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Research Article

# Evaluation of genotype by environmental interaction and stability of early maturing fodder oat genotypes in highland of Bale, Oromia, Ethiopia

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**ABSTRACT**

Selection of stable genotypes that interact less with the varying environment in which they are to be grown is required. The major objectives of the present study were to (i) assess the stability and yield performance of advanced Early maturing fodder Oat accessions evaluated in multiple environments, and (ii) identify stable high biomass yielding candidate cultivar(s) for possible release. A total of 19 fodders Oat accessions were evaluated against Dumant-2007 across four locations from 2022 to 2023 main cropping seasons. Randomized complete block designs (RCBD) with three replications were used. The AMMI analysis of variance for forage dry matter yield revealed highly significant ($P<0.05$) differences for days to flowering, days to maturity, plant height, leaf to steam ratio, seed yield, thousand seed weight and dry matter yield. The findings revealed that the highest forage dry matter yield was recorded for genotype 5448 (21.6 t/ha) and genotype 5447(21.5 t/ha) respectively. The higher leaf to steam ratio was recorded from both genotype 5447 and genotype 5448. Numerically the higher seed yield was obtained from 5447 (32.6 qt/ha), whereas the lowest seed yield was produced from genotype 5460 (21.2 qt/ha). The analysis of chemical compositions showed significant ($p<0.05$) differences for CP parameters among tested genotypes. The highest (12.290%) CP content was recorded from genotype 5448 followed by genotype 5447 (11.963%) whereas the lowest (9.41%) CP was recorded from 5449. The analysis of variance for AMMI also revealed significant variation for genotypes, environment and genotypes by environment interaction. The sum of squares for the first two IPCAs cumulatively contributed to 90.2% of the total GEI. Generally the mean performance, yield and stability of genotype 5448 and genotype 5447 were high and stable across the tested locations. Therefore, genotypes genotype 5448 and genotype 5447 were recommended to be promoted to a variety verification trial for further evaluation and possible release.

**Key words:** AMMI Stability, Dry matter, Early Maturity, Quality Parameters

## INTRODUCTION

Ethiopia has a large livestock population and diverse agroecological zones suitable for livestock production and for growing diverse types of food and fodder crops. However, livestock production has mostly been subsistence-oriented and characterized by very low reproductive and production performances due to primarily shortages of quality and quantity of animal feed (Maleda & Mastewal, 2013), due to land degradation, land shortage and poor soil fertility (Tewodros *et al.,* 2007). Due to rapidly increasing human population pressure, cropping is expanding and grazing areas are shrinking (Adugna, 2007). Nowadays Livestock production systems are threatened by population pressure, climate change, recurrent droughts and degradation of natural resources. These pressures are more acute in Bale Zone, where population pressure and grazing land change into arable land are the major problem.

Addressing these issues will lead to improved sustainability, food security and rural livelihoods through cultivated forage crop like fodder oats (*Avena sativa* L.). Oat is an important multi-purpose cereal crops cultivated for grain, feed and straw over more than 9 million hectares globally (McLeod, 2011). Traditionally oats have been cultivated in cropping areas not appropriate for wheat, barley or maize, and it is adapted to a wide range of soil types and can better perform than other small-grain cereals on marginal land (Buerstmayr *et al.,* 2007). It is also the most important winter cereal fodder crop (Lodhi *et al.,* 2009). Due to climate variability, it is paramount to evaluate early and late maturing fodder oat accessions to develop improved fodder oat varieties used when rainfall is in deficit and excess. Therefore, the major objectives of the present study were to assess the stability and yield performance of advanced early maturing fodder oat genotype(s) evaluated in multiple environments, and to identify stable high biomass yield, disease tolerant and high quality candidate cultivar(s) for possible release.

## MATERIALS AND METHODS

The activity was conducted at four locations Sinana, Agarfa, Goba and Adaba with nineteen (19) early maturing fodder oat accessions from RVT with one standard check Dumant 2007 and one local check Bonsa were used as a treatment (Table 1). Fodder Oat genotypes were planted in a randomized complete block design (RCBD) on the plot area of 2 m * 3 m. Seeds were drilled in a row with a spacing of 20 cm with a seeding rate of 80 kg/ha (Dawit & Teklu, 2014). Recommended fertilizer rate of 100 kg/ha NPS and 50 kg/ha urea was used.

## Data collected

Data such as germination emergence, Days to flowering, plant height, days to maturity, seed yield, dry biomass yield, and disease tolerance was taken. Forage quality parameters such as DM, CP, NDF, ADF and ADL were done.

**Table 1:** List of nineteen early matured oat genotypes with their origins for the experiment

| S. No. | Genotype code | Genotype code | Source of Material |
|---|---|---|---|
| 1 | G1 | 5464 | ILRI |
| 2 | G10 | Bareda | ILRI |
| 3 | G11 | 5445 | ILRI |
| 4 | G12 | 5447 | ILRI |
| 5 | G13 | 5449 | ILRI |
| 6 | G14 | 5534 | ILRI |
| 7 | G15 | 5511 | ILRI |
| 8 | G16 | 5520 | ILRI |
| 9 | G17 | 5448 | CIMMT |
| 10 | G18 | 5495 | ILRI |
| 11 | G19 | Dumant #2007 | ILRI |
| 12 | G2 | 5446 | ILRI |
| 13 | G3 | 5451 | ILRI |
| 14 | G4 | 5523 | ILRI |
| 15 | G5 | 5460 | ILRI |
| 16 | G6 | 5504 | ILRI |
| 17 | G7 | 5515 | ILRI |
| 18 | G8 | 5456 | ILRI |
| 19 | G9 | Bonsa | ILRI |

## Statistical data analysis

Data was analyzed by the R 4.3.3 software program mean analysis package and mean separation was carried out using the Least Significant Difference (LSD) test at 5% probability. Analysis of chemical composition was done for ash, crude protein, NDF, ADF and ADL contents. 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). Combined analysis of agronomic parameters for early maturing oat accessions from the four locations and draw AMMI and GGE bi-plots.

Data were analyzed with the model

$$Yijk = \mu + Gi + Ej + (GE)ij + B(k) + eijk$$

Where, Yijk=Measured response of accessions (i) in Block (k), of environment (j), μ=grand mean Gi=effect of the genotype (i), Ej=Effect of the environment (j), GEij=genotype and environment interaction; Bk, (j)=effect of block k in environment j; eijk=random error of genotype i in block k of environment j.

# RESULTS AND DISCUSSIONS

## Agronomic and yield performance of the early mature fodder Oat genotypes in two years and across four location

Analysis of variance of the mean square shows a highly significant plant height ($p<0.01$), days to dough stage ($p<0.01$), leaf to stem ratio ($p<0.01$) dry matter yield ($p<0.01$) and seed yield oat ($p<0.01$) (Table 2). The effect of year also had a significant effect on all parameters. A significant effect was observed on days to dough stage and leaf to stem ratio

**Table 2:** Agronomic and yield performance of the early mature fodder Oat genotypes in two years and across four location

| Location | Days to seed maturity | Days to 50% head | Plant height in (cm) | Leaf to stem ratio | Biomass yield in ton/ha | Seed yield (Quintal $ha^{-1}$) | 1000 seed wt (g) |
|---|---|---|---|---|---|---|---|
| E1 | 138.6 | 95.6 | 133.3 | 0.6 | 23.7 | 34.9 | 31.9 |
| E4 | 142.6 | 97.2 | 152.2 | 0.7 | 14.5 | 25.6 | 30.5 |
| E2 | 142.1 | 96.9 | 169.6 | 0.7 | 21.5 | 28.4 | 24.9 |
| E3 | 141.3 | 96.6 | 163.4 | 0.7 | 15.9 | 24.5 | 30.1 |
| Mean | 141.2 | 96.6 | 154.6 | 0.7 | 18.9 | 26.8 | 24.4 |
| LSD (0.05) | 0.67 | 0.28 | 3.3 | 0.87 | 0.06 | 4.2 | 0.63 |
| CV | 2 | 1.1 | 6.5 | 16.5 | 33.2 | 52.5 | 9.9 |
| Sig. (0.05) | *** | *** | *** | ** | *** | *** | *** |
| Year | | | | | | | |
| 1 | 141.4 | 96.8 | 161.0 | 0.6 | 17.6 | 29.6 | 25.6 |
| 2 | 140.8 | 96.2 | 143.9 | 0.8 | 21.0 | 22.2 | 22.3 |
| Mean | 141.1 | 96.5 | 152.5 | 0.7 | 19.3 | 25.9 | 23.9 |
| CV | 1.5 | 1.2 | 7.5 | 0.03 | 4.5 | 6.5 | 9.9 |
| Sig. (0.05) | * | *** | *** | ** | *** | *** | *** |

E1=Sinana, E2= Goba, E3=Agarfa, E4=Adaba significant highly significant. In line with this finding, Dawit *et al.* (2022) also reported that dry matter was highly significant with year and location at Kofele.

## Agronomic and dry matter yield performances of early maturing fodder oat genotypes

A combined analysis of variance for measured agronomic traits of early maturing fodder oat genotypes tested over environments is presented in Table 3. The genotypes revealed highly significant differences ($p<0.05$). This might be due to the influence of the environment during forage crop physiological growth and development. The shortest number of days heading for seed obtained from genotype 5448 (95 days) and 5447 (95.5) respectively, whereas, the standard check Dumant-2007 variety (97.4 days) took a longer number of days. The observed differences could be related to the differences in number of days taken to flowering. Early flowering results in early physiological maturity for seed harvest. The result was in line with Gemechis *et al.* (2024) reported that the Bonsa variety took 95 to attain 50% flowering days whereas, Dawit *et al.* (2023) reported a high number of days for 50% of flowering (100 to 102.8 days).

The mean of leaf to steam ratio ranged from 0.613 to 0.743. Significantly ($p<0.05$) differ among the tested genotypes. A higher number of leaf to stem ratio was recorded from Genotype-5447 (0.743) and genotype-5448 (0.722) respectively, whereas the lowest leaf to stem ratio was obtained from Dumant-2007 standard check (0.649). Plant leaves play a great role in the growth and development of plants thereby influencing forage biomass yield. This result agrees with (Gebremedhn *et al.,* 2015).

The composite mean dry matter yield of the tested genotypes across different environments ranged from 16.5 to 21.6t/ha. Significantly ($p<0.05$) the highest 21.6 t/ha) dry mater yield was recorded from genotype 5448 followed by genotype 5447 (21.5 t/ha) while the lowest (16.5 t/ha) was recorded from check Dumant-2007. This difference could be due to the genetic potential of the genotypes.

Genotype 5448 showed a 24.1% dry matter yield advantage over the standard checks Dumant-2007, while genotype 5447 showed a yield advantage of 23.7% over the standard check of Dumant-2007. The current result is inconsistent with the previous report of Muleta *et al.* (2022) where Bonsa and CI-2291 varieties produced maximum dry matter yield of 15.4 t/ha and 14.4 t/ha, respectively at the highlands of the study areas.

Disease score was significantly ($p < 0.05$) different among the tested genotypes. A higher number of disease reaction were obtained from genotype 5448 (2, 3) crown rest and leaf rest respectively, whereas the lowest disease reaction was produced from Dumant-2007 standard check (7, 8) crown rest and leaf rest respectively.

**Table 3:** Agronomic performance of the early mature fodder Oat genotypes

| Genotype code | DH | DM | PH | DMY | LSR | Disease score(1-9) | | SY | TSW | BYA |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | CR | LR | | | |
| 5464 G1 | 96.8 | 142 | 147 | 18.4 | 0.647 | 3 | 4 | 26 | 23.5 | 10.9 |
| Bareda | 96.7 | 144 | 162 | 19.4 | 0.65 | 4 | 4 | 24.9 | 21.4 | 15.5 |
| 5445 G11 | 96.9 | 142 | 168 | 19.2 | 0.613 | 6 | 5 | 26.1 | 23.6 | 14.6 |
| 5447 G12 | 95 | 137 | 155 | 21.5 | 0.743 | 3 | 3 | 32.6 | 25.6 | 23.7 |
| 5449 G13 | 96.8 | 141 | 152 | 20.5 | 0.673 | 6 | 6 | 29.4 | 21.1 | 20.0 |
| 5511 G14 | 96.4 | 141 | 158 | 19.2 | 0.679 | 7 | 8 | 27.1 | 22.9 | 14.6 |
| 5520 G15 | 96.5 | 141 | 153 | 19.9 | 0.614 | 3 | 3 | 30 | 26.9 | 17.6 |
| 5534 G16 | 97.2 | 142 | 150 | 18 | 0.658 | 4 | 3 | 31 | 26.6 | 8.9 |
| 5448 G17 | 95.5 | 138 | 152 | 21.6 | 0.722 | 2 | 3 | 22.8 | 25.6 | 24.1 |
| 5495 G18 | 96.4 | 141 | 154 | 18.1 | 0.675 | 3 | 4 | 24 | 26.3 | 9.4 |
| Dumant-2007 | 97 | 143 | 149 | 16.4 | 0.628 | 5 | 6 | 21.3 | 23.9 | 0.0 |
| 5446 G2 | 97.1 | 141 | 146 | 18.8 | 0.631 | 6 | 7 | 25.8 | 23.2 | 12.8 |
| 5451 G3 | 96.6 | 145 | 160 | 18.5 | 0.691 | 3 | 3 | 21.2 | 22.9 | 11.4 |
| 5460 G4 | 96.8 | 142 | 158 | 18.5 | 0.674 | 3 | 3 | 27.1 | 23.9 | 11.4 |
| 5504 G5 | 97 | 140 | 154 | 18.6 | 0.631 | 4 | 3 | 26.3 | 22.7 | 11.8 |
| 5523 G6 | 96.7 | 140 | 156 | 18.1 | 0.671 | 3 | 4 | 30.6 | 23.7 | 9.4 |
| 5515 G7 | 96.3 | 140 | 151 | 18.4 | 0.708 | 4 | 4 | 29.9 | 27.5 | 10.9 |
| 5454 G8 | 96.2 | 140 | 160 | 19.5 | 0.642 | 3 | 2 | 25.4 | 25.6 | 15.9 |
| Bonsa | 97.4 | 143 | 151 | 16.5 | 0.649 | 3 | 4 | 28.4 | 25.9 | 0.6 |
| Mean | 96.6 | 141.2 | 154.5 | 18.9 | 0.7 | 4.3 | 4.3 | 26.8 | 24.4 | 12.7 |
| LSD (0.05) | 0.28 | 0.67 | 3.3 | 0.06 | 0.87 | 1.2 | 0.9 | 4.2 | 0.63 | |
| CV | 1.1 | 1.8 | 8.1 | 25.21 | 17.8 | 1.1 | 1.3 | 6.37 | 9.9 | |
| Sig. 0.05 | *** | *** | no | *** | * | * | ** | *** | *** | |

Sig. codes: 0-no, '***'-0.001, '**'-0.01, '*'-0.05, '.'-0.1, ' '-1, CR=Crown rust, BY=Biomass yield in ton/ha, LR=Leaf rust, DH=Days to 50% head, DM=Days to seed maturity, PH=Plant height in (cm), BYA=Biomass Yield advantage (%), LSR=Leaf to stem ratio, Seed yield (Quintalha-1), TSW=Thousand seed Weight (g), Disease score based on 1-9 scale where 1 is highly resistant and 9 is highly susceptible, Dry matter and seed yield are mean of 4 locations and 2 years

Thousand seed weight (g) was significantly (p<0.05) different among the tested genotypes. A higher thousand seed weight was recorded from genotypes 5448 and 5447 (25.6 g), whereas the lowest thousand seed weight was obtained from Dumant-2007 standard check (23.9 g). The thousand seed weight observed in the present study was lower than that of Gemechis *et al.* (2024) who reported a thousand seed weight of Under mixed, oat Bonsa variety + vetch Gebisa variety recorded the highest thousand seed weight of 66.6 g, while the pure stand Bona-bas variety recorded the lowest thousand seed weight of 37.6 g at Bale high land of Ethiopia. This result was higher because of mixed with legume.

Seed yield did not show significant (p>0.05) differences among the tested genotypes. Numerically the highest seed yield was obtained from 5447 (32.6 qt/ha), whereas the lowest seed yield was produced from genotype 5451 (21.3 qt/ha) quintal. This agrees with Muleta *et al.* (2022) reported that optimum seeds yield of 31.02, 30.14 and 28.58 were recorded for variety CI-2291, CI-2806 and Bonsa, respectively at highland areas of Gechi and Hurumu districts.

## Combined analysis of variance for chemical composition of nineteen early maturing fodder oat genotypes tested in four environments

The chemical composition of the oats samples is presented in Table 4. The Crude protein content average ranges from (11.96%) to (12.290%) for genotypes ILRI#5447 and ILRI#5448 genotypes that have 15.8% and 18.97% yield advantages over the standard check (Dumant-2007) respectively. As regards to fiber quality, the lowest ADF and NDF were displayed by ILRI#5504, Bareda genotypes and (54.8% and 32.1%), respectively and the highest were recorded from ILRI#5523 and ILRI#5534 genotypes (37.6% and 61.2%) in that order.

## AMMI analysis of Biomass yield of early matured fodder Oat Genotypes

The AMMI analysis showed that AMMI 1and AMMI 2 biplots explained 58.2% and 32% AMMI of the biplots respectively (Figure 1 & Table 5). Figure 1 helps visualize the dry matter yield performance and stability of high dry matter yield oat genotypes. Accordingly, the AMMI biplot showed the (ILRI#5448) genotype and (ILRI#5447) genotype was in the first concentric circle, close to the horizontal line, which indicates these genotypes were stable and high yielder among tested genotypes. The important feature of the AMMI biplot is the average environment coordinates (AEC) view of genotypes to identify desirable genotypes in an ideal environment. Genotypes proximal to the arrow at the center of the concentric circle (ideal genotypes) are assumed to the suitable. The important factors AMMI biplot was the best way to visualize the interaction patterns between genotypes and environments.

**Table 4:** Combined analysis of variance for chemical composition of 19 early maturing fodder oat genotypes tested in four environments

| Genotypes | DM | Ash | CP | NDF | ADF | ADL |
|---|---|---|---|---|---|---|
| 5464 G1 | 93.5 | 8.6 | 10.363 | 57.3 | 34.5 | 4.2 |
| Bareda | 93.7 | 8.5 | 9.7567 | 54.8 | 32.2 | 3.6 |
| 5445 G11 | 92.4 | 9.0 | 09.41 | 55.6 | 31.6 | 2.7 |
| 5447 G12 | 93.5 | 8.8 | 11.963 | 58.5 | 33.5 | 4.2 |
| 5449 G13 | 93.7 | 8.1 | 11.260 | 58.2 | 34.5 | 5.6 |
| 5511 G14 | 93.6 | 7.8 | 10.570 | 56.7 | 34.2 | 3.7 |
| 5520 G15 | 93.6 | 8.3 | 9.6567 | 56.4 | 32.6 | 3.7 |
| 5534 G16 | 93.1 | 7.6 | 11.447 | 61.2 | 37.6 | 3.7 |
| 5448 G17 | 92.5 | 7.6 | 12.290 | 57.8 | 34.8 | 3.7 |
| 5495 G18 | 92.7 | 8.4 | 10.743 | 57.2 | 33.4 | 3.2 |
| Dumant-2007 | 92.2 | 7.4 | 10.33 | 56.0 | 33.4 | 3.7 |
| 5446 G2 | 93.4 | 8.8 | 10.997 | 55.4 | 33.2 | 3.3 |
| 5451 G3 | 93.5 | 9.0 | 9.7433 | 57.6 | 33.4 | 3.4 |
| 5460 G4 | 93.7 | 8.7 | 10.463 | 55.6 | 33.2 | 3.6 |
| 5504 G5 | 93.6 | 8.4 | 10.470 | 54.8 | 32.1 | 2.7 |
| 5523 G6 | 93.6 | 8.8 | 10.077 | 55.6 | 37.6 | 4.2 |
| 5515 G7 | 93.1 | 9.1 | 10.950 | 58.5 | 34.8 | 5.6 |
| 5454 G8 | 92.5 | 8.3 | 10.24 | 58.2 | 33.4 | 5.2 |
| Bonsa | 93.2 | 8.4 | 11.440 | 55.4 | 33.4 | 6.0 |
| Means | 93.2 | 8.2 | 10.685 | 57.1 | 33.8 | 3.8 |
| 5% LSD | 5.0 | 3.0 | 5.44 | 1.5 | 6.0 | 0.52 |
| C.V. | 12.0 | 2.5 | 0.4745 | 2.5 | 1.8 | 0.7 |
| Sing | ns | ns | 0.001 | ns | ns | Ns |

ADF=Acid detergent fiber, CP=Crude protein, DM=Dry matter, NDF=Neutral detergent fiber, ADL=Acid detergent lignin

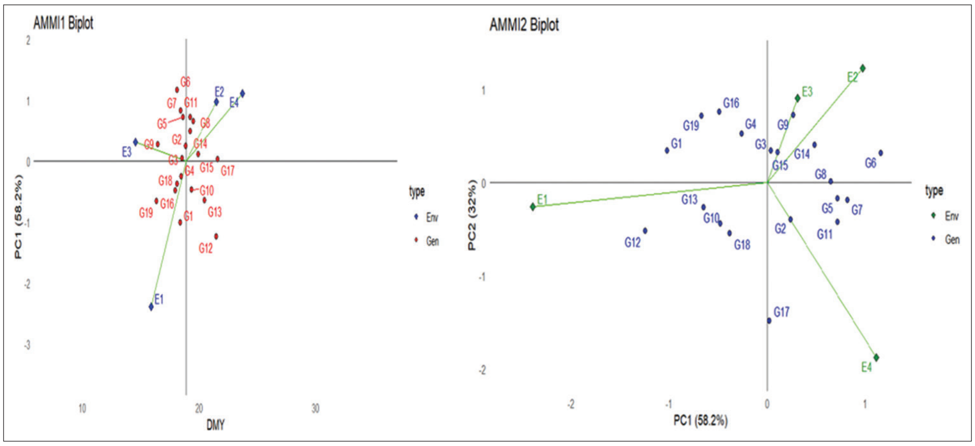


**Figure 1:** AMMI biplot stability

**Table 5:** AMMI analysis of Biomass yield of early matured fodder Oat Genotypes

| Sources of Variation | Df | Sum sq | Mean sq | F value | Pr(>F) | Proportion | Accumulated |
|---|---|---|---|---|---|---|---|
| ENV | 3 | 6600.9 | 2200.31 | 92 | 1.53E-06 | NA | NA |
| REP(ENV) | 8 | 191.3 | 23.92 | 2.23 | 2.50E-02 | NA | NA |
| GEN | 18 | 806.5 | 44.81 | 4.17 | 4.83E-08 | NA | NA |
| GEN:ENV | 54 | 656.8 | 12.16 | 1.13 | 2.54E-01 | NA | NA |
| PC1 | 20 | 191.3 | 9.56 | 0.89 | 6.00E-01 | 58.2 | 58.2 |
| PC2 | 18 | 104.9 | 5.83 | 0.54 | 9.38E-01 | 32 | 90.2 |
| PC3 | 16 | 32.2 | 2.01 | 0.19 | 1.00E+00 | 9.8 | 100 |
| Residuals | 372 | 3996 | 10.74 | NA | NA | NA | NA |
| Total | 509 | 12579.9 | 24.72 | NA | NA | NA | NA |

## CONCLUSIONS AND RECOMMENDATION

The genotype, environment, and their interaction effects (GEI) showed significant differences for measured agro-morphological traits and fodder nutritive values of oat genotypes. Most of the studied genotypes performed inconsistently across environments due to the presence of significant interaction effects. Due to the significant GEI effect, simultaneous consideration of both superior genotypes and stability performance using the first two AMMI-IPCAs is very important for fodder yield improvement in oat genotypes. Genotypes which produced fodder yield above the grand mean were G17, G12, G13, G15 and G9 but most of these genotypes perform inconsistently compared to some genotypes which produced fodder yield below the grand mean. The most stable genotypes based on the first two AMMI biplot analyses were G3, G4, G15, G12, G13, G17 and G9 but some of these genotypes fodder yield G3 and G4 perform below the total mean. Therefore, G17 (ILRI#5448) and G12 (ILRI#5447) which gave the highest mean biomass yield than the rest of the accessions with yield advantage of 24.1% and 23.3% respectively over the standard checks, and showed moderate stability over the testing sites, is identified as candidate genotypes to be verified in the coming cropping season for possible release and could be recommended for commercial production for Southeastern Ethiopia and similar agro-ecologies.

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