

## Genotype by Environmental Interaction Stability Analysis of Oat (*Avena Sativa L*) Genotypes in Highland of Guji zone, Southern Oromia

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### Abstract

### Original Research Article

Feed scarcity in terms of quantity and quality is the key factors that hinders animal production which needs advancement of forage technology that an able to fulfill the feed gaps. Thus the study was conducted to identify high yielding and stable genotype/s. Twelve oat genotypes including standard checks were laid out in randomized complete block design (RCBD) with three replications. Agronomic performances and yield showed significant difference in genotypes and environments but not their interactions. The additive main effect and multiplicative interactions (AMMI) analysis of variance revealed significant variations for environment effect account for 19.5%, genotypes G x E interaction effect accounted for 8.34% and 3.12% of the total variations respectively. This indicated that the major factor that influenced the yield performance of the tested genotypes was the environment. The higher dry matter yield of the combined mean was obtained from genotype ILRI-5433(9.64 tha) followed by genotype ILRI-5444(9.58 tha) among the tested genotypes across the environment. From stability analysis point of view genotype ILRI-5433 followed by genotype ILRI-5444 were stable genotypes with a high mean dry matter yield advantage of 20.85% and 20.35% over the standard check respectively. Therefore, genotype ILRI-5433 and ILRI-5444 because of their yielding potential and stability in the testing environments were selected as candidate genotypes to be verified for possible release in southern Oromia and other area with similar agro-ecology.

**Keywords:** Agronomic, *Avena Sativa*, Dry Matter, Genotypes, Interaction, Oat, Stability.

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## INTRODUCTIONS

Ethiopia has a huge livestock population that requires considerable amounts of good quality feed and appropriate feeding systems for increased production, productivity, and transformation of the livelihood of the farmers. However, inadequate supply of feed for the existing livestock population and poor quality of the available feed resources are the main factors contributing to the low production and productivity of livestock in Ethiopia (Alemayehu *et al.*, 2017). Due to the lack of availability of quality feed, the livestock production system of the country is generally characterized by a low input-output production system (Getahun, 2019). Feed resources are available only in particular seasons and contain limited nutrients (low crude protein, minerals, and vitamins), resulting in lower intake and digestibility (Talore, 2015). Therefore, this case is reported as a major problem in livestock production in developing countries like Ethiopia, particularly during the long dry season, when there is insufficient plant biomass carried over from the wet season to support domestic livestock species (Kebede *et al.*, 2021).

However, the problem of feed shortage both in quantitative and qualitative dimensions can be addressed through the cultivation of improved forage crops. Cultivated forage crops have a tremendous contribution to boosting and sustaining livestock productivity by filling the gap of good quality feed resources available in the country. The overall average productivity of the improved forage crops per unit area in Ethiopia has been found to exceed the productivities of seasonally rested and continuously grazed natural pastures by about 3 and 10 folds per single harvest under rain fed conditions, respectively (Fekede *et al.*, 2015). Among cultivated forage crops, the common oat (*Avena sativa L.*) is one of the potential fodder crops for livestock feed and has been growing in Ethiopia for about five decades (Gezahagn *et al.*, 2016). Oat can produce a substantial amount of biomass yield but its productivity varies with species, varieties, soil, weather, and management factors. The cultivated oat (*Avena sativa L.*) is a self-pollinated annual crop (Rines *et al.*, 2006) and is used as forage and grain worldwide (Fekede, 2004). Green fodder also contains around 10%-12% protein and 30%-35% dry matter.

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Oat (*Avena sativa* L.) is excellent fodder for animals and is cultivated in different regions of the country due to its diverse adaptability; it can grow in a wide range of soil types, rainfall situations, and altitudes. However, moderate and cool climate conditions are ideal for its development (Beyene *et al.*, 2015). Compared to other cereals such as barley and wheat, oats are resistant to both drought and moisture stress. It is characterized by the growth habit of erect and bunch to basal. It can be a good source of animal feed in the dry season if harvested at the right stage of growth, cured, and stored as hay (Tulu *et al.*, 2020). It is also a quick-growing, palatable, succulent, and nutritious fodder crop (Wada *et al.*, 2019). Therefore, to understand the quality of fodder, the current study was undertaken to identify the best adaptable, good nutritive value and digestibility characteristics of oat genotypes grown under different locations of Guji zone, Southern Oromia.

## MATERIALS AND METHODS

### Description of the Study Locations

The trial was conducted for two main cropping seasons (2023 and 20224) at Bore, Yirba and Ardajila Mea Boko) woredas on farmers land located in Guji zone southern part of Oromia. Bore Agricultural Research on station (BORC) is geographically, situated at the latitude of 24°06'23"55" N-06°24'15" N and longitude of 38°34'45" E-38°35'5" E at an altitude of 2728 m.a.s.l. Mean and maximum temperature of the last 5 years is 13.1 and 28.4°C, respectively. Yirba on farm is also found and lies at 5°52'N/38°29'E with altitude of 2575 m.a.s.l. The average rainfall of 1000 mm per annum and Orthic Acrosol property. The average temperature was 20°C. Arda Jila Me'a Boko on farm coordinated at 5°51'N/38°28'E with altitude 2450 m.a.s.l. The three research site have unimodal pattern of rain distribution, with the rainy period running from April to October.

### Experimental Materials and Treatments

Genetic materials comprised 12 Oat genotypes including standard checks (ILRI-5490, ILRI-5513, ILRI-5513, ILRI-5492, ILRI-5433, ILRI-5454, ILRI-5454, ILRI-5489, ILRI-5444, ILRI-5443, ILRI-5475, Bate, Bareda and Bonsa) were evaluated at 6 locations over two consecutive years (2023 to 2024). The planting materials used for this study were obtained initially from the international livestock research institute (ILRI) and Bako agricultural research center. Oat genotypes were evaluated for herbage yield, seed yield, and other agronomic parameters and stability across environments.

### Treatments and Experimental Design

The genotypes were arranged in randomized complete block (RCBD) with three replications was used across all locations. Each genotype was sown in 6 rows; 2m length with 1.8m width and 30cm inter-row spacing. Seed rates of 80 kg ha<sup>-1</sup> and 50 kg ha<sup>-1</sup> urea and 100 NPS Kg ha<sup>-1</sup> fertilizer rate were applied at the time of planting.

### Methods of Data Collections

Data like date of 50% flowering, Date of maturity, Cover (%), Vigor (%) Leaf to stem ratio, plant height (cm), dry matter yield (t/ha), and seed yield (qt/ha) was carefully collected. Forage sampling was collected at the 50% flowering stage and seed sampling was conducted at the maturity stage of the plant. In all plots, sampling was done from the middle four rows excluding the guard rows.

### Biomass Yield Determination

Herbage yield was harvested 10 cm above the ground and weighed in the field using a sensitive balance. Fresh sub-samples will be taken from each plot separately, weighed, and chopped into pieces (2-5 cm) for dry matter determination. The weighed fresh sub-samples (FWss) were oven-dried at 60°C for 72 hours and re-weighed (DWss) to estimate dry matter yield. The dry matter yield (t/ha) = (10 x TotFW x DWss / HA x FWss) (Tarawali *et al.*, 1995).

Where: TFW = total fresh weight from the plot in kg

DWss = dry weight of the sample in grams

FWss = fresh weight of the sample in grams.

HA = Harvest area in meter square and

10 is a constant for the conversion of yields in kg m<sup>2</sup> to tone/ha

### Chemical Compositions Analysis

The total ash and crude protein contents were determined according to the procedures described by (AOAC, 1990). Neutral detergent fiber (NDF), acid detergent fiber (ADF), and acid detergent lignin (ADL) were analyzed following the procedures described by (Van Soest *et al.*, 1991). The in vitro dry matter digestibility (IVDMD) and IVOMD was determined according to Tilley and Terry (1963).

### METHODS OF DATA ANALYSIS

Hartley's test (F-max test) was used to assess the homogeneity of error variance prior to computing the combined analysis (Hartley, 1950). Then, pooled analysis was performed that partitioned the total variation into components due to (G), (E), and G x E interaction effects. ANOVA for each location and combined ANOVA over locations was computed using the SAS statistical program version (2002). GenStat 18<sup>th</sup> edition (2012) was used to draw AMMI and GGE bi-plots.

## RESULTS AND DISCUSSIONS

### Analysis of variance (ANOVA)

The combined analysis of variance (ANOVA) showed significant (P < 0.01) variations for genotype and environment for herbage DM yield, plant height and, leaf to stem ratio (Table 1). The results of the genotype by environment (G\*E) interaction were significantly (P<0.01) affected dry matter yield, plant height, and seed yield, while the leaf-stem ratio showed non-significant results. These results illustrated the evidence for genetic

variability among oat genotypes and the diversity of locations.

**Table 1: Combined ANOVA results of Oat genotypes over locations and year**

Sources of variations	Df	Mean square			
		DMY	PH	LSR	SY
Rep	2	8.35**	1976.8**	0.34ns	321.96**
Genotype	11	8.35**	1976.8**	0.339ns	321.96**
Environment (L)	5	19.56**	1976.8**	0.34ns	321.96**
Year (Y)	1	8.35**	1976.8**	0.34**	321.96**
G*Y	22	4.98ns	2321.6**	0.34**	260.39**
G*E	55	9.54**	1895.5**	0.45ns	238.74**
Residue	201	3.336	223	0.38	41.51

## Yield and Yield Components

### Herbage Dry Matter Yield Performance

The composite mean dry matter yield tone/hectare was shown significant ( $P<0.05$ ) differences among the genotypes (Table 2). Out of the total average mean value, the highest DMY was recorded from genotype ILRI-5433 (9.64 t/ha) followed by ILRI-5444 (9.58 t/ha), whereas the lowest DMY was obtained from Bareda (7.6 t/ha) followed by Standard check Bate (7.63 t/ha), with overall mean value 9 t/ha. Out of the nine genotypes considered in the trial, only three (ILRI-5433, ILRI-5444, and ILRI-5513) genotypes produced more DMY than the overall mean value. It showed 20.85% and 20.35% dry matter yield advantage checks (Bate)

respectively. Concerning the environmental grouping for the trial, the highest DMY was recorded from ILRI-5433 (11.4 t/ha) at the Me'ee Boko location in 2023, followed by ILRI-5433 (10.9 t/ha) at the Yirba location in 2023. The lowest mean value of DMY was recorded from Bonsa (6.7 t/ha) at Me'e Bokko in 2023. Generally, the results conforms to the findings reported by Dawit and Mulusew (2017) and Numan *et al.*, (2016) reported in a range from 7.7 to 10.3 t/ha and 7.5 to 12.8 t/ha, respectively. However, the finding reported by Getnet *et al.*, (2003), was relatively higher (10.13 to 15.39 t/ha) than the yield obtained in the present study and is might be attributed the variability in the amount and distribution of rainfall, locations, and genetic difference.

**Table 2: Mean dry matter yield (tha-1) for Oat genotypes tested at six locations (Bore, Yirba and Mea Boko) during 2023 and 2024 years**

Genotypes	2023			2024			Mean	Yield adv.%
	Bore	Yirba	Me'e Bokko	Bore	Yirba	Mea Boko		
ILRI-5490	8.3 <sup>ab</sup>	8.67 <sup>ab</sup>	8.4 <sup>abc</sup>	7.19 <sup>b</sup>	8.5	6.92 <sup>ab</sup>	7.88 <sup>bcd</sup>	3.12
Bonsa	7.7 <sup>ab</sup>	7.2 <sup>b</sup>	6.7 <sup>c</sup>	8.08 <sup>ab</sup>	7.8	7.33 <sup>ab</sup>	7.71 <sup>cd</sup>	1.03
Bate	7.6 <sup>ab</sup>	7.9 <sup>ab</sup>	7.3 <sup>bc</sup>	9.21 <sup>ab</sup>	8.02	5.37 <sup>b</sup>	7.63 <sup>d</sup>	-
ILRI-5513	7.06 <sup>b</sup>	9.3 <sup>ab</sup>	9.86 <sup>abc</sup>	8.5 <sup>ab</sup>	9.9	7.69 <sup>ab</sup>	9.04 <sup>ab</sup>	15.56
ILRI-5492	8.1 <sup>ab</sup>	8.8 <sup>ab</sup>	6.7 <sup>c</sup>	8.35 <sup>ab</sup>	8.7	6.77 <sup>ab</sup>	7.91 <sup>bcd</sup>	3.5
ILRI-5433	9.6 <sup>a</sup>	10.9 <sup>a</sup>	11.4 <sup>a</sup>	8.62 <sup>ab</sup>	9.77	9.41 <sup>a</sup>	9.64 <sup>a</sup>	<b>20.85</b>
ILRI-5454	8.83 <sup>ab</sup>	8.43 <sup>ab</sup>	8.4 <sup>abc</sup>	11.01 <sup>a</sup>	9.73	5.82 <sup>ab</sup>	8.88 <sup>abc</sup>	14.07
ILRI-5489	7.8 <sup>ab</sup>	9.03 <sup>ab</sup>	8.7 <sup>abc</sup>	6.83 <sup>b</sup>	8.84	5.2 <sup>ab</sup>	8.23 <sup>bcd</sup>	7.3
Bareda	8.6 <sup>ab</sup>	8.43 <sup>ab</sup>	7.5 <sup>bc</sup>	6.52 <sup>b</sup>	7.98	5.37 <sup>b</sup>	7.6 <sup>b</sup>	-
ILRI-5444	9.03 <sup>ab</sup>	10.17 <sup>ab</sup>	8.7 <sup>abc</sup>	9.87 <sup>ab</sup>	10.3	6.71 <sup>ab</sup>	9.58 <sup>a</sup>	<b>20.35</b>
ILRI-5443	8.4 <sup>ab</sup>	9.63 <sup>ab</sup>	10.3 <sup>ab</sup>	7.87 <sup>ab</sup>	9.3	6.64 <sup>ab</sup>	8.67 <sup>abcd</sup>	11.9
ILRI-5475	7.2 <sup>b</sup>	9.07 <sup>ab</sup>	7.8 <sup>bc</sup>	7.95 <sup>ab</sup>	11.4	6.58 <sup>ab</sup>	8.32 <sup>bcd</sup>	8.3
<b>Mean</b>	8.18	8.96	8.49	8	9	7	9	
<b>CV (%)</b>	1.24	1.97	2.01	23.2	2.48	2.62	2.13	
<b>LSD</b>	**	**	**	**	**	**	*	

Mean of different letters within a column significantly different at ( $P<0.05$ ). CV=Coefficient of variation; LSD= least significant difference; ILRI= international livestock research institute.

### Seed Yield

The combined analysis of seed yield was showed significant ( $P<0.05$ ) difference among the oat genotypes tested across the environment and year (Table 3). The highest seed yield was recorded from genotype ILRI-5433 (29.1) qt/ha and genotype ILRI-5444 (21.83) qt/ha respectively, whereas the standard check (Bate)

variety recorded the lowest seed yield (11.42) qt/ha with an overall mean of 19.2 qt/ha. The current finding on seed yield was comparable with the result of Dawit and Mulusew (2014) who reported an oat seed yield ranges from 21.7 to 29.8 qt/ha in Bale zone, Ethiopia and lower than the result of Mesgana *et al.*, (2020) who reported a combined seed yield performance ranged from 39.04 to

30.45 qt/ha. The difference could be due to the genetic difference, environmental factor, and interaction of genotype with environmental effects.

**Table 3: Mean seed yield (qt/ha) of Oat genotypes tested at six locations (Bore, Yirba and Me'ee Bokko) during 2023 and 2024**

Genotypes	Bore		Yirba		Mea Boko		Mean
	2023	2024	2023	2024	2023	2024	
ILRI-5490	14.67d	22.77bc	30.13ab	17bcd	22.77 <sup>bc</sup>	17bcd	17.72bc
Bonsa	22.67bc	24.33bc	28.77ab	15.67bcd	24.33 <sup>bc</sup>	15.67bcd	20.41bc
Bate	8.6d	14.83c	15.17	10.78d	14.83 <sup>c</sup>	10.78d	11.42d
ILRI-5513	9.1d	28ab	25.6	19.44bc	28 <sup>ab</sup>	19.44ab	17.88bc
ILRI-5492	20.53bc	28.1ab	30.77ab	20bc	28.1 <sup>ab</sup>	20ab	20.96bc
ILRI-5433	37.87a	35a	32.2a	28.44a	35 <sup>a</sup>	28.44a	29.1a
ILRI-5454	28.97ab	24.57bc	26.67abc	18.33bcd	24.57 <sup>bc</sup>	18.33bcd	21.31b
ILRI-5489	20.27bc	19.17bc	19.2	22.67ab	19.17 <sup>bc</sup>	22.67ab	18.2bc
Bareda	18.8c	21.83bc	20.57	17.89bcd	21.83 <sup>bc</sup>	17.89bcd	17.96bc
ILRI-5444	28.8ab	28.3ab	26.47	17.33bcd	28.3 <sup>ab</sup>	17.33bcd	21.83b
ILRI-5443	18.27c	23.03bc	19.07	16.44bcd	23 <sup>bc</sup>	16.44bcd	18.14bc
ILRI-5475	7.73d	27.17ab	24.6	12.67cd	27.17 <sup>ab</sup>	12.67cd	15.32 cd
<b>Mean</b>	19.69	24.76	24.9	18	24.76	18.06	19.2
<b>CV (%)</b>	14.5	21.	25.5	23.1	21	23.1	39.7
<b>LSD</b>	NS	*	NS	*	*	*	**

Mean of different letters within a column significantly different at (P<0.05). CV=Coefficient of variation; LSD= least significant difference; NS; Not significant, ILRI= international livestock research institute.

#### Leaf to Steam Ratio

The mean Leaf-to-stem ratio of oat genotypes didn't shown significant (P>0.05) differences in all locations and combined over years (Table 4). The leaf to stem ratio has significant implications on the nutritive quality of the forage as leaves contain higher levels of nutrients and less fiber than stems. The mean of leaf to steam ratio ranged from 1.4 to 1.8. Numerically the higher leaf to steam ratio was recorded from both genotype ILRI-5433 and the other genotypes was almost comparable with each other. The leaf to stem ratio is an important factor affecting diet selection, quality and

intake of forages (Zailan *et al.*, 2018). The mean value of leaf-to-stem ratio in the current finding was higher than the result of Abate and Wegi (2011) who reported in the range of 0.64 to 0.78 with an overall mean value of 0.72. Similarly, Sharma *et al.*, (2019) reported oat leaves to stem ratio 0.73 to 0.88, whereas Befekadu and Yunus (2015) reported a lower leaf-to-stem ratio (0.43) in Arsi highland, Ethiopia. The numerical differences observed in leaf to steam ratio among oat genotypes tested could be due to the potential variations of the genotypes with environmental interactions.

**Table 4: Leaf to stem ratio (LSR) of Oat genotypes tested at six locations (Bore, Yirba and Mea Boko) during 2023 and 2024**

Genotypes	Bore		Yirba		Me'ee Boko		Mean
	2023	2024	2023	2024	2023	2024	
ILRI-5490	1.14	1.14	1.140	1.1	1.42	1.5	1.4
Bonsa	1.37	1.36	1.567	1.012	2.07	1.67	1.7
Bate	1.34	1.34	1.000	1.2	1.183	1.17	1.7
ILRI-5513	1.65	1.65	0.953	1.2	2.08	1.17	1.5
ILRI-5492	1.67	1.67	1.157	1.43	1.73	1.5	1.7
ILRI-5433	1.00	1.00	1.390	1.71	2.33	1.43	1.8
ILRI-5454	1.77	1.77	1.057	1.1	2.18	1.25	1.6
ILRI-5489	1.04	1.04	1.110	1.1	1.73	1.17	1.4
Bareda	1.03	1.03	1.167	1.1	1.57	1.5	1.4
ILRI-5444	1.49	1.49	1.383	1.5	2.15	1.33	1.6
ILRI-5443	1.48	1.48	1.380	1.12	1.92	1.17	1.6
ILRI-5475	1.17	1.17	1.293	1.13	1.92	1.08	1.5
<b>Mean</b>	1.35	1.35	1.216	1.22	1.86	1.33	1.5
<b>CV (%)</b>	4.77	4.77	21.5	33.2	36.9	22.9	40.4
<b>LSD</b>	NS	NS	NS	NS	NS	NS	NS

Mean of different letters within a column significantly different at (P<0.05). CV=Coefficient of variation; LSD= least significant difference; ILRI= international livestock research institute.

## Agronomic Performances

### Days of 50% Flowering and Maturity Days

The combined analysis of oat genotypes was revealed significant ( $P < 0.05$ ) variation on days to 50% flowering however didn't revealed significant ( $P > 0.05$ ) variation on days to maturity among the genotypes (Table 5). The mean value of genotype ILRI-5445 (88 days) was reached early at the days of 50% flowering stage, followed by ILRI-5444 (88.1 days) and ILRI-5492 (88.1 days), with a mean value of 90 days. From the total genotypes tested, eight genotypes including standard checks earlier reached the days of 50% flowering stage than the overall mean value. This result indicated that the genotypes are distinctly different for days of 50% flowering stage attributes. The current result is taken an early day to attain 50% flowering than the report by (Tessema and Getinet, 2020) who reported 147 days to 92 days. The variation among oat genotypes in days taken to flower may be due to their genetic makeup

(Nazakat *et al.*, 2004). The differences observed in the current study might be due to genetic makeup of the genotypes and environmental conditions of the tested area.

### Plot Cove and Stand Vigor

The combined analysis across year and locations of the oat genotypes was revealed significant ( $P < 0.05$ ) variation on plot cover and stand vigor of the plants (Table 5). The best genotypes with plot cover and poorest plot cover was recorded from genotype ILRI-5433 (93.25%) followed by ILRI-5443 (92.01%). The smallest plot cover was also recorded from standard check Bonsa variety (80.98%). The good genotypes with vigor was recorded from genotype ILRI-5433 (95.7%) followed by Bonsa check (90.15%). The smallest plot cover was also recorded from standard check Bate variety (75.36%).

**Table 5: Combined agronomic traits of Oat genotypes tested at six locations (Bore, Yirba, and Me'e Bokko) over two years 2023 and 2024**

Genotypes	Days of Flowering (DF)	Days of maturity (DM)	Cover (%)	Vigor (%)
ILRI-5490	88.8 <sup>ab</sup>	152.2	88.94 <sup>ab</sup>	83.37 <sup>bc</sup>
Bonsa	93.72 <sup>ab</sup>	159.6	80.97 <sup>c</sup>	90.15 <sup>ab</sup>
Bate	94.39 <sup>a</sup>	156.3	90.77 <sup>ab</sup>	75.36 <sup>c</sup>
ILRI-5513	88.78 <sup>ab</sup>	151.9	88.93 <sup>ab</sup>	84.6 <sup>abc</sup>
ILRI-5492	88.1 <sup>b</sup>	157.8	87.7 <sup>ab</sup>	88.93 <sup>ab</sup>
ILRI-5433	88 <sup>b</sup>	155.4	93.25 <sup>a</sup>	95.7 <sup>a</sup>
ILRI-5454	88.3 <sup>b</sup>	159.1	85.27 <sup>bc</sup>	87.07 <sup>ab</sup>
ILRI-5489	90.6 <sup>ab</sup>	159.6	87.71 <sup>ab</sup>	85.83 <sup>abc</sup>
Bareda	92.6 <sup>ab</sup>	158.4	91.4 <sup>ab</sup>	88.3 <sup>ab</sup>
ILRI-5444	88.2 <sup>b</sup>	160.6	88.33 <sup>ab</sup>	89.53 <sup>ab</sup>
ILRI-5443	89.6 <sup>ab</sup>	158.1	92.01 <sup>a</sup>	85.2 <sup>abc</sup>
ILRI-5475	88.2 <sup>ab</sup>	151.7	92.62 <sup>a</sup>	81.53 <sup>bc</sup>
<b>Mean</b>	90	157	89	86
<b>CV (%)</b>	8.9	17.8	9.7	17.9
<b>LSD</b>	**	NS	**	**

Mean of different letters within a column significantly different at ( $P < 0.05$ ). CV=Coefficient of variations; LSD= least significant difference; ILRI= international livestock research institute.

### Plant Height

The result of combined analysis of variance indicated a highly significant ( $P < 0.01$ ) difference in plant height among genotypes. From the total genotypes tested in this trial, Bate standard check was revealed a higher mean value of plant height than the other genotypes. Concerning environmental grouping, the measured mean value of plant height ranged lowest 121.1 cm from ILRI-5513 at Bore in 2024 to 177.2 cm from ILRI-5444 at Yirba in 2024 with an overall mean

value of 150 cm. The current finding was higher than the result of Mesgana *et al.*, (2020) who reported 89.2 cm to 153.1 cm plant height for different oat genotypes in the Amhara region, Ethiopia. Wada *et al.*, (2019) reported 123 cm from the Lampton variety Abate and Wegi (2011) reported 128.4 cm from the Bonsa variety and 156.2 cm from the Bona-bas variety. The difference observed probably due to harvesting age, environmental conditions and edaphic factor.

**Table 6: Plant height (PH cm) of Oat genotypes tested at six locations (Bore, Yirba and Mea Boko) during 2023 and 2024**

Genotypes	Bore		Yirba		Mea Boko		Mean
	2023	2024	2023	2024	2023	2024	
ILRI-5490	138b	120.5b	147cd	137.2de	147.3cd	127.1e	136.6 <sup>f</sup>
Bonsa	155.3ab	127ab	160.3abc	137.2de	158.3bc	131.2de	149 <sup>bcd</sup>
Bate	146.3ab	159.4a	171ab	174.7a	182a	155b	168.9 <sup>a</sup>
ILRI-5513	137.7b	121.1b	156.7abc	129.9e	152bcd	156.5b	138.1 <sup>ef</sup>
ILRI-5492	151ab	135ab	164.7abc	142.2de	150.7bcd	146.1bcd	148.3 <sup>cde</sup>
ILRI-5433	151.2ab	127.8ab	136.7d	132.2e	139.3d	156.5b	156.3 <sup>bc</sup>
ILRI-5454	147.3ab	152.2ab	167.7ab	155.5bcd	160.3bc	146.5bcd	154.8 <sup>bc</sup>
ILRI-5489	162.7ab	143.8ab	176a	171.1ab	166.3b	131.7de	162.5 <sup>ab</sup>
Bareda	173a	152.2ab	154.7bcd	163.3abc	154.3bcd	153.8 b	158.6 <sup>bc</sup>
ILRI-5444	152ab	146.7ab	172.3ab	177.7a	160.3bc	177.2a	136.5 <sup>f</sup>
ILRI-5443	142ab	162.2a	162abc	148.8cde	157bc	144.3bcd	152.7 <sup>bcd</sup>
ILRI-5475	141.3ab	122.2b	160.3abc	144.4cde	157.3bc	134.4cde	143.3 <sup>def</sup>
<b>Mean</b>	149.8	139	160.8	150	157.1	146	150
<b>CV (%)</b>	11.3	13	6.3	7.1	5.5	6.3	9.9
<b>LSD</b>	NS	**	**	**	**	**	**

Mean of different letters within a column significantly different at (P<0.05). CV=Coefficient of variation; LSD= least significant difference; NS= not significant deference; ILRI= international livestock research institute.

#### Disease Severity and Reaction of Food Oat Genotypes

Yellow rust is economically importance disease of fodder oat. The fodder oat yellow rusts (stem and leaf) were recorded according to Cob modified scoring method. The response of the genotypes to stem and leaf rusts were varied in severity scores (0-90%) and their reaction. Among 12 tested oat genotypes ILRI-5433, ILRI-5454 and Bonsa were moderately resistant (MR) to leaf rust while genotypes ILRI-5443, ILRI-5475, Bareda, ILRI-5489, ILRI-5492, ILRI-5513, ILRI-5490 and Bate

variety were susceptible(S) to leaf rust. On the other hand genotypes ILRI-5444, ILRI-5433, ILRI-5454, ILRI-5489, ILRI-5443 and Bareda, were moderately resistant (MR) to stem rust whereas Bonsa and ILRI-5475 was moderately susceptible (MS) and Bate, ILRI-5513 and ILRI-5490 were susceptible (S) to stem rust (Table 7). The studies illustrated that oat rusts (leaf and steam) could cause economical yield losses when the oat genotypes are susceptible (Paul, 2019; Bowen *et al.*, 2016).

**Table 7: Disease severity and reaction of food oat genotypes**

Genotypes	Yellow rust (FS) Rust Disease			
	Leaf rust	CRXN	Stem rust	RCXN
ILRI-5490	55.3 <sup>ab</sup>	S	30.2 <sup>a</sup>	S
Bonsa	29.2 <sup>cde</sup>	MR	24.1 <sup>ab</sup>	MS
Bate	65.8 <sup>a</sup>	S	30.31 <sup>a</sup>	S
ILRI-5513	67.78 <sup>a</sup>	S	19.43	S
ILRI-5492	43.8 <sup>bc</sup>	S	18.99 <sup>ab</sup>	MR
ILRI-5433	2.78 <sup>f</sup>	MR	9.14 <sup>b</sup>	MR
ILRI-5454	23.9 <sup>e</sup>	MR	29.5 <sup>a</sup>	MR
ILRI-5489	33.6 <sup>cde</sup>	S	24.2 <sup>ab</sup>	MR
Bareda	40.1 <sup>cd</sup>	S	9.87 <sup>ab</sup>	MR
ILRI-5444	24.89 <sup>de</sup>	MS	17.4 <sup>ab</sup>	MR
ILRI-5443	32.6 <sup>cde</sup>	S	13.7 <sup>ab</sup>	MR
ILRI-5475	59.56 <sup>a</sup>	S	19.9 <sup>ab</sup>	MS
MEAN	39.9		21.4	
CV (%)	35.1		76.1	
LSD (5%)	**		**	

Mean of different letters within a column significantly different at (P<0.05). CV= coefficient of variation; LSD= least significant difference; CRXN= Coefficient of reaction; MS = moderately susceptible; MR = moderately resistant; and S = Susceptible

#### AMMI Analysis of Variance

The AMMI analysis of variance for forage dry matter yield revealed that significant (P<0.05)

differences for genotype, environment and G x E interaction effects (Table 8). Environment captured 19.5% of the total variation, whereas genotype and

genotype by environment interaction captured 8.34% and 3.12 %, respectively. A large total variation due to environment indicated that overwhelming influence of environments on forage dry matter yield performance of oat genotypes. The significance among environments demonstrated that genotypes responded differently to different environments confirming the need to assess the performance of oat genotypes across environments to identify genotypes with stable and superior yield across environments. The current study was in line with this different authors (Birmaduma *et al.*, 2023; Abuye *et al.*, 2018) reported large yield variation of oat genotypes due to environments were observed.

Further AMMI revealed the significant G x E interaction effect was decomposed into PCA. The first IPCA explained 37.17% and the second IPCA additionally explained 22.94%, the first two IPCA totally 60.11%. Different scholar (Temesgen *et al.*, 2014) suggested the most accurate model for AMMI could be predicted by using the first two IPCA. The more the IPCA scores approximate to zero, the more stable or adapted the genotypes are over all the environments sampled. The variation of dry matter yield for each genotype was significant in the different environments was in line with the study (Arega *et al.*, 2023).

**Table 8: AMMI ANOVA for herbage dry matter yield of 12 oat genotypes evaluated at 6 environment over two consecutive years (2023 and 204)**

Source of variation	Df	SS	MS	% Explained			P- values
				Total variations	G X E	G X E cumulative	
Total	215	83.57	0.3887				
Genotypes	11	3.73	0.339*	8.34			0.0018
Environments	5	35.13	7.026*	19.5			<0.001
G x E Interactions	55	8.56	0.156*	3.12			0.00951
Blocks (Envts)	12	5.61	0.47*	3.2			0.027
IPCA 1	15	2.82	0.19*	4.24	37.17		0.663
IPCA 2	13	2.64	0.2*	3.02	22.94	60.11	0.576
Residuals	27	3.10	0.1148				0.982

DF= degree of freedom; SS= total sum of square; MS= mean sum of square; GXE= genotype with environmental interaction; IPCA= principal component analysis

### Stability Analysis for Dry Matter Yield AMMI Bi-Plot Analysis

The GGE bi-plot has therefore, been used in crop genotypes trials to effectively identify the best performing genotype(s) across environments, identify the best genotypes for specific environments delineation, whereby specific genotypes can be recommended to specific environments and can be used to evaluate the yield and stability of genotypes (Yan and Kang, 2003). Genotype ILRI-5444, ILRI-5490 and Bonsa variety had broad adaptability across the environments as they were located closer to the center of the bi-plot. However, the genotypes were less sensitive to environmental factors may not be higher in dry matter yield response. As Crossa (1990) and Voltas (2002) reported that genotypes near the origin/center of the biplot are not sensitive to environmental interaction, whereas genotypes distant from the origin of the biplot are sensitive and have large interaction effects. This mean genotypes; with small value of IPCA1 have consistent responses to the changing environment. Environment; Bore-24 and Me'ee Bokko-23 were considered highly discriminating

for the tested materials since they had longer vectors (Potential environments). As Akter *et al.*, (2014) report environments with short spokes exert small interactive forces, whereas environments with long spokes exert strong interaction on the performance of oat genotypes.

### AMMI Stability Value (ASV) and Genotype Selection Index for Dry Matter Yield

Genotypes with the lowest AMMI value were the most stable for dry matter yield performance across the test environments. In this study genotype ILRI-5433 was the most stable whereas, the standard checks Bareda and Bonsa were relatively less stable (Table 7). In most studies the genotypes with a lower ASV has the lowest mean value of dry matter yield indicating that ASV was not the only genotype selection criteria. The genotypes selection index was the criteria selection comparison of genotypes stability which is steamed from the mean performance of the genotypes and ASV. Thus genotypes ILRI-5533 and ILRI-5544 had better mean value for dry matter yield which was above the ground mean and relatively stable across the test environment.

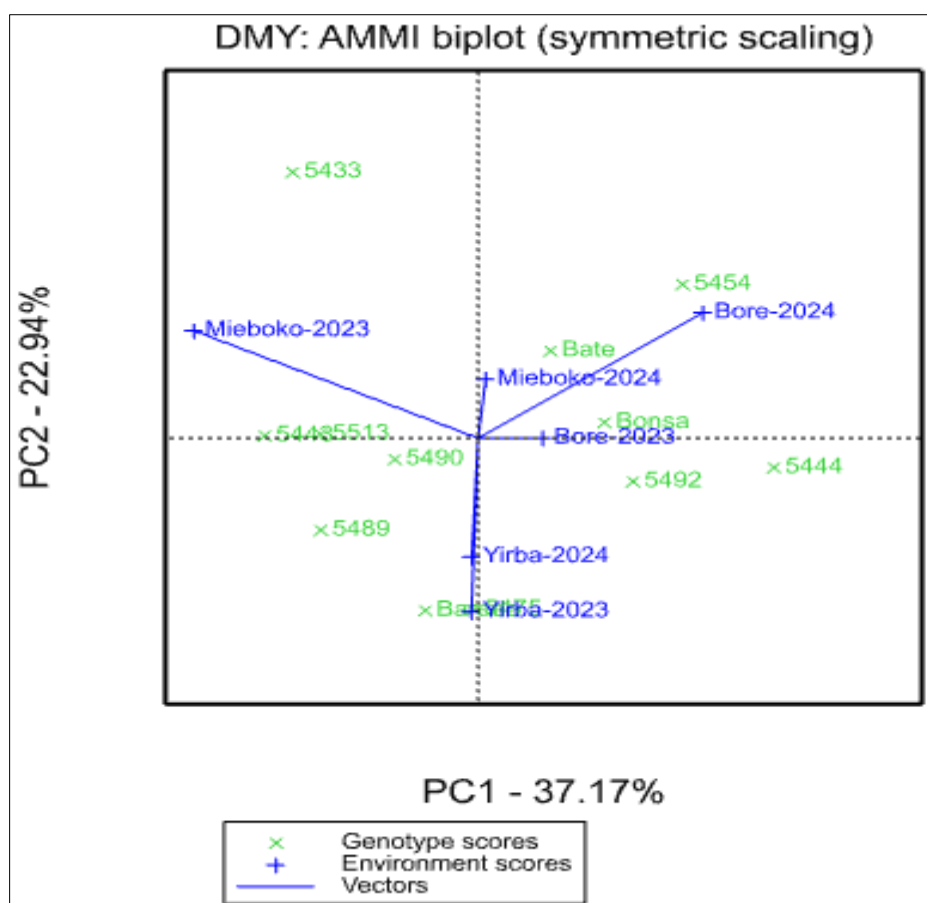


Fig.1: AMMI 2 bi-plot for IPCA 1 against IPCA 2 scores for 12 genotypes and six environments

Table 9: AMMI Stability value (ASV) for Dry matter yield

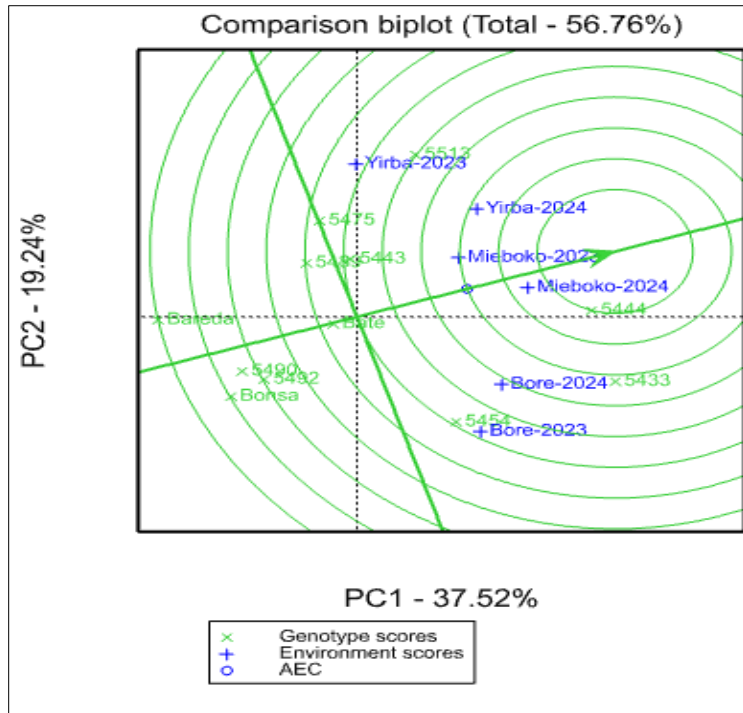
Genotype	Mean dry matter yield (tha)	Rank dry matter yield (tha)	IPCag1	IPCag2	ASV	Rank ASV
IRLI-5443	8.671	(5)	0.81749	0.01173	2.203	(5)
IRLI-5444	9.582	(2)	-1.13350	-0.13445	1.544	(1)
IRLI-5454	8.877	(4)	-0.78312	0.70282	1.880	(4)
IRLI-5475	8.324	(8)	0.01940	-0.78368	3.320	(8)
IRLI-5489	8.248	(7)	0.60141	-0.42028	3.158	(7)
IRLI-5433	9.643	(1)	0.70963	1.21625	0.755	(2)
IRLI-5490	7.881	(9)	0.31945	-0.09658	3.941	(11)
IRLI-5492	7.909	(10)	-0.59342	-0.19822	4.069	(9)
IRLI-5513	9.004	(3)	0.60274	0.01873	1.719	(3)
Bareda	7.633	(12)	0.20214	-0.78730	5.457	(10)
Bate	8.528	(6)	-0.27768	0.39918	2.493	(6)
Bonsa	7.713	(11)	-0.48454	0.07179	4.613	(12)

### Evaluation of Genotypes

Genotype IRLI-5444 and genotype IRLI-5433 which fell into the center of concentric circles, was the ideal genotype in terms of higher dry matter yielding ability and stable. In addition, Genotype IRLI-5443 and IRLI-5454 located on the next consecutive concentric circle might be regarded as desirable genotype showed higher interaction to the environmental factors and also higher in dry yielding than the remaining tested out

genotypes across the tested environments. Genotypes those very distant from the first concentric and the second circle; (Bonsa, Bareda and the other) genotypes were undesirable genotypes compared to other genotypes. The genotypes closest to the ideal genotype drawn on the center of concentric and/or average environmental coordinate (AEC) are highest yielder. The current result is corresponding to different authors (Zerihun, 2011; Kaya *et al.*, 2006).





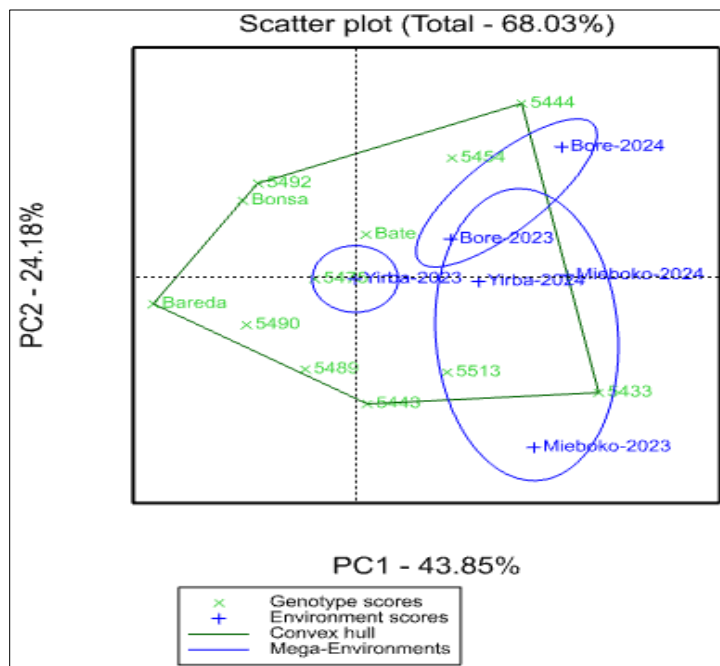
**Fig. 2:** GGE-bi-plot based on genotype focused scaling for comparison of the genotypes

**GGE Bi-Plot Analysis**

**Which-Won-Where' Patterns Analysis**

The genotypes located at the vertex of the polygon performed either best-performance in the mega-environments (MGE). Yan *et al.*, (2000) and Yan and Kang (2003) reported the polygon view of GGE bi-plot as the best way for identification of winning genotypes with visualizing the interaction patterns between genotypes and environments. Genotypes ILRI-5433,

ILRI-5433, Bareda, ILRI-5459 and genotype ILRI-5449 were the vertex (winning genotypes) in the sector where environments located in the MGE. Genotypes located at the vertices of a polygon had the highest dry matter yield in one or all environments that fell in the sector. This result is in agreement with the findings of Yan (2002); Yan *et al.*, (2010); Kebede *et al.*, (2023) and Wondimu *et al.*, (2022).



**Fig. 3:** The GGE-bi-plot for which won-where pattern for genotypes and environments

## Discriminating and Representativeness of Test Environments

Ideal test environment, which is the center of the concentric circles, has more power to discriminate genotypes in terms of the genotypic main effect as well

as able to represent the overall environments. Among the testing environments (Me'ee Bokko-24 and Me'ee Bokko-23) was highly to discriminate genotypes as well as the representative testing site.

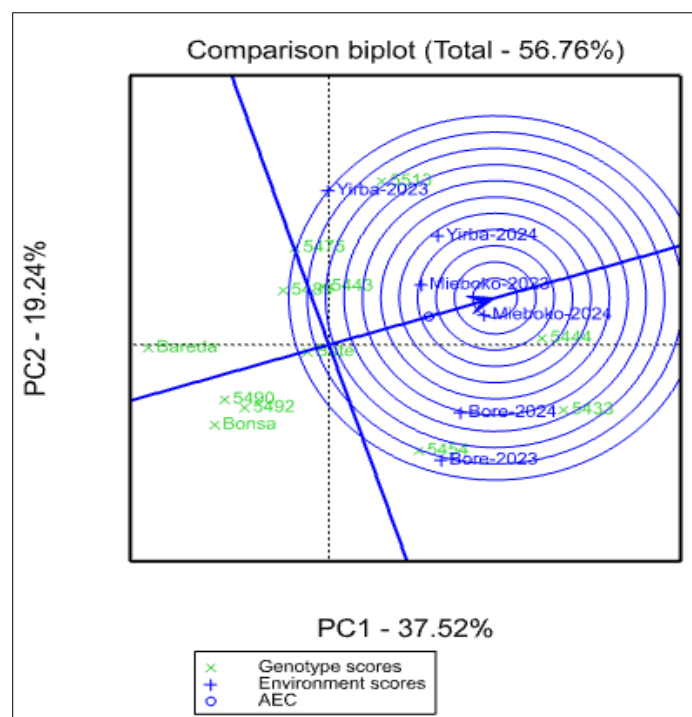


Fig. 4: GGE-bi-plot based on environment focused scaling for comparison of the environments.

## Chemical Composition

The combined analysis of variance for dry matter percentage (DM), crude protein (CP), neutral detergent fiber (NDF), and in vitro organic matter digestibility (IVOMD) showed significant differences among each other's (Table 9). The mean value of DM % was ranging 91.95% from Bonsa (check) to ILRI 5492 (94.53%) with a mean value of 93.64%. This result is higher than that of Tulu *et al.*, (2020) who reported 50.73% recorded DM% from different oat genotypes around southern Oromia. However comparable to the result of Birmaduma *et al.*, (2023) who reported (92.27%) in Haraghe, eastern part of Oromia region. The variation might be related to the difference in rainfall, genetic variability, soil fertility, forage harvesting stage, and other climatic conditions.

The crude protein content was shown significant ( $P < 0.05$ ) differences among the genotypes. The average mean value of the current CP content was ranging from 9.58 to 13.45 with a mean of 12%. This result was lower than the result of Mosissa *et al.*, (2018) who reported 10-16.6 g/100 and higher than the result of Kebede *et al.*, (2021) who reported 6.9-8.1 with a mean of 7.7%. The difference might be related to the genetic differences among oat genotypes studied and agronomic practices applied during the production and harvesting stage.

Neutral detergent fiber (NDF) content varied between 71.64 % to (51.06 %) with a mean of 64 %. A higher result was reported by Kebede *et al.*, (2021) who reported a mean value ranging from 70.1 to 74.8 with a mean value of 72.8%. The higher NDF is mostly affected by harvesting time (Molla *et al.*, 2018). However, the mean NDF content of oat genotypes in the current study was higher than that of Negash *et al.*, (2017) who reported a mean NDF content of 56.95%, and but lower than that of Wada *et al.*, (2019) who reported NDF mean ranging between 41.6% and 51.4% for different oat varieties. The variations might be due to genetic materials, harvesting stage, climatic conditions, and soil factors are the major causes of the difference in NDF content in oat genotypes. The IVOMD was shown significant ( $P < 0.05$ ) differences among the genotypes. Lowest to highest IVOMD was recorded from genotype ILRI-5475 (38.23%) and Bate variety (46.2%).

The in vitro organic matter digestibility (IVDMD), acid detergent fiber (ADF), acid detergent lignin (ADL), Ash and organic matter content (OM) didn't showed significant ( $P > 0.05$ ) differences among the genotypes. Similarly, Kebede *et al.*, (2021) reported a non-significant difference ( $P > 0.05$ ) IVDMD among 15 oat genotypes under vertisols conditions in the Central Highlands of Ethiopia.

**Table 10: Composite mean chemical compositions of oat genotypes tested in regional variety trial from six locations (Bore, Yirba, and Me'e Bokko) during 2023**

Genotypes	DM (%)	CP (%)	NDF (%)	ADF (%)	ADL (%)	IVDMD (%)	IVOMD (%)	ASH (%)	OM (%)
ILRI-5490	93.4 <sup>ab</sup>	10.61 <sup>b</sup>	70.15 <sup>a</sup>	45.9	6.8	48.9	38.7 <sup>b</sup>	11.01	89
Bonsa	91.95 <sup>b</sup>	11.94 <sup>ab</sup>	62.56 <sup>ab</sup>	44.04	5.4	55.8	45.8 <sup>a</sup>	11.4	88.6
Bate	93.05 <sup>ab</sup>	10.82 <sup>b</sup>	65.38 <sup>ab</sup>	44.2	6.9	54.2	46.2 <sup>a</sup>	11.9	88.1
ILRI-5513	93.1 <sup>ab</sup>	11.01 <sup>b</sup>	44.25 <sup>b</sup>	47.4	6.8	50.2	41 <sup>ab</sup>	10.81	89.2
ILRI-5492	94.53 <sup>a</sup>	11.13 <sup>b</sup>	64.74 <sup>ab</sup>	44.9	6.3	53.2	43.9 <sup>ab</sup>	10.7	89.3
ILRI-5444	94.07 <sup>ab</sup>	12.27 <sup>ab</sup>	55.29 <sup>ab</sup>	44.9	5.8	56.7	44.7 <sup>a</sup>	12.2	87.8
ILRI-5454	94.01 <sup>ab</sup>	9.85 <sup>b</sup>	70.37 <sup>a</sup>	47.2	5.6	53.4	42.8 <sup>ab</sup>	11.4	88.6
ILRI-5489	93.43 <sup>ab</sup>	10.96 <sup>b</sup>	68.89 <sup>a</sup>	45.6	6.9	55.5	43.9 <sup>ab</sup>	12.7	87.32
Bareda	93.12 <sup>ab</sup>	11.31 <sup>ab</sup>	63.61 <sup>ab</sup>	43.9	4.8	55.5	44.3 <sup>ab</sup>	11.94	88.06
ILRI-5433	94.33 <sup>ab</sup>	13.45 <sup>a</sup>	51.06 <sup>ab</sup>	46.2	5.2	50	39.9 <sup>ab</sup>	11.24	88.8
ILRI-5443	94.42 <sup>ab</sup>	12.32 <sup>ab</sup>	65.63 <sup>a</sup>	45.6	6.7	52.4	42 <sup>ab</sup>	11.27	88.73
ILRI-5475	94.23 <sup>ab</sup>	10.64 <sup>b</sup>	71.64 <sup>a</sup>	46.7	5.2	48.5	38.23 <sup>b</sup>	11.6	88.41
MEAN	93.64	12	64	45.53	6.04	52.84	42.61	11.5	88.5
CV (%)	1.3	15.9	17	5.2	1.98	8	7.4	1.89	2.5
LSD	*	*	**	NS	NS	NS	**	NS	NS

Means in a column within the same category having different superscripts differ ( $P < 0.05$ ); DM = Dry Matter; CP = Crude Protein; OM = Organic matter; NDF = Neutral detergent fiber; ADF = Acid Detergent Fiber; ASH = Total ash; ADL = Acid detergent lignin; IVOMD = In vitro Organic Matter Digestibility; IVDMD = In-vitro dry matter digestibility CV = Coefficient of variation; LSD = Least Significance difference.

## CONCLUSIONS AND RECOMMENDATION

Significant variations were observed among oat genotypes tested together in six environments. There were also significant genotype, environment and their interactions for most of the traits evaluated in diverse locations. Oat genotypes responded differently on agronomic performance, herbage dry matter, seed yield, and yield stability across the test environment due to deferential responses of the genotypes to various edaphic, climatic and biotic factors. Genotypes, environments and their interactions represented 8.34%, 19.5% and 3.12% of the total variance respectively. The AMMI statically model has shown that the largest proportion of the total variation in DM yield was attributed to genotypes. Different stability parameters and models indicated that oat genotypes ILRI-5433 and ILRI-5444 were considered the most desirable and stable among the tested genotypes evaluated with each other. On the other hand Bareda and Bonsa varieties were considered as the most unstable across the test environments. Accordingly genotype ILRI-5433 and ILRI-5444 the highest herbage DM yields and were most stable in the test environments. Therefore the production of stable, high yielding oat genotypes is of paramount importance to fill the gaps in the improved variety of forages. Thus, it is advised to cultivate and release as varieties in the tested locations and other areas with similar agroecology's of the country.

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