 51.1 q/ha at Bekoji (Table 6). Highest grain yield was recorded for KARC-C001/08-KU-11 (51.1 q/ha), Msel/Ocra-E (48.7 q/ha), KARC-C001/08-KU-06 (48.3) ranked first, second and third respectively while the lowest yield was recorded for KARC-C001/08-KU-11 (Fig. 4a and b). The analysis result revealed that there is a highly significant difference between genotypes in hectoliter weight (Table 4). The genotypes indicated in HLW ranging from 55.3 to 62.8 at Bekoji. The highest hectoliter weight was recorded for KARC-C001/08-KU-19 while the lowest was recorded for Msel/Ocra-E. Even though there is a difference between genotypes, the whole genotypes met the Ethiopian Quality Standards Authority, the acceptable test weight (HLW) of raw malt barley ranges from 48 to 62 kg/HL (EQSA, 2006).

The evaluated genotypes showed a highly significant difference between genotypes in thousand kernel weight at Bekoji. Mean value of thousand kernel weight of genotypes ranged from 41.3 to 54.06. The highest thousand kernel weight was recorded for 29IB20/Ocra-J and the lowest were recorded for KARC-C001/08-KU-12. The acceptable range of thousand seed weight is ranged from 25 to 35 (EQSA, 2006). This study agrees with results indicated significant differences among cultivars in grain yield and quality parameters *(*Lalic *et al.,* 2008 and Aynewa *et al*., 2013*)*.




(a)




(b)

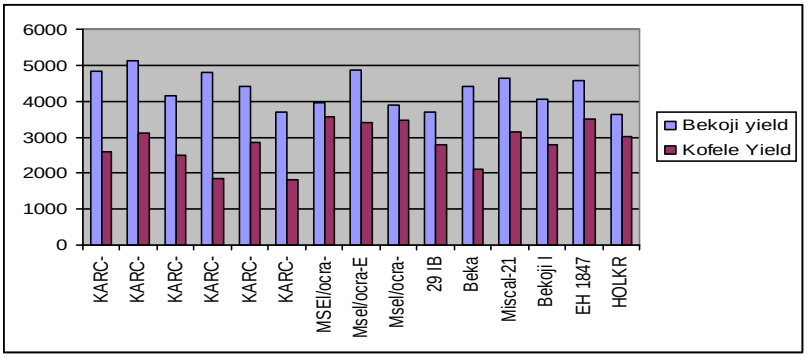
Fig 4. Yield difference between genotypes at Bekoji

Table 6. Malt Barley National Variety Trial III Mean comparison location Bekoji

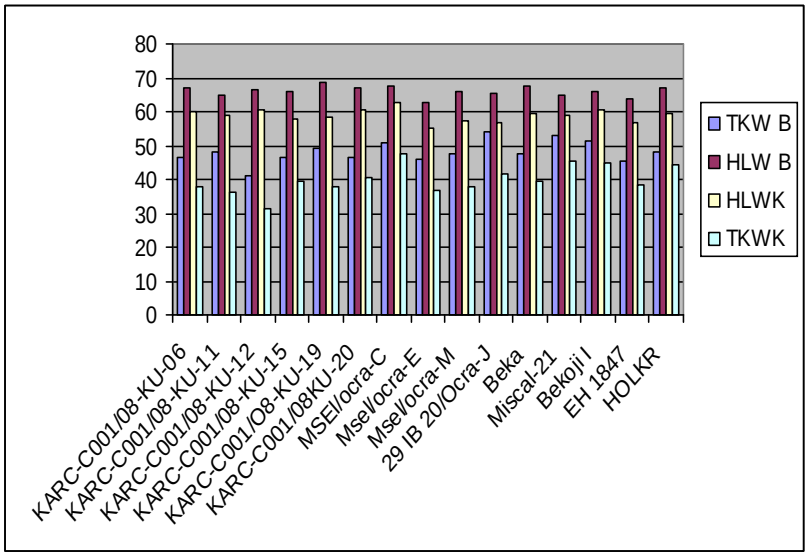
| Treatments | GY | TKW | HLW | PH |
|---|---|---|---|---|
| KARC-C001/08-KU-06 | 4837.8BA | 46.3ED | 67.0BAC | 113.3B |
| KARC-C001/08-KU-11 | 5114.8A | 48.0EBDC | 65.1DEC | 107.6CB |
| KARC-C001/08-KU-12 | 4164.0EBDC | 41.3F | 66.6BAC | 101.3ED |
| KARC-C001/08-KU-15 | 4808.7BAC | 46.6EDC | 66.0BDAC | 106.0CD |
| KARC-C001/O8-KU-19 | 4411.7EBDAC | 49.2EBDAC | 68.6A | 99.0E |
| KARC-C001/08KU-20 | 3693.7ED | 46.4EDC | 67.2BAC | 105.3CD |
| MSEl/ocra-C | 3958.5EBDC | 50.8BDAC | 67.7BA | 83.3F |
| Msel/ocra-E | 4873.8BA | 46.0EDF | 62.5E | 84.6F |
| Msel/ocra-M | 3887.3EDC | 47.6EDC | 66.0BDAC | 86.6F |
| 29 IB 20/Ocra-J | 3711.0ED | 54.06A | 65.3BDC | 97.6E |
| Beka | 4402.0EBDAC | 47.7EDC | 67.3BAC | 132.0A |
| Miscal-21 | 4627.2BDAC | 52.9BA | 65.1DEC | 101.3ED |
| Bekoji I | 4040.7EBDC | 51.2BAC | 66.1BDAC | 108.6CB |
| EH 1847 | 4584.8BDAC | 45.6EF | 63.7DE | 99.0E |
| HOLKR | 3629.5E | 48.0EBDC | 66.9BAC | 106.0CD |
| Mean | 4316.3 | 48.1 | 66.11 | 102.13 |
| CV | 12.9 | 6.07 | 2.3 | 3.7 |
| LSD | 935.6 | 4.8 | 2.5 | 6.3 |

*HLW= Hectoliter weight, TKW= Thousand kernel weight, GY= Grain yield, CV=coefficient of variation, LSD=Least Significant difference*

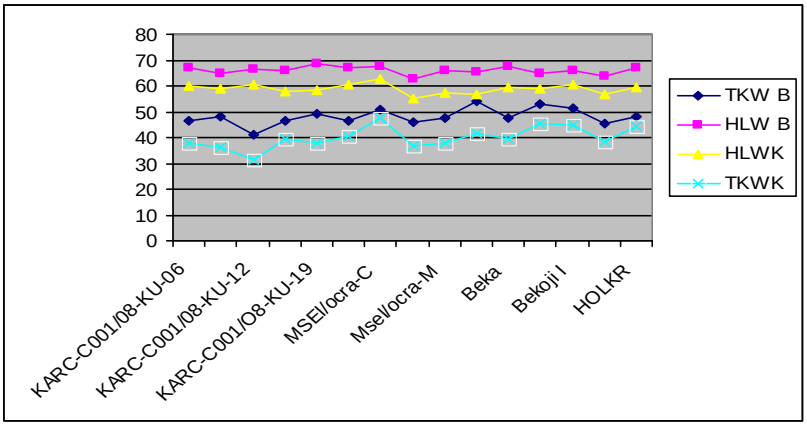
Yield potential of the evaluated genotypes showed better performance at Bekoji than Koffele (Fig. 5a). The analysis result of genotypes had better yield at Bekoji indicated that environmental conditions affect Yield potential of genotypes. In test weight and thousand kernel weight of the evaluated genotypes had better quality at Bekoji than Koffele (Fig. 5b and c). Bekoji had more suitable environmental condition than Koffele for yield and quality of Kulumsa crosses and US Davis.




(a)




(b)




(c)

Fig. 5. Comparison of mean genotype potential from Bekoji and Kofele

## Conclusion and Recommendations

Highest yield was recorded for KARC-C001/08-KU-11, Msel/Ocra-E, and KARC-C001/08-KU-06 ranked first, second and third respectively while the lowest yield was recorded for KARC-C001/08-KU-11. The highest hectoliter weight was recorded for KARC-C001/08-KU-19 while the lowest was recorded for Msel/Ocra-E. Even though there is a difference between genotypes, the whole genotypes were met the acceptable range of national quality standards requirement based on Ethiopian quality standard authority standards. Yield potential of evaluated genotypes showed better performance at Bekoji than Koffele. The analysis result of genotypes had better yield at Bekoji indicated that environmental conditions affect Yield potential of genotypes. In test weight and thousand kernel weight evaluated genotypes had better quality at Bekoji than Koffele. Bekoji had more suitable environmental condition than Koffele for yield and quality for Kulumsa crosses and US Davis.

To conclude, it can be affirmed that estimation of genetic factors help in understanding the role of various plant traits in establishing the growth behavior of cultivars under a given set of environmental conditions. Thus development of genotypes through crossing and evaluation should be done every year in each research center because introduced materials are susceptible to different leaf diseases.

## References


Ellis, M.H., W. Spielmeyer, K.R. Gale, G.J. Rebetzke, and R.A. Richards. 2002. 'Perfect' markers for the Rht-B1b and Rht-D1b dwarfing genes in wheat. Theor. Appl. Genet. 105:1038-1042.

EQSA., 2006. Ethiopia Quality Standards Authority. Malting Barley Specification. Addis Ababa, Ethiopia.

Gomez, K.A. and A.A. Gomez., 1984. Statistical procedures for agricultural research, 2nd edition. John Wiley and Sons Inc., New York.680 pp.

Lalic A., Kovacevic, J., Simic, G., Novoselovic, V. G., 2008. Spring Barley Genotypes Traits Regarding Genotype Environment Interaction to Croatian Environments. Alps-Adria Scientific Workshop Stara Lesna, Slovakia, 3-17.

Lupton,F.G.H., and R.N.N. Whitehouse, 1957. Studies on the breeding of self Pollinated cereals.I. Selection methods in breeding for yield. Euphytica 6: 169-185.

.

Newton, A.C., Swanston, J.S., Guy, D.C., and Ellis, R.P. 1998. Journal of the Institute of Brewing 104, 41-45.

P.M. Anderson, E.A. Oelke, and S.R. Simmons 1985, Growth and Development Guide for Spring Barley (Reviewed 2008).

Reid, D.A., and Weibe, G.A. 1978. Taxonomy, botany, classification and world collection. Pages 78-104 in: Origin, Botany Culture, Winter Hardiness, Genetics, Utilization Pests. Agriculture Handbook 338. US Department of Agriculture Washington, DC.

SAS. 1999. SAS/STAT user's guide, Version 8. SAS Institute Inc., Cary, NC.

Thomas, W.T.B.2003. Prospects for molecular breeding of barley. Ann.Biol.142:1-12.

Yetsedaw A., Tadesse D. and Wondimu B., 2013. Participatory Varietal selection of malt Barley (*Hordeum vulgare* L.) genotypes for yield and other agronomic traits at North West Ethiopia. Wudpecker Journal of Agricultural Research ISSN 2315-7259 Vol. 2(8), pp. 218 - 222, August 2013



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