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Yield and Nutritional Quality of Oat (*Avena sativa*) Genotypes under Vertisols Conditions in the Central Highlands of Ethiopia

Gezahagn Kebede[1]*, Mulisa Faji[1], Fekede Feyissa[2], Kedir Mohammed[1], Getnet Assefa[3], Diriba Geleti[2], Muluneh Minta[1], Mesfin Dejene[1], Mengistu Alemayehu[4], Alemayehu Mengistu[5], Aschalew Tsegahun[1] and Solomon Mengistu[1]

[1]Holetta Agricultural Research Center, P.O Box, 31, Holetta, Ethiopia.
[2]Ethiopian Institute of Agricultural Research, P.O. Box, 2003, Addis Ababa, Ethiopia
[3]Livestock specialist, Addis Ababa, Ethiopia
[4]Ethiopian Agricultural Research Council Secretariat, Addis Ababa, Ethiopia
[5]Forage and Rangeland Scientist, Urael Branch, P.O. Box 62291, Addis Ababa, Ethiopia
***Corresponding author:** gezk2007@yahoo.co.uk

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Abstract: *Shortage of feed is a critical problem for livestock production in Ethiopia. However, the selection of oat genotypes that perform better under vertisol conditions is very important to mitigate the feed shortage problem in the central highlands of Ethiopia. So, the study was designed to evaluate the agro-morphological and nutritional performance of fifteen oat genotypes under vertisol conditions during the main cropping seasons of 2015 and 2016 at Kuyu and Ginchi sub-stations of Holetta Agricultural Research Center. Randomized complete block design replicated three times was used for evaluating the genotypes. The genotypes were sown with the recommended seeding rate of 100 kg ha^{-1} using an inter-row spacing of 20 cm. Diammonium phosphate (DAP) fertilizer at the rate of 100 kg ha^{-1} was uniformly applied at sowing for all genotypes at both locations and years. Data were collected on plant height, dry matter yield, leaf to stem ratio, straw yield, seed yield, thousand seed weight, harvest index, and nutritive values. All measured data were subjected to analysis of variance using procedures of SAS general linear model. The genotypes responded differently ($P<0.001$) for plant height, leaf to stem ratio, straw yield, seed yield, thousand seed weight, and harvest index. All measured agro-morphological traits of oat genotypes were significantly influenced by genotype by location by year interaction. In both cropping seasons, the genotypes produced relatively better dry matter yield at Kuyu than Ginchi indicating the performance of genotypes was highly hampered by heavy vertisol characteristics of Ginchi location. In the over years and locations combined analysis, genotypes 1600, 1740, 2596, 79983, 1493, and 1742 produced more than 15 t ha^{-1} dry matter yield at the soft dough stage. Oat genotypes that had relatively higher plant height and better dry matter yield showed higher straw yield when compared with small plant height and lower dry matter-producing genotypes. The mean seed yield performance of oat genotypes in the combined analysis was 2250 kg ha^{-1} and the highest seed yield was recorded for genotype 2806 followed by 79983, 2291, 8251, and 1742. Moreover, the chemical and in-vitro dry matter digestibility analysis of oat genotypes was done and genotype 1486 produced the highest crude protein and in-vitro dry matter digestibility contents while the lowest was recorded from genotype SAIA. The highest crude protein yield was recorded for oat genotype 2291 followed by 2596, 2806, 1506, and 1742 and oat genotypes that produced the highest crude protein yield also gave the highest digestible yield. Generally, better dry matter yield, crude protein yield, digestible yield, and seed yield performances were recorded from genotypes 2291, 2596, 2806, 1506, 1742, 8251, and 79983. Therefore, these oat genotypes were recommended for vertisol conditions of the study areas and similar agro-ecologies.*

Keywords: Forage yield, Harvest index, Herbage quality, Leaf to stem ratio, Seed yield, Straw yield

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1. Introduction

Feed shortage in terms of both quantity and quality is the leading problem affecting the livestock productivity in Ethiopia (Aduga, 2007; Fekede et al., 2015a). Traditional livestock production system mainly depends upon poor pasturelands and crop residues which are usually inadequate to support reasonable livestock production (Tsige, 2000). During the latter part of the dry season, livestock feed is normally in short supply and is also of poor quality. Residues from cereals are the main source of forage but these are low in protein and have poor digestibility. The production of adequate quantities of good quality dry season forages to supplement crop residues and pasture roughages is the only way to economically overcome the dry season constraints affecting livestock production in Ethiopia. Much of the available feed resources are utilized to support the maintenance requirement of the animals with little surplus left for production. Poor animal nutrition and productivity arising from the inadequate supply and low-quality feed are among the major constraints facing livestock production in developing countries (Fekede et al., 2015b).

Screening of different forage crops was made both at accessions and species level and promising materials were promoted for production (Getnet and Gezahagn, 2012). A wide range of annual and perennial forage species were evaluated in areas ranging in altitude from 600-3000 meters above sea level, and many promising species have been selected for high, medium, and low altitudes. The selected forage crops are generally well adapted to the different agro-ecologies and high-yielding and have better quality compared to natural pasture (Getnet et al., 2012). Among the different forage crops recommended for various agro-ecological zones of Ethiopia, common oat (*Avena sativa*) is abundantly grown in the central highlands of Ethiopia. Oat is a potential fodder crop for livestock feed and has been growing in the central highlands of Ethiopia for about five decades. It has been well accepted by the farming community because of its hardy nature which performs better under stressful conditions with very minimal managerial inputs. It is used as livestock feed in the form of hay, silage, and grazing or green feed and provides an abundance of excellent forage at a time when other succulent, high-protein feeds are scarce. Its grain also makes part of the staple diet of human beings in some parts of the country (Lulseged, 1981).

In Ethiopia, vertisol covers 10.2% or 12.5 million ha of which 7.6 million ha occur in the Ethiopian highlands and are the fourth most important soil. Despite this soil is very fertile, its productivity is constrained by unique soil physical properties. Due to the high water holding capacity of this soil, aeration becomes a limiting factor for root growth and activity. Soil type was found to be the most important factor affecting forage biomass yield and seed production. Different varieties respond differently to different soil types, climatic, and management conditions. Thousands of oat lines have been collected and tested for environmental adaptation and forage yield in the highlands (Astatke, 1976). Several reports have indicated that there is a considerable variation in agronomic and quality traits between oats genotypes under a given environmental condition. Until recently, the focus of research works on oat has been limited to evaluation and selection varieties in terms of adaptation to edaphic and agro-ecological conditions as well as herbage yield potential. However, the number of oat genotypes tested and recommended for vertisol conditions is highly limited. So, evaluation of promising oat genotypes under vertisol conditions is vital to improving oat production and productivity. Therefore, the study was designed to evaluate the performance of different oat genotypes under vertisol conditions and to select promising genotypes of oat for utilization in the study areas and similar agro-ecologies of the country.

2. Materials and Methods

2.1. Description of the study areas

The experiment was conducted under field conditions at the Kuyu and Ginchi sub-station of Holetta Agricultural Research Center during the main cropping seasons of 2015 and 2016. The test locations represent the highland areas ranging in altitude from 2200 to 2400 masl. The farming system of the study areas is a mixed crop-livestock production system. The long-term (30 years) average annual rainfall and minimum and maximum air temperatures and the descriptions of the study sites are indicated in Table 1.

Table 1: Descriptions of the test environments

Parameter	Kuyu[a]	Ginchi[b]	References
Latitude	9° 00'N	9° 02'N	
Longitude	38° 30'E	38° 12'E	
Altitude (masl)	2400	2200	
Distance from Addis Ababa (km)	29	75	
Annual rainfall (mm)	1044	1095	EIAR, 2005
Daily minimum temperature (°C)	6.2	8.4	EIAR, 2005
Daily maximum temperature (°C)	21.2	24.6	EIAR, 2005
Soil type	Vertisol	Vertisol	EIAR, 2005
Textural class	Clay	Clay	EIAR, 2005
pH (1:1 H2o)	5.63	6.50	Desta, 1982; Getachew *et al*., 2007
Total organic matter (%)	5.63	1.30	Desta, 1982; Getachew *et al*., 2007
Total nitrogen (%)	0.16	0.13	Desta, 1982; Getachew *et al*., 2007
Available phosphorous (ppm)	6.95	16.50	Desta, 1982; Getachew *et al*., 2007

2.2. Experimental treatments and design

The fifteen genotypes of oat considered for this experiment were 633, 1486, 1488, 1493, 1506, 1589, 1600, 1740, 1742, 2291, 8251, 2806, 2596, 79983 and SAIA. The genotypes were planted at the beginning of the main rainy season at the two locations. The genotypes were sown in rows of 20 cm with seed rate of 100 kg ha^{-1} on a plot size of 1.8 m x 3 m= 5.4 m^2 consisting of nine rows. However, the seven rows with a net plot size of 1.4 m x 3 m = 4.2 m^2 were used for data collection. The experiment was conducted on randomized complete block design (RCBD) with three replications and the genotypes assigned randomly to plots within the block. At sowing, 100 kg ha^{-1} Diammonium phosphate (DAP) fertilizer was uniformly applied using the broadcast method for all treatments at both locations and years. Generally, all crop management was uniformly applied for all genotypes and maximum care was taken in the experimental plots to reduce the possible yield-limiting factors which could affect the yield performance of the genotypes.

2.3. Data collection and measurements

For plant height determination, the mean height of five randomly selected plants from net plot area was recorded for each plot. At the forage harvesting stage (soft dough), four interior rows were clipped at 5cm above the ground level to determine the biomass yield. The weight of the total fresh biomass yield was recorded from each plot in the field and the estimated 500 g sample was taken from each plot to the laboratory. The sample taken from each plot was weighed to know the total sample fresh weight and oven-dried for 24 hours at a temperature of 105°C for herbage dry matter yield determination. The herbage sample taken from each plot was weighed to know the total sample fresh weight and manually fractionated into leaf, stem, and panicle. The morphological parts were separately weighed to know their sample fresh weight, oven-dried for 24 hours at a temperature of 105°C, and separately weighed to estimate the proportions of these morphological parts. Accordingly, leaves were separated from stems, and the leaf to stem ratio (LSR) was estimated based on the dry matter basis of each component.

The remaining inner three rows of each plot were harvested at grain maturity to assess the grain and straw yield performances of the genotypes. To isolate the seed from the total biomass, the panicle portion of the plant was first cut apart and separately collected. The remaining aftermath was harvested from ground level and its fresh biomass was measured and recorded in the field. About 300 g samples of the aftermath were taken and oven-dried at 65°C for 72 hours to determine the straw dry matter yield. The residue remaining after grain threshing (chaff) was oven-dried at 100°C overnight and added to the aftermath dry matter for estimation of straw dry matter yield. Seed samples were taken and oven-dried at 100°C for 48 hours to adjust the moisture content of 12.5%, a recommended percentage level for cereals (Biru, 1979). Seed yield and thousand seed weight were then calculated at 12.5% moisture content. Harvest index was calculated as the ratio of grain yield to total above-ground biomass yield per unit area multiplied by 100.

2.4. Nutritional quality analysis

Harvesting for chemical analysis was undertaken as the genotypes reached the soft dough stage, as recommended for forage harvesting for oat genotypes (Astatke, 1976; Lulseged, 1981; Fekede, 2004). The fresh weights of the samples were recorded, and they were then oven-dried at a temperature of 65^{o}C for 72 hours for laboratory analysis to determine the chemical composition and *in-vitro* organic matter digestibility of the genotypes. The oven-dried samples were then ground to pass a one mm sieve and used for laboratory analysis. The chemical analysis and *in-vitro* dry matter digestibility of oat genotypes were done following the standard laboratory procedures as indicated in Table 2.

Table 2: Laboratory procedures for chemical and *in-vitro* organic matter digestibility analysis

Parameters	Procedures
Total ash	By combusting the samples at 550°C for 6 hours (AOAC, 1990)
CP	N determination (AOAC, 1995) and the CP content estimated by N * 6.25.
NDF, ADF, ADL	Van Soest and Robertson (1985)
IVDMD	Tilley and Terry (1963)
Hemicellulose	NDF - ADF
Cellulose	ADF - ADL
CP yield	(CP% * DM yield)/100
Digestible yield	(IVDMD% * DM yield)/100

2.5. Statistical analysis

Analysis of variance (ANOVA) procedures of SAS general linear model (GLM) was used to compare treatment means (SAS, 2002). For the combined analysis of variance, the homogeneity of error variance was tested (Gomez and Gomez, 1984). The least significant difference (LSD) at a 5% significance level was used for comparison of means. For each year and location analysis, the model below [1] was used.

$$Y_{ij} = \mu + G_i + B_j + e_{ij} \qquad [1]$$

Where:

Yij = Dependent variable;
μ = overall mean;
Gi = effect of genotype i;
Bl = effect of block l
eij is a random error

For the combined analysis, the model below was used [2].

$$Y_{ijkl} = \mu + G_i + Y_j + L_k + (GY)_{ij} + (GL)_{ik} + (YL)_{jk} + (GYL)_{ijk} + B_l + e_{ijkl} \qquad [2]$$

Where

Yijkl = Dependent variable;
μ = overall mean;
Gi = effect of genotypei;
Yj = effect of year j;
Lk = effect of location k;
(GY)ij = the interaction effect of genotype i and year j;
(GL)ik = the interaction effect of genotype i and location k;
(YL)jk = interaction effect of year j and location k;
(GYL)ijk = interaction effect of genotype i, year j and location k;
Bl = the effect of the block I
eijkl = random error

3. Results and Discussion

3.1. Analysis of variance

The combined analysis of variance for plant height, dry matter yield, leaf to stem ratio, straw yield, seed yield, thousand seed weight, and harvest index of oat genotypes tested over locations and years are indicated in Table 3. The genotypes showed a non-significant (P>0.05) difference for only dry matter yield. The location didn't significantly (P>0.05) affect the seed yield and thousand seed weight of oat genotypes. Harvest index and dry matter yield were not affected significantly by the interaction effects of genotype by location and genotype by year, respectively.

On the other hand, the tested genotypes responded differently (P<0.001) for plant height, leaf to stem ratio, straw yield, seed yield, thousand seed weight, and harvest index. Similarly, all the measured agro-morphological traits of oat genotypes were significantly influenced (P<0.001) by cropping season. Moreover, plant height, dry matter yield, leaf to stem ratio, straw yield, and harvest index were significantly affected (P<0.001) by location, indicating the two locations varied in edaphic and climatic conditions. Some genotypes exhibit a highly specific response to a particular environment (soil, rainfall, and temperature), others are uniform in performance over a range of environments (Gezahagn *et al*., 2017a). Generally, all measured agro-morphological traits of oat genotypes were significantly influenced by genotype by location by year interaction. The selection of better performing genotypes in one environment may not enable the identification of genotypes that can repeat nearly the same performances in other environments (Gemechu, 2012; Gezahagn *et al*., 2017a).

Table 3: Combined analysis of variance for measured agro-morphological traits of oat genotypes

Parameters	G	L	Y	G*L	G*Y	L*Y	G*L*Y
PH	***	***	***	***	***	NS	*
DMY	NS	***	***	**	NS	**	**
LSR	***	***	***	**	**	NS	*
StY	***	***	***	***	***	***	***
SY	***	NS	***	**	***	***	*
TSW	***	NS	***	***	***	***	***
HI	***	***	***	NS	**	***	*

PH= plant height; DMY= dry matter yield; LSR= leaf to stem ratio; StY= straw yield; SY= seed yield; TSW= thousand seed weight; HI= harvest index; G= genotype; L= location; Y= year; G*L= genotype by location interaction; G*Y= genotype by year interaction; L*Y= location by year interaction; G*L*Y= genotypeby location by year interaction; NS = non-significant; * = significant at 0.05; ** = significant at 0.01; *** = significant at 0.001

3.2. Forage Yield and Yield Components

The plant height of oat genotypes tested over years and across locations is indicated in Table 4. The result indicated that the genotypes respond differently (P<0.05) in terms of plant height for both cropping seasons and locations at the forage harvesting stage. Moreover, the plant height in the combined analysis showed significant variation (P<0.05) for tested genotypes. The genotypes produced relatively higher plant height at Kuyu than the Ginchi location in both cropping seasons. The combined analysis indicated that the SAIA genotype produced the highest plant height followed by 2596, 2291, 1486, and 8251. On the other hand genotypes 1506, 1740, 633, 2806, and 1488 had the lowest plant height while the remaining genotypes had intermediate plant height. Variation in plant height was observed among the tested oat genotype in the present study agrees with previous findings (Fekede 2004; Getnet *et al*., 2004; Gezahagn *et al*., 2016). In addition to genetic variability, soil fertility and environmental conditions could also contribute to the difference in plant height (Gezahagn *et al*., 2017a). Plant height may differ in varieties due to environmental conditions which in turn cause variation in hormonal balance and cell division rate (Zaman *et al*., 2006). Generally, the presence of genetic variation among the tested genotypes, response of genotypes to environmental factors, and their interactions are the major reason for plant height differences in oat genotypes.

The response of oat genotypes for herbage dry matter yield performance at the forage harvesting stage across locations and over years is indicated in Table 5. The result revealed that the dry matter yield of oat genotypes varied significantly (P<0.05) only at Ginchi in both cropping seasons. In 2015, the oat genotypes produced better dry matter yield at both locations when compared with the 2016 growing season. The dry matter yield ranged from 20.0 – 31.1 with a mean of 24.4 t ha^{-1} and from 9.6 – 18.6 with a mean of 14.6 t ha^{-1} at Kuyu and Ginchi, respectively, in 2015 cropping season. Similarly, in the 2016 growing season, the dry matter yield ranged from 3.9 – 17.0 with a mean of 13.3 t ha^{-1} at Kuyu and from 4.8 – 7.7 with a mean of 6.1 t ha^{-1} at Ginchi. In the combined analysis, the genotypes responded nonsignificantly ($P>0.05$) for dry matter yield. In both cropping seasons, the genotypes produced relatively better dry matter yield at Kuyu than Ginchi. The overall mean dry matter yield of oat genotypes at Kuyu had a 67% yield advantage over Ginchi in the 2015 cropping season. Similarly, the dry matter yield of oat genotypes at Kuyu had a 118% yield advantage over Ginchi in the 2016 cropping season. Among the tested oat genotypes, 1600, 1740, 2596, 79983, 1493, and 1742 were produced better dry matter yield. The yielding ability of the genotype is the result of its interaction with the environment and environmental factors such as soil characteristics, moisture, and temperature (Gezahagn *et al*., 2017b). Yield is a complex quantitative character and is greatly influenced by environmental fluctuations; hence, the selection for superior genotypes based on yield *perse* at a single location in a year may not be very effective (Shrestha *et al*., 2012). Generally, considerable variation in terms of dry matter yield was observed among the tested oat genotypes and this result is in close conformity with the findings of Fekede (2004) and Getnet *et al*. (2004).

Table 4: Mean plant height (cm) of oat genotypes tested over years and locations

SN	Genotypes	2015		2016		Combined
		Kuyu	Ginchi	Kuyu	Ginchi	
1	2806	162.5^{c}	136.7^{abcd}	161.7^{a}	90.6f	137.9^{cde}
2	79983	177.8^{abc}	127.6^{de}	155.5^{ab}	119.4^{bc}	144.9^{abcd}
3	8251	176.7^{abc}	130.6^{cde}	165.5^{a}	111.7^{bcd}	146.1^{abcd}
4	1493	175.0^{abc}	147.8^{ab}	147.2^{abc}	100.0^{def}	142.5^{bcde}
5	2291	169.6^{bc}	152.2^{a}	146.7^{abc}	120.0^{bc}	147.1^{abc}
6	1742	187.2^{a}	130.0^{cde}	151.7^{ab}	109.4^{bcde}	144.6^{abcd}
7	1488	185.6^{ab}	121.7^{de}	154.4^{ab}	100.0^{def}	140.4^{bcde}
8	1740	177.8^{abc}	119.4^{e}	135.5^{bc}	108.9^{bcdef}	135.4^{de}
9	633	167.2^{c}	137.3^{abcd}	123.9^{c}	122.2^{ab}	137.7^{cde}
10	1486	186.7^{ab}	145.0^{abc}	152.2^{ab}	102.2^{cdef}	146.5^{abcd}
11	2596	187.2^{a}	131.1^{bcde}	170.0^{a}	117.2^{bcd}	151.4^{ab}
12	SAIA	161.7^{c}	144.4^{abc}	170.6^{a}	140.6^{a}	154.3^{a}
13	1506	166.1^{c}	131.7^{bcde}	136.7^{bc}	91.1^{ef}	131.4^{e}
14	1600	178.3^{abc}	136.7^{abcd}	146.7^{abc}	101.7^{cdef}	140.8^{bcde}
15	1589	173.3^{abc}	121.1^{de}	155.5^{ab}	115.0^{bcd}	141.3^{bcde}
	Mean	175.5	134.2	151.6	110.0	142.8
	P-value	0.0378	0.0072	0.0242	0.0006	0.0102

Means followed by a common superscript letter within a column are not significantly different from each other at $P<0.05$

Table 5: Mean dry matter yield (t ha^{-1}) of oat genotypes tested over years and locations

SN	Genotypes	2015		2016		Combined
		Kuyu	Ginchi	Kuyu	Ginchi	
1	2806	20.0	17.5^{ab}	15.2	5.0^{cd}	14.4
2	79983	24.7	14.5^{abcd}	15.1	7.3^{abc}	15.4
3	8251	24.2	13.0^{bcde}	13.8	7.5^{ab}	14.6
4	1493	23.3	14.7^{abcd}	17.0	5.2^{cd}	15.0
5	2291	21.8	18.6^{a}	10.3	6.3^{abcd}	14.3
6	1742	23.3	16.9^{abc}	14.4	5.2^{bcd}	15.0
7	1488	23.6	14.6^{abcd}	15.1	4.8^{d}	14.5
8	1740	31.1	9.6^{e}	13.6	7.6^{a}	15.5
9	633	22.7	14.7^{abcd}	3.9	4.9^{d}	11.5
10	1486	25.7	14.8^{abcd}	13.9	5.1^{cd}	14.9
11	2596	25.0	17.2^{abc}	13.3	6.0^{abcd}	15.4
12	SAIA	21.9	12.4^{cde}	13.5	6.5^{abcd}	13.6
13	1506	26.5	14.8^{abcd}	10.7	7.7^{a}	14.9
14	1600	25.5	14.5^{abcd}	15.8	6.4^{abcd}	15.6
15	1589	26.8	11.8^{ed}	13.1	5.2^{bcd}	14.2
	Mean	24.4	14.6	13.3	6.1	14.6
	P-value	0.1077	0.0496	0.1224	0.0673	0.4768

Means followed by a common superscript letter within a column are not significantly different from each other at P<0.05

The leaf to stem ratio of oat genotypes varied significantly (P<0.05) in both locations during the 2016 cropping seasons and in the combined analysis (Table 6). The result showed that the highest leaf to stem ratio at the forage harvesting stage was recorded at Ginchi than Kuyu in both cropping seasons. The mean leaf to stem ratio of oat genotypes in the 2015 cropping season was 0.76 and it increased to 1.06 in 2016 at Kuyu. Similarly, the mean leaf to stem ratio of oat genotypes increased from 1.11 in 2015 to 1.20 in the 2016 cropping season at Ginchi. The combined analysis indicated that genotype 1600 produced the highest leaf to stem ratio followed by 1506 1486, 2596, and 633. On the other hand genotypes SIAI, 79983, 1740, 2291, and 2806 had the lowest leaf to stem ratio while the remaining genotypes had intermediate leaf to stem ratio. The mean leaf to stem ratio of oat genotypes at Ginchi had 46% higher than Kuyu in the 2015 cropping season. Though it decreased in 2016, the tested genotypes had a 13% higher mean leaf to stem ratio at Ginchi than Kuyu. The leaf to stem ratio was directly proportional to the proportion of leaf and inversely proportional to the proportion of stem. Due to the presence of genetic variations, the tested oat genotypes respond differently for the leaf to stem ratio. Growth characteristics and management such as tillering performance, plant height, and age of harvesting also affect the proportion of leaf and stem of the plant. The leaf to stem ratio also varied among tested oat varieties (Fekede, 2004). The leaf to stem ratio has significant implications on the chemical composition of any forage crop as leaves contain higher levels of nutrients and less fiber than stems. The result indicated that the leaf to stem ratio is an important factor affecting diet selection, quality, and intake of forage (Smart *et al.*, 2004). The leaf to stem ratio is associated with the high nutritive value of the forage because the leaf is generally of higher nutritive value (Tudsri *et al.*, 2002) and the performance of animals is closely related to the amount of leaf in the diet.

The straw yield of oat genotypes tested across locations and over years is indicated in Table 7. The result indicated that the genotypes responded differently (P<0.05) for straw yield at Kuyu in both cropping seasons and Ginchi only in the 2016 growing season. The combined analysis also showed that the straw yield at the grain harvesting stage varied significantly (P<0.05) among the tested oat genotypes. The straw yield was higher in the 2015 cropping season than in 2016 in both locations indicating the climatic conditions of the first year were conducive for the tested genotypes. The mean straw yield of oat genotypes had 100 and 94% yield advantages at Kuyu than Ginchi in 2015 and 2016 cropping season, respectively. Among the tested genotypes, 1742, 1493, 1506, 1600, and 2806 genotypes which had relatively higher plant height and better dry matter yield showed higher straw yield. On the other hand, genotypes 2291, 1488, 633, 1589 and SAIA produced lower straw yield while the remaining oat genotypes were intermediate in straw yield performance.

In general, all the oats varieties included in this study gave higher straw yield than the values reported for different cultivars of barley in the highlands of Ethiopia (Seyoum *et al*., 1995) and maize in mid-altitude areas of southern Ethiopia (Adugna and Sundstol, 1999). Oat straw is used as animal feed because it is softer and has more digestible organic matter and metabolic energy to livestock than other cereal crops. It is a preferred feed of all animals and its straw is soft and superior to wheat and barley. Moreover, the straw is used as a bedding material (Fekede, 2004) due to its softness and better absorbent nature.

Table 6: Mean leaf to stem ratio of oat genotypes tested over years and locations

SN	Genotypes	2015		2016		Combined
		Kuyu	Ginchi	Kuyu	Ginchi	
1	2806	0.74	1.25	1.01^{bcd}	0.63^{b}	0.91^{bcde}
2	79983	0.72	0.91	0.78^{d}	0.85^{b}	0.82^{de}
3	8251	0.79	1.06	0.99^{bcd}	0.94^{b}	0.95^{bcde}
4	1493	0.74	1.03	1.20^{bc}	1.00^{b}	0.99^{bcde}
5	2291	0.65	0.91	0.84^{cd}	1.10^{b}	0.88^{cde}
6	1742	0.84	1.10	0.90^{bcd}	1.30b	1.04^{bcde}
7	1488	0.81	1.18	0.98^{bcd}	1.04^{b}	1.00^{bcde}
8	1740	0.65	0.94	0.92^{bcd}	0.89^{b}	0.84^{cde}
9	633	0.64	0.95	1.94^{a}	0.73^{b}	1.07^{bcd}
10	1486	0.74	1.56	0.98^{bcd}	1.62^{b}	1.23^{ab}
11	2596	0.79	1.22	1.25^{b}	1.42^{b}	1.17^{bc}
12	SAIA	0.64	0.78	0.66^{d}	0.72^{b}	0.70^{e}
13	1506	0.97	1.30	1.24^{b}	1.49^{b}	1.25^{b}
14	1600	0.90	1.27	1.22^{b}	3.13^{a}	1.63^{a}
15	1589	0.86	1.21	0.93^{bcd}	1.16^{b}	1.04^{bcde}
	Mean	0.76	1.11	1.06	1.20	1.03
	P-value	0.1844	0.4564	<.0001	0.0054	0.0001

Means followed by a common superscript letter within a column are not significantly different from each other at $P<0.05$

Table 7: Mean straw yield (t ha^{-1}) of oat genotypes tested over years and locations

SN	Genotypes	2015		2016		Combined
		Kuyu	Ginchi	Kuyu	Ginchi	
1	2806	19.5^{bc}	11.5	11.1^{bcd}	4.8^{ab}	11.7^{abcd}
2	79983	18.5^{cd}	10.1	9.0^{cde}	5.8^{ab}	10.8^{abcdef}
3	8251	17.7^{cd}	8.2	8.5^{de}	5.9^{a}	10.1^{bcdef}
4	1493	24.1^{a}	10.5	9.0^{cde}	6.0^{a}	12.4^{ab}
5	2291	11.0^{f}	9.7	5.8^{ef}	4.1^{b}	7.7^{g}
6	1742	22.5^{ab}	11.1	13.1^{abc}	4.6^{ab}	12.8^{a}
7	1488	13.5^{ef}	8.3	8.6^{de}	4.3^{ab}	8.7^{fg}
8	1740	19.6^{bc}	9.8	9.8^{bcde}	5.3^{ab}	11.1^{abcde}
9	633	18.5^{cd}	9.4	3.3^{f}	5.0^{ab}	9.1^{efg}
10	1486	16.6^{cde}	7.0	17.0^{a}	5.4^{ab}	11.5^{abcd}
11	2596	17.2^{cde}	9.7	8.5^{de}	5.8^{ab}	10.3^{bcdef}
12	SAIA	15.0^{de}	7.7	11.7^{bcd}	4.9^{ab}	9.8^{cdefg}
13	1506	24.3^{a}	8.7	10.1^{bcde}	5.2^{ab}	12.1^{abc}
14	1600	19.5^{bc}	9.4	14.1^{ab}	4.3^{ab}	11.8^{abcd}
15	1589	17.6^{cd}	7.5	8.5^{de}	4.8^{ab}	9.6^{defg}
	Mean	18.36	9.2	9.9	5.1	10.6
	P-value	<.0001	0.3178	0.0002	0.4834	0.0005

Means followed by a common superscript letter within a column are not significantly different from each other at $P<0.05$

3.3. Seed yield and yield components

The seed yield of oat genotypes harvested at the seed harvesting stage differed significantly ($P<0.05$) across locations and over years as shown in Table 8. The genotypes produced better seed yield in the 2015 cropping season when compared to 2016 indicating favorable climatic conditions in the first year assisted the genotypes to express the genetic potential. The genotypes gave the highest seed yield at Kuyu than Ginchi in the 2015 cropping season. However, the seed yield obtained in 2016 was highest at Ginchi than at Kuyu. The combined analysis also showed that the seed yield performance of oat genotypes varied significantly ($P<0.05$). The seed yield performance of oat genotypes in the combined analysis ranged from 1460 – 3210 with a mean of 2250 kg ha^{-1}. Oat genotype 2806 produced the highest seed yield followed by 79983, 2291, 8251, and 1742. On the other hand genotypes 1589, SAIA, 1600, 1740, and 1486 gave the lowest seed yield while the remaining oat genotypes had intermediate seed yield performance. The variability among the oat genotypes in seed yield performance was mainly due to their genetic difference and their differential response to the growing environments. The seed yield difference among oat genotypes is also reported in different research studies (Fekede, 2004; Getnet et al., 2004). The significant effect of oat genotypes on seed yield performance in the present study is also in agreement with the previous findings in other countries (Singh and Singh, 1992; Lupingan et al., 1999; Naeem et al., 2002).

Thousand seed weight of oat genotypes tested across locations and over years is indicated in Table 9. The result showed that the genotypes responded differently ($P<0.05$) for thousand seed weights at each location and over years. The genotypes gave relatively higher mean thousand seed weight in the 2015 cropping season than in 2016. This indicates that in the 2015 cropping season, the climatic conditions such as amount and distribution of rainfall and minimum and maximum temperatures were favorable for oat production. In the combined analysis, significant ($P<0.05$) variation was also observed among oat genotypes for thousand seed weight. Thousand seed weights of oat genotypes in the combined analysis ranged from 22.6 – 34.7 with a mean of 30.2 g. The highest thousand seed weight was recorded for oat genotype 633 followed by 2806, 1742, 8251, and 1493. On the other hand, the lowest thousand seed weight was recorded for oat genotypes SAIA, 1589, 1600, 1740, and 1506 while the remaining genotypes produced intermediate thousand seed weight. Oat genotypes with high grain yield showed higher 1000 kernel weight (Fekede, 2004; Getnet et al., 2004). The difference could be due to the inherent variation in seed size complemented with the environmental and soil conditions. Thousand seed weight has got practical significance in estimating the seeding rate for each oat genotype to ensure that an equal number of seeds could be sown per unit area (Fekede, 2004).

Table 8: Mean seed yield (kg ha^{-1}) of oat genotypes tested over years and locations

SN	Genotypes	2015		2016		Combined
		Kuyu	Ginchi	Kuyu	Ginchi	
1	2806	6280^{a}	5040^{a}	250^{ab}	1240^{a}	3210^{a}
2	79983	5480^{ab}	4390^{ab}	190^{abcd}	1100^{ab}	2790^{ab}
3	8251	5480^{ab}	4180^{abc}	110^{cdef}	880^{bcd}	2660^{abcd}
4	1493	4210^{cdef}	3890^{abcd}	130^{cdef}	860^{bcd}	2270^{bcdef}
5	2291	5910^{ab}	3880^{abcd}	190^{abcd}	1080^{ab}	2760^{abc}
6	1742	5390^{abc}	3800^{bcd}	230^{bcd}	890^{bcd}	2580^{abcde}
7	1488	3920^{ef}	3530^{bcde}	80^{def}	830^{bcd}	2090^{cdefg}
8	1740	3160^{fg}	3460^{bcde}	130^{cdef}	950^{abc}	1920^{efg}
9	633	4900^{bcde}	3450^{bcde}	70^{ef}	910^{abcd}	2330^{bcde}
10	1486	4040^{edf}	3110^{cdef}	150^{bcdef}	870^{bcd}	2040^{defg}
11	2596	5260^{abcd}	3070^{cdef}	180^{abcde}	1090^{ab}	2400^{bcde}
12	SAIA	2240^{g}	2900^{cdef}	170^{bcde}	950^{abc}	1590^{g}
13	1506	4820^{bcde}	2680^{edf}	300^{a}	590^{d}	2100^{cdefg}
14	1600	3130^{fg}	2350^{ef}	150^{bcdef}	790^{bcd}	1610^{fg}
15	1589	3040^{fg}	2090^{f}	50^{f}	660^{cd}	1460^{g}
	Mean	4480	3460	160	910	2250
	P-value	<.0001	0.0025	0.0075	0.0398	<.0001

Means followed by a common superscript letter within a column are not significantly different from each other at $P<0.05$

Table 9: Mean thousand seed weight (g) of oat genotypes tested over years and locations

SN	Genotypes	2015		2016		Combined
		Kuyu	Ginchi	Kuyu	Ginchi	
1	2806	30.3^{ef}	36.3^{a}	34.0^{a}	36.3^{a}	34.3^{ab}
2	79983	35.3^{c}	31.3^{cde}	29.7^{c}	31.3^{c}	31.9^{cd}
3	8251	35.7^{bc}	30.3^{def}	30.0^{bc}	32.3^{bc}	32.1^{bcd}
4	1493	32.0^{de}	33.3^{b}	30.3^{bc}	32.7^{bc}	32.1^{bcd}
5	2291	25.3^{h}	33.7^{b}	30.7^{bc}	32.7^{bc}	30.0^{cde}
6	1742	32.0^{de}	32.0^{bcd}	31.7^{abc}	33.7^{abc}	32.3^{bc}
7	1488	32.3^{d}	33.0^{bc}	29.7^{c}	31.3^{c}	31.6^{cd}
8	1740	29.0^{fg}	28.0^{hi}	25.7^{d}	27.7^{d}	27.6^{fg}
9	633	34.7^{c}	36.3^{a}	32.7^{ab}	35.0^{ab}	34.7^{a}
10	1486	38.0^{a}	29.0^{fgh}	25.7^{d}	27.0^{de}	29.9^{de}
11	2596	37.3^{ab}	30.0^{efg}	29.0^{c}	31.3^{c}	31.9^{cd}
12	SAIA	25.7^{h}	23.0^{k}	20.3^{e}	21.3^{f}	22.6^{h}
13	1506	38.0^{a}	25.3^{j}	25.0^{d}	26.7^{de}	28.8^{ef}
14	1600	28.0^{g}	28.3^{gh}	25.3^{d}	27.0^{de}	27.2^{fg}
15	1589	31.0^{de}	26.3^{ij}	23.0^{de}	24.7^{e}	26.3^{g}
	Mean	32.3	30.4	28.2	30.1	30.2
	P-value	<.0001	<.0001	<.0001	<.0001	<.0001

Means followed by a common superscript letter within a column are not significantly different from each other at $P<0.05$

The harvest index of oat genotypes tested across locations and over years is indicated in Table 10. The result showed that the genotypes responded differently ($P<0.05$) for harvest index at both locations in the 2016 cropping season. Moreover, the harvest index of oat genotypes was varied significantly ($P<0.05$) at Kuyu in the 2015 cropping season. The highest harvest index was recorded in the 2015 cropping season than in 2016. The combined analysis also showed that the tested oat genotypes varied significantly ($P<0.05$) for harvest index. The mean harvest index of oat genotypes in the combined analysis ranged from 12.4 – 22.0 with a mean of 16.1%. The highest harvest index was recorded for oat genotype 2291 followed by 2806, 8251, 79983, and 1488. On the contrary, oat genotypes 1589, 1600, 1506, 1740, and 1493 produced the lowest harvest index while an intermediate harvest index was obtained by the remaining oat genotypes. The harvest index obtained in the current study is lower when compared to the harvest index reported by another study (Fekede, 2004). Variation in genotypes, climate, and soil conditions could be the major reasons for harvest index differences in tested oat genotypes. Varietal differences in harvest index were also reported in maize (Adugna *et al*., 1999), in tef (Seyoum *et al*., 1996), and barley (Seyoum and Zinash, 1995). The general trend in this study indicated that high grain-producing oat genotypes had a higher harvest index than low grain-producing genotypes.

Table 10: Mean harvest index (%) of oat genotypes tested over years and locations

SN	Genotypes	2015		2016		Combined
		Kuyu	Ginchi	Kuyu	Ginchi	
1	2806	24.4^{b}	30.6	2.3^{abc}	20.8^{a}	19.5^{ab}
2	79983	22.8^{b}	30.7	2.1^{bcd}	16.1^{ab}	17.9^{bc}
3	8251	23.7^{b}	33.6	1.4^{cd}	12.9^{bc}	17.9^{bcd}
4	1493	14.7^{de}	27.6	1.5^{cd}	12.8^{bc}	14.2^{defgh}
5	2291	34.8^{a}	29.1	3.5^{a}	20.6^{a}	22.0^{a}
6	1742	19.4^{bcd}	26.6	1.7^{bcd}	16.7^{ab}	16.1^{bcdefgh}
7	1488	22.9^{b}	30.0	0.98^{cd}	16.2^{ab}	17.5^{bcde}
8	1740	13.9^{de}	26.2	1.3^{cd}	15.1^{bc}	14.2^{efgh}
9	633	21.0^{bc}	27.3	2.0^{bcd}	15.9^{ab}	16.6^{bcdef}
10	1486	19.5^{bcd}	30.5	0.98^{cd}	13.9^{bc}	16.2^{bcdefg}
11	2596	23.8^{b}	24.4	2.2^{abcd}	16.2^{ab}	16.6^{bcdef}
12	SAIA	12.9^{e}	27.9	1.8^{bcd}	16.4^{ab}	14.7^{cdefgh}
13	1506	16.7^{cde}	23.6	2.9^{ab}	10.3^{c}	13.4^{fgh}
14	1600	14.0^{de}	20.4	1.1^{cd}	15.6^{abc}	12.8^{gh}
15	1589	14.7^{de}	22.1	0.76^{d}	12.2^{bc}	12.4^{h}
	Mean	19.9	27.4	1.8	15.5	16.1
	P-value	<.0001	0.4830	0.0192	0.0310	<.0001

Means followed by a common superscript letter within a column are not significantly different from each other at $P<0.05$

3.4. Nutritional Characteristic of Oat Genotypes

The mean ash, crude protein (CP), *in-vitro* dry matter digestibility (IVDMD) contents, and CP yield and digestible yield of oat genotypes harvested at the soft dough stage are indicated in Table 11. The result revealed that ash, crude protein yield, and digestible yield varied significantly ($P<0.05$) among oat genotypes. On the other hand, the CP and IVDMD contents didn't vary ($P>0.05$) among the tested oat genotypes. The ash content of oat genotypes ranged from 9.4 – 12.5 with a mean of 10.8%. The amount of ash in forage is an indication of mineral concentrations in the feed. The mineral content is affected by the stage of maturity and the leaf to stem ratio of the forage plant. The plant developmental stage, morphological fractions, climatic conditions, soil characteristics, and fertilization regime are some of the potential factors causing variation in mineral concentration in forage plants (McDowell and Valle, 2000; Jukenvicius and Sabiene, 2007). Among the tested genotypes, genotype 1486 produced the highest CP and IVDMD contents while the lowest was recorded from genotype SAIA. When the plants matured, the proportion of leaves to stems declines, which reduces the CP and IVDMD contents (Mannetje, 1983; Humphreys, 1991). The highest CP yield was recorded for the oat genotype 2291followed by 2596, 2806, 1506, and 1742. On the other hand, oat genotypes 1589, SAIA, 1740, 1488, and 633 gave the lowest CP yield while the remaining genotypes produced an intermediate CP yield. Similarly, oat genotypes that produced the highest CP yield also gave the highest digestible yield. The nutritive value of forages is mainly determined by voluntary intake, crude protein, and structural carbohydrates. Forage intake is influenced by digestible dry matter and CP content and the extent of degradation (Minson, 1990).

Table 11: Mean ash (%), CP (%), IVDMD (%), CP yield (t/ha) and digestible yield (t/ha) of oat genotypes

SN	Genotypes	Ash	CP	IVDMD	CPY	DY
1	2806	10.9^{abcde}	7.9	53.7	0.89^{ab}	6.0^{abc}
2	79983	11.0^{abcde}	7.6	53.6	0.84^{abc}	5.9^{abcd}
3	8251	9.4^{e}	7.3	53.2	0.74^{bc}	5.4^{bcde}
4	1493	9.8^{de}	7.5	53.4	0.75^{bc}	5.3^{bcde}
5	2291	10.7^{abcde}	7.9	54.1	0.98^{a}	6.7^{a}
6	1742	10.8^{abcde}	7.9	53.4	0.87^{ab}	5.9^{abc}
7	1488	10.3^{bcde}	7.5	53.5	0.73^{bc}	5.2^{bcde}
8	1740	10.9^{abcde}	7.7	53.7	0.67^{c}	4.7^{de}
9	633	12.5^{a}	7.6	53.6	0.74^{bc}	5.2^{bcde}
10	1486	11.0^{abcde}	8.1	54.3	0.81^{abc}	5.4^{bcde}
11	2596	9.8^{de}	7.8	53.8	0.90^{ab}	6.3^{ab}
12	SAIA	10.2^{cde}	6.9	52.4	0.65^{c}	5.0^{cde}
13	1506	11.9^{abc}	7.8	53.8	0.88^{ab}	6.0^{abc}
14	1600	11.5^{abcd}	7.8	53.8	0.81^{abc}	5.6^{abcde}
15	1589	12.1^{ab}	7.7	53.7	0.65^{c}	4.6^{e}
	Mean	10.8	7.7	53.6	0.79	5.5
	P-value	0.0455	0.2154	0.2184	0.0333	0.0478

Means followed by a common superscript letter within a column are not significantly different from each other at P<0.05. CP = crude protein; IVDMD = in-vitro dry matter digestibility; CPY = crude protein yield; DY = digestible yield

The mean neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL), cellulose, and hemicellulose contents of oat genotypes harvested at the soft dough stage are indicated in Table 12. The result indicated that except for the ADL content, the fiber contents didn't vary significantly (P>0.05) among the tested oat genotypes. The ADL content of oat genotypes ranged from 9.1 – 11.7 with a mean of 10.5%. The general trend showed that the NDF>ADF> Cellulose > Hemicellulose >ADL content and the trend conform with other studies done on oat varieties (Fekede, 2004). The mean NDF content of oat genotypes in the current study is higher than the mean NDF content (63.5%) reported on oat varieties (Fekede, 2004). Variations on genetic materials, harvesting stage, climatic conditions, and soil factors are the major causes of difference for NDF content in oat genotypes. The NDF content of all the oat genotypes in this study lies within the range (55 to 76%) reported for high-quality roughages (Nsahlai *et al.*, 1996). The ADF content of the oat genotypes in this study falls in the range of 33.30 to 59.40% reported for high-quality roughages (Nsahlai *et al.*, 1996). The comparatively lower ADF content in oats could be indicative of its better digestibility than the other roughages (Fekede, 2004). ADL content value above 60 g/kg DM can negatively affect the digestibility of forage (Van Soest, 1982). Generally, the presence of insoluble fiber, particularly lignin, lowers the overall digestibility of the feed by limiting nutrient availability (Van Soest, 1994; Mustafa *et al*., 2000). The higher cellulose and hemicelluloses contents in the feed limit forage intake and digestibility (Wolf *et al*., 1993; Lundvall *et al*., 1994) and its content in the feed varies among morphological fractions (Seyoum *et al*., 1996; Fekede, 2004) and increased with harvesting stage (Adane, 2003).

Table 12: Mean NDF (%), ADF (%), ADL (%), cellulose (%) and hemicellulose (%) contents of oat genotypes

SN	Genotypes	NDF	ADF	ADL	Cellulose	Hemicellulose
1	2806	73.3	52.0	10.5^{abc}	41.5	21.2
2	79983	72.7	46.5	10.2^{abc}	36.4	26.1
3	8251	70.1	45.4	11.7^{a}	33.8	24.7
4	1493	71.6	45.7	11.5^{a}	34.2	25.9
5	2291	72.7	50.9	11.2^{a}	39.8	21.8
6	1742	73.1	49.1	10.3^{abc}	38.8	24.0
7	1488	71.1	45.8	9.6^{bc}	36.2	25.3
8	1740	74.0	50.7	11.0^{ab}	39.7	23.3
9	633	73.4	48.7	9.4^{c}	39.3	24.6
10	1486	73.0	48.1	10.6^{abc}	37.6	24.9
11	2596	71.3	48.3	11.5^{a}	36.8	23.0
12	SAIA	74.1	49.4	10.2^{abc}	39.2	24.6
13	1506	74.8	48.5	10.5^{abc}	38.0	26.2
14	1600	74.2	50.2	10.3^{abc}	39.9	24.0
15	1589	72.5	47.8	9.1^{c}	38.8	24.7
	Mean	72.8	48.5	10.5	38.0	24.3
	P-value	0.5778	0.4892	0.0361	0.6087	0.4936

Means followed by a common superscript letter within a column are not significantly different from each other at $P<0.05$. NDF = neutral detergent fiber, ADF = acid detergent fiber, ADL = acid detergent lignin

4. Conclusions and Recommendation

Oat genotypes respond differently for agro-morphological performance and nutritive values on vertisol conditions at Kuyu and Ginchi during the main cropping seasons of 2015 and 2016. Plant height, dry matter yield, leaf to stem ratio, straw yield, seed yield, thousand seed weight, harvest index, chemical composition, and in-vitro dry matter digestibility showed variations among the tested oat genotypes on vertisol conditions. The result revealed that genotypes such as 1600, 1740, 2596, 79983, 1493, and 1742gave better forage dry matter yield on vertisol conditions. On the other hand, 2806, 79983, 2291, 8251, and 1742 produced better seed yields. The highest crude protein yield was recorded for oat genotype 2291 followed by 2596, 2806, 1506, and 1742 and oat genotypes that produced the highest crude protein yield also gave the highest digestible yield. Generally, better dry matter yield, crude protein yield, digestible yield, and seed yield performances were recorded from genotypes 2291, 2596, 2806, 1506, 1742, 8251, and 79983. Therefore, these oat genotypes can be recommended for vertisol conditions of the study areas and similar agro-ecologies.

Conflict of Interest

The authors declared that there is no conflict of interest.

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