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Research Article

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Genotype X environment interaction analysis on dry biomass yield of late maturing fodder oat (*Avena sativa L.*) genotypes in mid and highland areas of West Arsi and Bale, South East Ethiopia

Aliyi Kedu, Gemechis Lencho*, Wubshet Tesfaye, Teklu Wegi

Oromia Agricultural Research Institute, Sinana Agricultural Research Center, P.O.Box. 208, Robe Bale, Ethiopia

ABSTRACT

Eleven genotypes of fodder Oat (*Avena sativa* L.) were evaluated across four locations with one standard checks Bona-bas under rainfall conditions from 2022 to 2023. Both agronomic and chemical composition data were collected. The analysis of the data indicated a statistically significant difference($P<0.05$) between genotypes in the days of 50% heading, plant height, biomass yield, date to seed maturity, thousand kernel weight and seed yield. The overall mean of Biomass yield (15.8 ton ha^{-1}) and Seed yield (29.3 quint ha^{-1}). Quality parameters such as ash, crude protein(CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL) and dry matter content is not significantly different ($P>0.05$) between genotypes. The additive main effects and multiplicative interaction (AMMI) analysis of the dry Biomass yield indicated significant influence by genotype, Environment and year interaction. Among the Eleven genotypes and Bona-bass standard check evaluated in the trial the ILRI #5427 and ILRI #5524 has indicated higher biomass yield and Better stability were selected for variety registration and further promotion.

KEYWORDS: Fodder oat, Genotypes, Biomass yield, Bona-bass, Quality

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***Corresponding Author:**
Gemechis Lencho
E-mail: lenchoabdibor041@gmail.com

INTRODUCTION

Fodder Oat (*Avena sativa*) is one of the most important annual fodder crops for the cool highlands of Ethiopia. Like other cereal crops Oats were well adapted to wide range of soils, are resistant to moisture stress and relatively tolerant to water logging and frost. So far few varieties of Oat were evaluated and recommended for Bale highland areas (Tekl yohannes and worku.1999). In addition fodder Oat varieties Bonsa (Acc. No. 79AB384) and Bona-bas (Acc. No. 1660) were evaluated and nationally released for Bale and west Arsi highland areas (Abate & Teklu, 2011).

However, different varieties of Oat have different yield performance and adaptation to specific situation. Moreover, the performances of some of the earlier released varieties have been declining with time due to problems including leaf and stem rust attack. Therefore, it is an appropriate time to look for other high yield and disease resistant varieties of oat for fodder production in the Bale highlands.

In the past, genotypes were selected only by comparing their average productivity, but nowadays genotype x environment interaction (GEI) and stability are required as a basis for an adequate breeding program to serve as a decision tool in releasing improved varieties and deciding the adaptation domain of such varieties (Yan, 2011).

Analysis of genotypes by environmental data is often limited to evaluation based on genotype main effect (G), while GEIs are disorder factors. A large value of GEI usually has a negative effect on the yield estimate precision and indicates a decreased genotype effect on the value of the phenotypic trait.

Therefore; analysis of yield data through all three sources of variance, namely the genotype main effect, the environment main effect, G x E interaction and prediction of stability is essential to select the genotypes for the next breeding stage. The objective of this study is to identify the stable, disease tolerant

and superior late maturing fodder Oat genotypes for highland areas of west Arsi and Bale.

MATERIALS AND METHODS

Eleven Oats (*Avea sativa* L.) genotypes, including one standard check (Bona-bass) were evaluated. The experiment were conducted under rain feed condition at four location for the two consecutive years (2022-2023) during main cropping season Bona (June to November) at Sinana (SARC on station), Goba (Alloshe village), Agarfa (Agarfa SARC sub-site) and Adaba (Adaba SARC sub-site). The altitude of the places ranges 2400-2700 m.a.s.l. The areas are mainly covered by dark to deep black verity soil type.

Planting Materials

The planting materials used for this study were initially obtained from the international Livestock research Institute (ILRI). Out of 164 fodder Oat accessions obtained from ILRI those genotypes listed in Table 1 selected during pre-Variety trial screening was used for this experiment and the standard check was Bona-bass.

Experimental Land Preparation and Planting

The appropriate sites for the trial were selected in four locations and the lands were well prepared for the experiment. The planting were carried out during the end of June to mid-July in both 2022 and 2024. The planting and weed control were manually done and the experiments were managed under rain feed only.

Experimental Design and Layout

A randomize completed block design with three replications was used at all locations. The plot size of 6 rows; with 2 m length, at 20 cm interspacing with recommended fertilizer rate of 100 kg/ha NPS and 50 kg/ha Urea and seed rate of 80 kg/ha were used.

Data Collection

Days to 50% heading, plant height (cm), Dry biomass (t/ha), leaf to stem ratio, Days to seed maturity, Seed yield and disease score data were major data collected during the execution of the experiment.

Quality data such as CP, ADF, DM, Ash, NDF, were also collected. The oven-dried samples at a temperature of 65 °C for 72 hours were used for laboratory analysis to determine the chemical composition. The dried samples were then grounded to pass a one millimeter (mm) sieve, and the grounded samples were used for other quality parameters quantification. The samples were analyzed on a DM (%) basis for ash, crude protein (CP), neutral detergent fiver (NDF), acid detergent fiber (ADF) and acid detergent lignin (ADL). Total ash content was determined by oven drying the samples at 105 °C overnight and by combusting the samples in a muffle furnace at 550 °C for 6 hours (AOAC, 1990), The Nitrogen content was determined following the micro-kjeldahl digestion, distillation, and titration procedures (AOAC, 1990) and the CP% was estimated by multiplying the N content by 6.25. The plant tissue contents (NDF, ADF and ADL) were determined according to the Van Soest *et al.* (1991) procedure.

Statistical Analysis

Prior to inferential statistics the normality, homogeneity and sorting of the data were done. During data analysis consideration were given to location as random variable and genotypes as fixed variable. The soft were program R 4.3.3 metan analysis package were used for data analysis. The 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 DISCUSSION

Dry Biomass Yield (DMY)

The combined analysis of Biomass yield of late mature fodder Oat genotypes tested over four locations and for 2 years is presented in Table 1. The result of ANOVA showed that genotype, environment and their interaction were significantly ($P<0.05$) influenced the dry biomass yield (Table 2).

The average dry matter yield combined over location and over year (Table 3) were 15.3 t ha^{-1} and the recorded dry matter were higher than that of standard check of the late mature fodder Oat (Bona-bass) which is 14.5 t ha^{-1}. The result were higher than reports by Gadisa *et al.* (2023) as 7.61 t ha^{-1}, Dawit and Teklu (2011) as 10.1 t ha^{-1}, Genotype ILRI #5427 and ILRI #5524 were the highest Dry biomass yielders over all other accessions and they had dry biomass yield of 19.4 t ha^{-1} and 19.8 t ha^{-1}

Table 1: List of twelve oat genotypes with their origins for the experiment

S. No.	Genotypes	Source
1.	5427	ILRI
2.	6207	ILRI
3.	5524	ILRI
4.	5436	ILRI
5.	5538	ILRI
6.	5467	ILRI
7.	5451	ILRI
8.	Bona_Bas	FAO
9.	5429	ILRI
10.	5468	ILRI
11.	6206	ILRI
12.	5519	ILRI

respectively. They had dry matter yield advantage of 25.3% and 26.8% respectively over the standard check. The highest average biomass yield was recorded on Sinana followed by Goba and the less favorable environment was Adaba (Table 4).

Table 2: ANOVA of Dry biomass yield

Sources of variation	DF	Sum	Mean Sq	F Value	Sign.	Pr(>F)
Years	1	199	199	9.957	**	0.001985
Genotypes	11	979	86	4.452	***	1.08E^{-05}
Replication	2	19	9	0.47	ns	0.625978
Location	3	10109	3369	168.577	***	<2e^{-16}
GenxLocation	33	1611	49	2.442	***	0.000188
YearxGen	11	93	8	0.423	ns	0.943496
Gen x Rep x Location	22	326	15	0.742	ns	0.788432
Gen xRep x Location	72	1560	22	1.084	*	0.340692
Residuals	132	2638	20			

ns: non-significant. *p<0.05, **p<0.01, ***p<0.001. Gen: Genotype

AMMI Analysis

Dry biomass yield was investigated by AMMI ANOVA (Table 5). For the for biomass yield trait, we found significant differences between genotypes, locations, interactions and PC1 and PC2 parts. Because the cumulative contribution from PC1 and PC2 justified more than 91.1% of the interaction but IPC2 and the residuals were non-significant, the model of AMMI analysis variance with PC1 and IPC2 seems adequate.

According to the results shown in Table 5, when genotypes are examined in multi-location yield experiments, a cross over GEI most often happens (Ceccarelli, 1995). The cumulative percentage of the GXE interaction that was justified by PC1 and PC2 was 91.1.05%. Also, the contributions of IPC1 and IPC2 were 58.8% and 32.1%, respectively.

Table 3: Agronomic performance of the late maturing fodder oat genotypes

Entry	Days to 50% head	Days to seed maturity	Stand %	Plant height in (cm)	Biomass yield in ton/ha	Leaf to stem ratio	Disease score (1-9) LR, CR		Seed yield (Quintal ha^{-1})	1000 seed wt (g)	BM Yield advantage (%)
							CR	LR			
ILRI #5427	96.5	165.1	97.5	135.5	19.4^{a}	0.7	3.0	4.0	32.4^{abc}	26.8	25.3
ILRI #6207	76.0	136.4	102.9	143.3	14.9^{bc}	0.6	4.0	4.0	22.6^{e}	29.5	2.7
ILRI #5524	96.5	165.1	98.5	147.4	19.8^{a}	0.6	4.0	3.0	24.3^{de}	28.8	26.8
ILRI #5436	76.5	135.3	97.1	149.5	13.7^{c}	0.7	7.0	5.0	28.4^{cd}	30.7	-5.5
ILRI #5538	76.5	135.3	99.0	143.0	14.5^{bc}	0.6	6.0	6.0	33.1^{ab}	32.1	-0.3
ILRI #5467	76.3	135.1	97.5	151.1	15.8^{bc}	0.8	7.0	5.0	34.4^{a}	30.0	8.0
ILRI #5451	76.9	135.7	98.5	146.0	15.0^{bc}	0.7	5.0	6.0	26.9^{de}	26.8	3.6
Bona_Bas	86.3	163.5	98.1	149.6	14.5^{bc}	0.5	7.0	8.0	26.3^{de}	21.3	0.0
ILRI #5429	76.8	135.7	97.9	138.8	14.3^{bc}	0.7	5.0	6.0	32.8^{abc}	32.7	-1.1
ILRI #5468	76.9	135.6	97.9	142.5	15.9^{bc}	0.7	3.0	4.0	35.2^{a}	30.0	8.8
ILRI #6206	76.5	135.1	97.7	138.4	16.5^{b}	0.6	5.0	6.0	28.8^{bcd}	30.0	11.9
ILRI #5519	77.1	135.9	99.2	142.6	15.0^{bc}	0.6	6.0	7.0	26.5^{de}	28.6	3.5
Means	80.7	142.8	98.5	144.0	15.8	0.6	5.3	5.5	29.3	28.9	-
LSD.(5%)	1.9	2.0	2.0	10.0	2.57	0.06	1.2	0.9	4.6	1.9	-
C.V.	4.1	3.0	6.3	12.2	28.6	16.3	1.1	1.3	27.3	11.7	-
Sig.	***	***	.	*	***	.	**	*	***	***	-

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05'.' 0.1' ' 1; BM=Bio-mass, ADF=Acid detergent fiber, CP=Crude protein, CR=Crown rust, DM=Dry matter, LR=Leaf rust, NDF=Neutral detergent fiber. 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

Table 4: Performances of major yield parameters by year and location

Genotypes	Year 2022/23								Year 2023/24							
	Sinana		Goba		Agarfa		Adaba		Sinana		Goba		Agarfa		Adaba	
	DMY	SY/ha	DMY	SY/ha	DMY	SY/ha	DMY	SY/ha	DMY	SY/ha	DMY	SY/ha	DMY	SY/ha	DMY	SY/ha
ILRI #5427	22.3	49.2	23.2	42.4	20.9	17.2	9.8	24.5	26.1	48.4	26.8	42.4	16.1	18.4	9.7	16.4
ILRI #6207	18.5	18.5	16.7	24.2	14.6	22.7	5.8	25.5	23.7	29.7	18.4	24.3	16.1	17.5	5.4	18.3
ILRI #5524	12.0	20.8	24.4	24.9	22.9	26.3	13.0	20.0	16.9	40.9	33.4	24.7	24.5	19.5	11.1	17.3
ILRI #5436	18.2	19.5	16.6	30.9	11.3	21.4	5.2	28.3	20.4	47.0	17.4	31.2	15.8	23.8	5.0	25.3
ILRI #5538	16.7	27.9	17.3	46.8	17.0	28.3	4.1	25.2	19.8	36.0	11.6	46.8	26.2	30.3	2.9	23.7
ILRI #5467	22.5	27.5	17.0	40.2	15.7	26.0	5.4	36.2	22.3	33.0	20.9	45.7	17.6	37.9	4.8	28.8
ILRI #5451	17.9	14.5	17.7	30.7	12.5	16.8	4.2	30.2	22.0	49.1	18.3	30.7	22.9	22.7	4.8	20.5
Bona_Bas	19.6	26.7	15.9	24.5	14.8	14.4	4.6	29.9	23.2	37.4	14.3	24.5	18.9	22.0	4.8	30.7
ILRI #5429	20.8	34.8	19.4	39.9	12.6	28.1	5.4	25.9	16.9	46.0	17.7	39.9	18.9	31.5	3.0	16.3
ILRI #5468	21.5	30.0	20.0	42.5	17.4	41.1	3.6	31.1	17.7	41.3	17.3	35.6	24.2	31.7	5.5	28.3
ILRI #6206	21.7	22.4	22.1	30.7	14.8	23.3	3.4	29.0	22.7	38.7	25.7	30.7	18.1	26.7	3.1	28.7
ILRI #5519	18.0	40.7	18.6	21.7	14.3	16.5	5.0	27.0	21.0	41.3	20.0	22.7	18.2	20.7	5.2	21.5
Means	19.2	27.7	19.1	33.3	15.7	23.5	5.8	27.7	21.1	40.7	20.1	33.3	19.8	25.2	5.5	23.0
LSD.(5%)	2.5	4.0	2.5	4.0	2.5	2.5	2.5	2.5	2.5	4.0	4.0	4.0	2.5	2.5	2.5	4.0
C.V.	28.4	22.2	28.4	22.2	28.4	28.4	28.4	28.4	28.4	22.2	22.2	22.2	28.4	28.4	28.4	22.2
Sig.	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1; DMY=Dry biomass yield in tone ha^{-1}, SY/ha=Seed yield i Quintal ha^{-1}

Table 5: AMMI analysis of the dry biomass yield in tone ha^{-1}

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	Proportion	Accumulated
ENV	3	10108	3369.5	54.61	1.13e^{-05}	NA	NA
REP (ENV)	8	494	61.7	3.30	1.38e^{-03}	NA	NA
GEN	11	978	89.0	4.75	1.40e^{-06}	NA	NA
GEN: ENV	33	1614	48.9	2.61	1.63e^{-05}	NA	NA
PC1	13	475	36.6	1.95	2.59e^{-02}	58.9	58.9
PC2	11	259	23.6	1.26	2.49e^{-01}	32.1	91.1
PC3	9	72	8.0	0.43	9.18e^{-01}	8.9	100.0
Residuals	232	4341	18.7	NA	NA	NA	NA
Total	320	18342	57.3	NA	NA	NA	NA

Location-Environment represented by ENV, Genotype-Genotype represented by GEN

The dry biomass yield of genotypes and environments average was 15.8 ton ha^{-1}. The scatterplot of dry biomass vs. IPC1 (Figure 1) illustrates that the superior genotype had a higher agricultural yield (horizontal axis) and in terms of the first interaction item (IPC1), which is shown on the vertical axis, had a minimum value and was near zero. The vertical line that divides the horizontal axis into two parts is the mean of grain yield and the genotypes that are located on the right side had a higher grain yield than the average. Accordingly the superior genotypes are G3>G1>G11>G10 and G6 and where located on the right side of the graph and close to zero in terms of the IPC1 axis. On the other hand, the horizontal line that divided the vertical axis into parts is the zero line for IPC1. The stable genotypes are near to this line and have a minimum G X E interaction. Not only high dry biomass performance but also the stable genotypes need to be taken into consideration. The second high yielder and the lowest IPC1 on dry biomass among the genotypes belonged to G1. The labile locations were E2>E3>E4 and E1. E3 (Agarfa) is the 3rd productive and location.

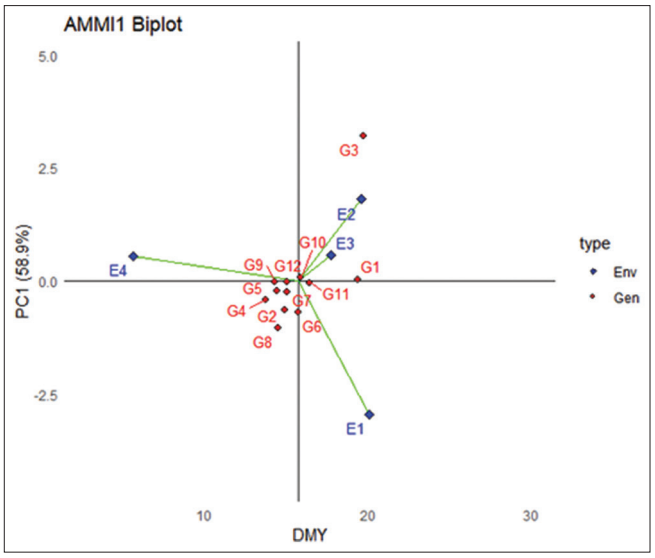

Figure 1: Scatter plot of IPC1 vs. Dry Biomass yield in AMMI analysis

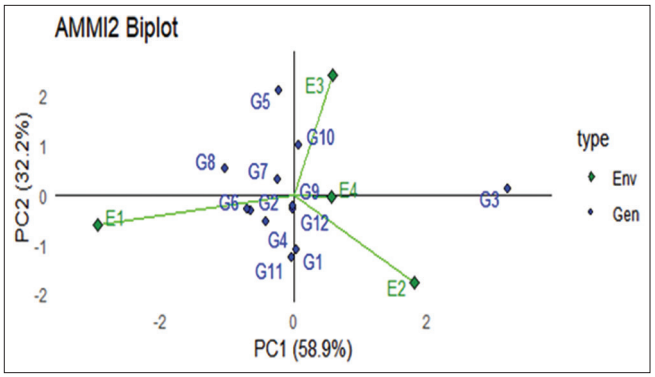

Figure 2: Scatterplot of IPC1 vs. IPC2 in AMMI analysis of grain yield

According to the correlation between IPC1 and IPC2, the genotypes that were positioned near the origin had the least interaction, and the genotypes positioned near to the axis had more general stability. Furthermore, any genotypes that are close to each location have specific stability in that environment (Nikkhah *et al.*, 2007). In terms of the dry biomass yield feature, G9>G12>G2>G7>G4>G1 and G6 showed minimum interplay between genotypes and locations. The genotypes that have more general stability included G1>G9>G3 and G10 (Figure 2).

In this study, G1-ILRI #5427 and G3-ILRI #5524 genotypes, G1-Sinana and G-2Goba environments were located at the right side of the ordinate indicating both these genotypes and environments had superior performance in fodder dry matter yield compared to the remaining genotypes and environments which were located at the left side of the ordinate.

Seed Yield

Likewise the average seed yield recorded for the two elite genotypes were ILRI #5427 (32.4 qt ha^{-1}) and ILRI #5524 (24.3 ha^{-1}) this is significantly higher than the standard check bona-bass 15.5 qt ha^{-1}. The overall mean of the seed yield were lower than reports by Gadisa *et al.* (2023) as 33.46 qt ha^{-1}, Dawit and Mulusew (2014) as 21.7 to 29.8 qt ha^{-1} and Mesgana *et al.* (2020) as 30.45 to 39.04 qt ha^{-1}.

Leaf to Stem Ratio

The average mean value (0.7) on the leafiness of the genotypes over four location in two years were shown significant variation (P<0.05) which falls in the range of 0.5-0.7. This is comparable with reports of Dawit and Teklu (2011) as 0.64-0.78, Sharma *et al.* (2019) as 0.73-0.88 and higher than Befekadu and Yunus (2015). The leaf to stem ratio data also showed a significant difference among the genotypes (P>0.05) and standard check. Genotype ILRI #5427 is more leafy than Bona-bass; has the leaf to stem ratio of 0.7 and 0.5 respectively.

Nutritional Quality

The major parameters considered under quality are ash, crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL) and Organic matter (OM) (Table 6). The result of the analysis of variance indicated

Table 6: ANOVA of the nutritional content of the genotypes

Genotypes	DM	Ash	CP	NDF	ADF	ADL
ILRI #5427	93.5	8.6	8.6	57.3	34.5	4.2
ILRI #6207	93.7	8.5	8.6	54.8	32.2	3.6
ILRI #5524	92.4	9.0	9.1	55.6	31.6	2.7
ILRI #5436	93.5	8.8	9	58.5	33.5	4.2
ILRI #5538	93.7	8.1	8.9	58.2	34.5	5.6
ILRI #5467	93.6	7.8	8.2	56.7	34.2	3.7
ILRI #5451	93.6	8.3	9.5	56.4	32.6	3.7
Bona_Bas	93.1	7.6	8.8	61.2	37.6	3.7
ILRI #5429	92.5	7.6	9.1	57.8	34.8	3.7
ILRI #5468	92.7	8.4	8.7	57.2	33.4	3.2
ILRI #6206	92.2	7.4	8.7	56.0	33.4	3.7
ILRI #5519	93.4	8.8	8.8	55.4	33.2	3.3
Means	93.2	8.2	8.83	57.1	33.8	3.8
5% LSD	5.0	3.0	0.8	1.5	6.0	0.52
C.V.	12.0	2.5	1.2	2.5	1.8	0.7
Sig.	ns	***	ns	*	**	*

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

that there were no statistically significant differences (P>0.05) in all chemical composition parameters among the genotypes. Data on the nutritional quality indicated that ILRI #5427, ILRI #5524 and the standard check bona-bass has CP of 8.6%, 9.1% and 8.8% respectively. The obtained result has shown lower crud protein than that of Dawit and Teklu (2011) as 12.4%, Mosissa *et al.* (2018) as 10-16.6%, and Gadisa *et al.* (2023) as 9.93% and better than Kebede *et al.* (2021) as 7.7%.

CONCLUSION AND RECOMMENDATION

In this study, we analysed 12 late maturing genotypes on four test locations in two years for the Dry biomass and Seed yield trait. All items of the combined ANOVA were significant; the interaction items in AMMI ANOVA were significant, too. The F-test indicated IPC3 as non-significant, and the cumulative percentage of IPC1 and IPC2 justified 91.1% of the G x E interaction, so IPC1 and IPC2 were sufficient for the AMMI ANOVA model. The dry biomass yield average was 15.8 tone ha^{-1}. The superior stable genotypes were G3>G1>G9>G10 >G15>G14and G7. The minimum interaction G x E of genotypes was observed for G4, G1, G13, G8 and G10. G1>G9>G3 and G10 had minimum interplay between genotypes and locations. Therefore, ILRI #5427 and ILRI #5524 can be recommended for further variety registration and further popularization.

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