Evaluation of Lablab (Lablab purpureus L.) genotypes for Fodder production and their Nutritive Values for low lands of Southwest Ethiopia

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Abstract

The study was conducted to evaluate thirteen pre-screened lablab purpureus (L) genotypes out of ninety eight genotypes that introduced from ILRI Addis Ababa, Ethiopia for their potentials on dry matter and forage yield and also chemical compositions and in-vitro dry matter digestibility under lowland conditions of South West Ethiopia. The experiment was performed in three locations for two consecutive years during 2018–2019 and 2020–2021 cropping season. It performed by using completely randomized block design with three replications and analyzed by using SAS software version 9.3. Dry matter yield was significant ($p < 0.001$) whereas, seed yield was not significant ($p > 0.05$) among the genotypes. The second level interaction effect genotype-year-location was not significant ($p > 0.05$) for both dry matter and seed yield. However, the first level genotype-location interaction effect was significant at ($p < 0.001$) for dry matter and ($p < 0.05$) for seed yield. Those show that the genotypes vary in performances across the condition of study location. Genotypes indicated in T6 and T8 were better yield advantage for dry matter and seed yield with 72.1% and 21.1% and also 62.2% and 8.9% over the standard check (Gebisa) respectively. The stability of genotypes was estimated using the mean yield of genotypes (x_i), regressing coefficient (b_i) and regression deviation mean square (s^2d_i). Stability analysis shows that even though the better stable genotypes are 11613 and 10953 genotypes in terms of dry matter yield, 11619 and 14459 were the most stable in terms of seed yield. These suggest that better performed and stabile genotypes need to be further evaluated on live animal performance through feeding trials including other agronomic activities for better production and productivity.

Introduction

The major livestock feed resources in Ethiopia are natural pasture, crop residues, improved pastures, forage crops and agro-industrial by products (Alemayehu, 2004). The utilization of those feed resources, however, depends up on agro-ecology and crops produced. The traditional livestock production systems depends upon pasturelands and crop residues which are usually inadequate and poor in quality to support reasonable livestock production (Habte, 2000).

According to Emana et al. (2017) seasonal variability in feeds availability and quality is the most common constraints that limit livestock productivity in Ethiopia. As a result of this, productivity of livestock lags behind requirements to feed the ever growth human population (Tsegay et al., 2015; Getahun and Tegene, 2018).

Legume forages are widely known for their vital contribution in farming systems. They provide quality feeds to livestock. Maintain soil fertility by minimizing erosion and Supply nitrogen for soil nitrogen fixing microbes and thereby reduces fertilizer (Abubakar et al., 2006). Therefore, introduction, evaluation and screening of legumes; under different environments appealing under Ethiopian conditions.

Among those forage legumes Lablab (*Lablab purpureus* (L) is self-fertilizing crop belong to the family leguminosae (Kshirsagar et al., 2018). It has higher grain yield when compared to that of cowpea with greater adaptation to rang of environment (Adebisi and Bosch, 2004)

Moreover Lablab helps to improve and balance nutritional requirement of livestock when fed together with other roughages dominated by fiber. Studies have shown that when ruminant animals are fed with crop residues and fibrous forage materials like maize stover supplemented with lablab forage, their performances. Its foliage also could be conserved as hay and silage for livestock feed and could also be used as green manuring crop (Kabirizi et al., 2007).

Wide diversity of lablab genotypes exists worldwide. However, those genotypes have not been evaluated under the different agro ecologies of Ethiopia and hence not much information is available for adaptation and performance (Taye et al., 2007).

Therefore, this paper presents results of experiments initiated to evaluate the fodder production potential of different varieties of lablab and their nutritive values for lowland agro-ecologies with specific objectives of generating information on growth characteristics and yield performance as well as nutritive values.

Materials And Methods

Description of the study area

The trial was conducted in three locations (Tepi Agricultural Research Center, Bechi and Kite) of the warm humid conditions of south western Ethiopia for two years (2019/20 to 2021). The description of testing site is presented in Table 1.

Table 1
Description of study areas

Location	Name	Latitude	Longitude	Altitude	Annual rain fall	Annual temperature (^{0}C)	Soil Ph	Soil type
1	Tepi	$7^0$19' N	$35^0$42' E	1200	1559	16.09–30.23	6.3	Clay
2	Bechi	$7^0$22' N	$35^0$53' E	1276	1574	16.5-35.25	5.9	Clay
3	Kite	$6^0$95' N	$35^0$51' E	1200	1200	15.1–27.5	5.1	C.loam

Experimental materials

Ninety eight lablab (*Lablab purpureus*) accessions, obtained from International Livestock Research Institute (ILRI) forage diversity gene bank in Addis Ababa, The accession were evaluated for two years at Tepi Agricultural Research Center (TARC). Genotypes for forage and grain yield performance as well as tolerance to disease. Based on outcome, twelve genotypes were advanced for further evaluation across different environment.

The twelve genotypes (11615, 14459, 6528, 11612, 14417, 11613, 14425, 10953, 14435, 11619, 14445, 11614) were evaluated with one check (variety Gebisa) for two consecutive years in three locations including Tepi, kite and Bechi in Sheka and Bench Sheko Zones of the South West region of Ethiopia.

Experimental Design

The experiment was laid out in a randomized complete block design (RCBD) in three replications. Seeds of twelve genotypes were sown each at a seeding rate of 20 kg/ha (Murphy and Colucci, 1999). Sowing was done in rows spaced at 40 cm between rows and plant spacing 30 cm with in rows. The plot size was 3 m x 2.4 m (Muhammad *et al*., 2017). The spacing between plots and blocks were 1m and 1.5m respectively. The twelve genotypes randomly assigned to the twelve plots in each of the three blocks or replications.

Data collected

At each of the three locations, data was collected on plant height numbers of branch per plant, number of leaves per plant, number of seed per pod, number of pod per plant, days fifty percent flowering, seed harvest, hundred seed weights were recorded using two middle rows from each plot (Pengelly and Maass, 2001). Harvesting for forage parameters were done at 50 percent flowering stage. Plant height was measured from ground to the tip from five plants in the middle rows.

Assessment of disease severity index

Assessment of disease symptom for leaf spot was recorded on 12 randomly pre-tagged plants in plots for each genotype. Descriptive scale developed by Sharma and Kolte (1994) were used for leaf spot scoring. The scoring was done using 0–5 scale every ten days stating from the date of first appearance. Where,

Table 2
Descriptive scale used for disease scoring

Disease score	Description
0	No symptom
1	1–10%
2	11–25%
3	26–50%
4	51–75%
5	> 75%
% = describe the infected plants from the total of pre-tagged plants	

The severity of grades was converted in to percentage severity index (PSI) for analysis (Wheeler, 1969).

$$PSI = \frac{\text{Sum of numerical ratings}}{\text{No. of plants scored X maximum score on scale}} x100$$

Laboratory analysis of quality attributes

The oven dried samples were ground to pass through a 1 mm sieve size and kept for laboratory chemical analysis. The samples were analyzed in % DM basis using a calibrated Near Infra-Red Spectroscopy (NIRS) Foss 5000 apparatus and Win ISI II software. The samples of lablab genotypes were also analyzed using conventional method to calibrate the NIRS apparatus. To do these samples were dried at 60^{o}c for overnight in an oven to standardize the moisture content and three gram of each sample was scanned using the NIRS at 1108–2492 nm, with an 8 nm step. The reference samples dry matter, crude protein and ash content were analyzed using a standard procedure of AOAC (2005). The fiber fractions (neutral detergent fiber, acid detergent fiber and lignin) were analyzed by using the standard procedures (Van Soest and Robertson, 1985). Two-stage technique (Tilley and Terry, 1963) was employed to analyze in vitro dry matter digestibility.

Data analysis

Statistical analysis

The two year data collected from each location was analyzed using general linear model (GLM) procedure of SAS and mean comparison was done using least significance difference test (Burlew, 2014), Version 9.3. Bartlett's test was used for homogeneity of variance analysis to determine the validity. Combined analyses of variance were performed using GLM procedures for those variables which exhibited homogeneity of variances. Different transformation methods were used to transform those data which couldn't exhibit homogeneity of variance for agronomic and nutritional parameters. Data on flowering date, plant height, leaf area, and number of leaf per plant, dry mater yield, fresh forage yield, number of pod per plant, number of branch per plant and number of seed per pod were log transformed. Whereas data on neutral detergent fiber, acid detergent fiber, crud protein yield and neutral detergent fiber yield were square root-transformed. Untransformed data were analyzed according to Gomez and Gomez (1984). Mean separation was carried out using Fisher's Least Significant Difference (LSD) test when the ANOVA showed significant difference among treatments at 5% level of significance. Simple pair-wise correlation and regression analyses were conducted using (SAS 2014) to show the relationship between yield and yield components and nutritional values. Genotypic responses to environmental changes were assessed using a linear regression coefficient (bi) and the variance of the regression deviations (S^2di) (Finlay and Wilkinson, 1963) and Eberhart and Russell (1966). The statistical model for data analysis was:

$$Y_{ijkl} = \mu + T_i + B_{j(kl)} + L_k + Y_l + (T*L)_{ik} + (T*Y)_{il} + (L*Y)_{kl} + (T*L*Y)_{ikl} + E_{ijkl}$$

Where: - Y_{ijkl} = the response variable (the observation in j^{th} block i^{th} treatment and l^{th} interaction effect);

μ = the overall mean;

T_i = the treatment effect;

$B_{j(kl)}$ = the effect of block j in year l and location k; and (gradient);

L_k= the location effect;

Y_l = the year effect;

$(T*L)_{ik}$ = interaction effect of treatment and location;

$(T*Y)_{il}$ = interaction effect of treatment and year;

$(L*Y)_{kl}$ = interaction effect of location and year;

$(T*L*Y)_{ikl}$ = interaction effect of treatment by location and year and

E_{ijkl} = the random error.

Result And Discussion

Combined analysis of variance and mean performance of genotypes across locations over two years

Days to fifty percent flowering and physiological maturity for seed

The results showed that days to 50% flowering were significant ($p < 0.001$) among the genotypes. However, the days to seed to physiological maturity for seed harvest didn't varied among genotypes ($p > 0.05$) (Table 3). This might be due to the influence of the environment during physiological maturity for seed. The shortest number of days physiological maturity for seed taken by genotype 14425 (T7) whereas, geno.14435 (T9) took longer number of days. The observed differences could be related to differences in number of days taken to flowering. Early flowering results in early physiological maturity for grain/ seed harvest. In line with this KC et al. (2016) reported that lablab genotypes took (81–130) in 50% flowering whereas, Kankwatsa (2018) reported shorter number of days to 50% flowering (52 to 69 days).

Plant height and number of branch per plant

Analysis data on plant height and number of branch per plant showed that there were significant variations among the genotypes (Table 3). The tallest and the shortest plant height recorded in the present study were (191.7 cm (T7) and (144.3 cm (T12) respectively with mean value of 179.7 cm. this is considerably higher than the reports of Salah (2015) who found that plant height of lablab varied from 38.0 to 86.3 cm with mean value of 63.81 cm. Contrary to this Shawe (2019) observed 169.0-565.9 cm with mean value of 355.6 cm.

On the other hand, (5.6 (T7) and (4.3 (T12) with mean value of 5.1 (Table 3). Lowest value reported in the present study is higher than what was (1.7) reported by Salah (2015). but it was less than the 11.1 reported by Shawe (2019). The study also showed that the taller the plant height, the more would the number of branch.

Number of pod per plant and seed per pod

The data on number of pod per plant and seed per pod is given in Table 3. The data showed that there were non-significant differences among genotypes for both the number of pod per plant and seed per pod ($p > 0.05$). Maximum and minimum values for the number of pod per plant and seed per pod were 28.5 (T12) and 3.4 (T9), whereas the lowest recorded were 20.7 (T9) and 3.0 (T3 and T12) with mean value of 25.7 and 3.2 respectively. The present study resulted in lower number of seed per pod

compared to results of 3.4–5.3 with mean value of 3.9 reported by Peer (2018) India. On the other hand wide rang number of seeds per pod of 2.1–5.7 reported by (Shawe, 2019).

Dry matter and seed yield and leaf to stem ratio

The dry matter yield and leaf to stem ratios were significantly different among genotypes (Table 3). The highest and lowest dry mater yields recorded were 10.5 t/ha (T6) and 6.1 t/ha (T12 and T13) respectively with mean value of 7.7 t/ha. Two genotypes (T6 and T8) have the highest yield advantage 72.1% and 62.2% over that of the standard check (Gebisa) respectively. The result of the present study is in line with the previous repot of Ogedegbe et al. (2011) where the highest reported dry yield was 10.2 t/ha. Muir (2002) also reported that dry matter yields of legumes in warm-season legumes are largely dependent on rainfall. On the other hand the dry matter yields of lablab observed in the present study was within the range of values (1.8–12.9 DM t ha^{-1}) reported by Mihailovic et al. (2016). However, lower dry mater yields of 6.8 and 6.0 t ha^{-1} were reported for *Lablab purpureus* and *lablab intoritum* respectively in South Omo Zone, SNNP region of Ethiopia (Hidosa et al., 2016). Similarly a forage dry matter yield of 5.4 t ha^{-1} was reported for lablab under sub-humid climatic condition of western Oromia (Tulu et al., 2018).

The heights and lowest leaf to stem ratio recorded were 1.7 by genotype T6 and 1.2 by genotype T12 respectively with mean value of 1.4. Genotypes with higher dry matter yield are likely to have higher photosynthesis that allows having more biomass yield. The results of the present study in range of values (1.4 with a range of 0.76–2.55) reported by Murphy *et al*. (1999).

Seed yield and hundred seed weight

Highly significant differences were observed for hundred seed weight among the genotypes but not that for the seed yields (Table 3). Genotypes that recorded highest seed yield scored more seed yields were also found to be possessing more seed weight of hundred seeds.

The mean seed yield of genotypes in the present study was 942.4 kg/ha with maximum 1080 kg/ha obtained from genotype T6 and the minimum of 777.3 kg/ha was recorded by genotype T1 (Table 3). Indicating a seed yield advantage of 8.9% -21.1% when compared to the check variety (Gebisa). Those yield advantage recorded by genotype T6 and T8, respectively, the range of seed yield recorded in the present study was in line with Adebisi et al (2004) who reported 450–1500 kg/ha seed yield in Netherland.

Genotypes T6 and T12 recorded the maximum (24.2 g) and minimum (21.7 g) respectively hundred seed weight with mean of 22.8 g. The hundred seed weight observed in the present study was comparable with that of Peer et al. (2018) who reported hundred seed weight of 16.1–37.9 g with a mean value of 24.8. However, Shawe (2019) reported higher hundred seeds weight 21.2–50 with mean value of 36 g for some lablab genotypes studied.

Disease severity index

The analysis of variance showed that the Disease Severity Index (DSI) significantly varied among the genotypes (Table 3). During the first cropping season leaf rust was observed among some genotypes. On the other hand relatively more infection was observed in genotype 11614 (4.5%) whereas genotypes 11612 and 14425 (2.1%) were among the least infected with DSI value 3.0%. the finding of the present study revealed less DSI when compared to the reports of Hidosa et al. (2016) who reported DSI of 6.5–13.6 among lablab genotypes.. In other study Kankwatsa (2018) observed existence some resistant lablab genotypes for disease.

Table 3

Agronomic performance and percent of disease severity index of lablab genotypes at Tepi during 2019 and 2021 main cropping seasons

Genotypes	FFD	PH (cm)	L:S	NBPP	DSH	NPPP	NSPP	DMY (t/ha)	HSW(g)	SY(kg/ha)	DSI (%)
11615	112.4^{abc}	181.4^{ab}	1.4^{cd}	5.1^{abc}	155.9	24.8	3.1	7.3^{bc}	23.1^{abc}	777.3	2.4^{cd}
14459	112.7^{abc}	185.2^{ab}	1.4^{cd}	4.9^{abcd}	158	25.7	3.2	7.8^{b}	22.9^{abc}	1062	2.8^{c}
6528	112.3^{abcd}	197.0^{a}	1.3^{de}	5.5^{ab}	156.3	26	3	7.8^{b}	23.1^{abc}	780.4	2.2^{d}
11612	103.2^{de}	174.3^{ab}	1.3^{d}	4.9^{bcd}	154.8	23.6	3.3	7.8^{b}	21.9^{bc}	972.7	2.1^{d}
14417	104.2^{cde}	183.3^{ab}	1.5^{bc}	4.7^{cd}	155.9	27.3	3.2	7.4^{bc}	23.1^{abc}	919.4	2.8^{b}
11613	109.2^{bcde}	183.0^{ab}	1.7^{a}	5.7^{a}	158.3	25.3	3.2	10.5^{a}	24.2^{a}	1080	2.2^{d}
14425	102.9^{e}	191.7^{a}	1.3^{de}	5.6^{a}	150.6	26.7	3.4	7.4^{bc}	22.1^{bc}	1013	2.1^{d}
10953	111.6^{abcde}	189.2^{a}	1.6^{b}	5.3^{abc}	160.7	26.9	3.2	9.9^{a}	24.1^{a}	970.5	2.4^{cd}
14435	119.3^{a}	183.0^{ab}	1.3^{de}	5.2^{abc}	167.3	20.7	3.1	6.0^{c}	21.5^{c}	933.1	2.2^{d}
11619	112.9^{abc}	178.8^{ab}	1.3^{d}	5.0^{abcd}	157.8	26.9	3.2	7.8^{b}	21.9^{bc}	1075.9	4.1^{ab}
14445	118.8^{a}	183.0^{ab}	1.4^{cd}	5.2^{abc}	164.3	25.6	3.2	7.7^{b}	23.6^{ab}	938.8	4.0^{ab}
11614	103.2^{de}	144.3^{c}	1.2^{e}	4.3^{d}	154.7	28.5	3	6.1^{c}	21.7^{c}	836.7	4.5^{a}
Gebisa	115.6^{ab}	162.4^{bc}	1.2^{de}	5.2^{abc}	158.3	26.5	3.1	6.1^{c}	23.6^{ab}	891.5	3.7^{b}
Mean	**110.6**	**179.7**	**1.4**	**5.1**	**157.9**	**25.7**	**3.2**	**7.7**	**22.8**	**942.4**	**3.01**
LSD	**9.1**	**23.2**	**0.2**	**0.73**	**16.9**	**6.9**	**0.34**	**1.38**	**1.8**	**367.1**	**0.46**
CV	**12.5**	**19.6**	**16.7**	**21.7**	**16.3**	**28.2**	**16.2**	**27.4**	**12.3**	**29.2**	**16.3**
P-value	***	**	***	*	NS	NS	NS	***	*	NS	***

Means followed by different letters within a column are significantly different ($P \leq 0.05$). *, **, *** and NS significant at 5%, 1% and 0.1% and non-significant respectively. FFD = days to fifty percent flowering, PH = plant height (cm), L: S = leaf to stem ration, NBPP = number of branch per plant, DSH = Days to seed harvest, NPPP = number of pod per plant, NSPP = number of seed per pod, DMY = dry matter yield (t/ha), HSW = hundred seed weight (g), SY = seed yield (kg/ha) and DSI = disease severity index (%).

Dry matter and seed yield across the study locations

The results of data analyzed for dry matter and seed yields are presented in Table 4). The dry matter and seed yield of genotypes varied significantly among the three locations ($p < 0.01$). The mean dry matter yield of the 13 genotypes varied from 10.2 t/ha recorded at Tepi in the first year of production to 2.6 t/ha recorded at Kite in the first year of harvest. The observed seed yield also varied from 1696.6 kg/ha recorded at Bechi in the second production year to 550.7 kg/ha noted at Bechi in the first year (Table 4).

Table 4
Mean maximum and minimum yields of dry matter and seed yields in the test locations

Location	Cropping season	Location	Dry matter yield (t/ha)			Seed yield (kg/ha)		
			Mean**	Maxi	Mini	Mean**	Maxi	Mini
L1	2018–2019	Tepi	10.2[a]	14.2	6.1	684.1[b]	1027.9	374.7
L2	2020–2021	Tepi	9.8[a]	13.1	6.3	1104.8[a]	1406.3	690.7
L3	2018–2019	Bechi	8.7[b]	12.6	4.7	550.7[c]	786.1	382.9
L4	2020–2021	Bechi	8.5[b]	11.7	6.0	1696.6[a]	2531.9	678.8
L5	2018–2019	Kite	2.6[d]	4.0	1.2	634.9[b]	967.1	417.2
L6	2020–2021	Kite	6.4[c]	8.7	5.2	983.3[b]	1274.3	479.6

Means followed by different letters within a column are significantly different ($P \leq 0.05$). ** Significant ($p < 0.01$).

Dry matter and seed yields

As the results presented in Table 5 indicated dry matter yield was significantly affected by year, location, genotype and the interaction effect of location and genotypes. At Tepi (Table 5) between the two years, significantly more forage dry matter was produced in 2019 compared to year 2020 for genotypes at Tepi and similarly at Bechi significantly more seed yields observed in 2020 over that of year 2019 (Table 5).

On the other hand, among the interaction effects of location x genotypes (Table 7), significantly more forage dry matter of 14.2 t/ha was produced by genotype 11613 at Tepi location, whereas significantly less forage dry matter of 1.2 t/ha was obtained from genotype 11614 at location Kite (Table 5).

Table 5
Dry matter yield across location and year of lablab genotypes during 2019/18 to 2021/20 cropping season

Genotypes	Dry matter yield (t/ha)								
	Tepi			Bechi			Kite		
	Year 1	Year 2	Combined	Year 1	Year 2	Combined	Year 1	Year 2	Combined
11615	10.1^{bc}	9.0^{bcd}	9.5^{c}	8.2^{bcde}	8.3^{bcd}	8.3^{cde}	2.1^{ef}	5.9^{cde}	3.9
14459	9.5^{bcd}	9.1^{bcd}	9.3^{cd}	10.5^{ab}	8.7^{bcd}	9.6^{bcd}	2.3^{def}	6.9^{bcd}	4.6
6528	11.2^{ab}	8.3^{bcd}	9.7^{c}	10.7^{ab}	9.7^{abc}	10.2^{abc}	1.6^{gf}	5.2^{e}	3.4
11612	10.8^{ab}	10.7^{ab}	10.8^{bc}	8.4^{bcd}	7.7^{cd}	8.1^{de}	3.2^{bcd}	6.3^{cde}	4.6
14417	10.7^{ab}	10.0^{abc}	10.4^{c}	7.4^{bcde}	7.7^{cd}	7.5^{def}	2.3^{def}	6.3^{cde}	4.3
11613	14.2^{a}	13.1^{a}	13.7^{a}	12.6^{a}	11.0^{ab}	11.8^{a}	4.0^{a}	8.2^{ab}	6.1
14425	9.9^{bc}	9.3^{bcd}	9.6^{c}	9.5^{abc}	8.7^{bcd}	9.1^{bcde}	1.7^{gf}	5.3^{e}	3.5
10953	12.8^{ab}	12.7^{a}	12.8^{ab}	10.1^{abc}	11.7^{a}	10.9^{ab}	3.2^{abc}	8.7^{a}	5.9
14435	7.1^{cd}	7.3^{cd}	7.2^{de}	5.7^{de}	6.0^{d}	5.9^{fg}	3.6^{ab}	6.6^{cde}	5.1
11619	9.6^{bcd}	6.2^{bcd}	9.4^{c}	9.3^{abcd}	9.0^{abc}	9.1^{bcde}	2.7^{cde}	7.0^{bc}	4.9
14445	10.8^{ab}	10.0^{abc}	10.4^{c}	8.7^{bcd}	8.0^{cd}	8.4^{cde}	3.4^{abc}	6.4^{de}	4.9
11614	9.8^{bc}	9.3^{bcd}	9.6^{c}	4.7^{e}	6.0^{d}	5.4^{g}	1.2^{g}	5.2^{e}	3.2
Gebisa	6.1^{d}	6.3^{d}	6.2^{e}	6.8^{cde}	7.5^{cd}	7.2^{def}	3.3^{abc}	6.5^{cde}	4.9
Mean	**10.2**	**9.6**	**9.9**	**8.7**	**8.5**	**8.6**	**2.6**	**6.4**	**4.5**
LSD	**3.5**	**3.3**	**2.2**	**3.7**	**2.8**	**2.1**	**0.8**	**1.5**	**2.6**
CV (%)	**20.6**	**20.3**	**18.9**	**25.4**	**19.8**	**21.1**	**17.5**	**14.1**	**28.6**
P-value	**	**	***	**	**	***	***	**	NS

Means followed by different letters within a column are significantly different ($P \leq 0.05$). **, *** and NS significant at 1% and 0.1% and non-significant respectively.

Table 6
Seed yield across location and year of lablab genotypes during 2019/18 to 2020/21 cropping season

Genotypes	Seed yield (kg/ha)								
	Tepi			Bechi			Kite		
	Year 1	Year 2	combined	Year 1	Year 2	combined	Year 1	Year 2	combined
11615	509.7^{de}	859.1	684.4	501.4^{cde}	1647.2^{bcd}	1074.3	557.4^{cd}	589	573.2
14459	526.3^{d}	1409.7	966.1	619.5^{bc}	2002.5^{abc}	1311	562.2^{cd}	1255.8	909
6528	536^{d}	1051.3	793.7	560.4^{cd}	1332.8^{cde}	946.6	417.2^{d}	874.6	600.9
11612	688.3^{c}	1258.2	973.3	509.7^{cde}	1677.9^{bcd}	10.93.8	583.9^{cd}	1118.2	875.2
14417	843.1^{b}	772.2	807.6	494.4^{cde}	1710.3^{bcd}	1102.4	967.3^{a}	728.8	848.1
11613	1026.9^{a}	1322.3	1174.6	786.1^{a}	1512.5^{cd}	1149.3	801.8^{ab}	1030.3	916.1
14425	452.8d^{e}	1487.2	970	526.4^{cde}	1800.7^{abcd}	1163.5	623.9^{bc}	1187.2	905.6
10953	1027.9^{a}	763	895.5	747.2^{ab}	1617.5^{bcd}	1182.6	793.2^{ab}	873.4	833.3
14435	374.7^{e}	776.3	575.5	489.6^{cde}	2413.9^{ab}	1451.7	637.8^{bc}	906.2	772
11619	775.7^{bc}	1077.6	926.7	543.1^{cd}	2531.9^{a}	1537.5	542.8^{cd}	984.3	763
14445	871.5^{b}	851.7	861.6	534.7^{cde}	2013.6^{abc}	1274.2	552.6^{cd}	808.3	680.5
11614	798.6^{bc}	1409.7	1104.1	382.9^{e}	6778.8^{e}	531	421.5^{d}	1329	875.2
Gebisa	461.3^{de}	1328	894.6	463.9^{de}	1116.1^{de}	790	792.8^{ab}	1187.2	990
Mean	**684.1**	**1104.8**	**894.4**	**550.7**	**1696.6**	**1123.7**	**634.9**	**983.3**	**809**
LSD	**151.6**	**827.6**	**557.6**	**153**	**817.9**	**873.4**	**195.2**	**685.4**	**454.5**
CV	**13.2**	**24.5**	**29**	**16.5**	**28.6**	**28.7**	**18.2**	**27.1**	**28**
P-value	***	**NS**	**NS**	***	**	**NS**	***	**NS**	**NS**

Means followed by different letters within a column are significantly different (P ≤ 0.05). **, *** and NS significant at 1% and 0.1% and non-significant respectively.

Genotype and environment interaction effect on dry matter and seed yield

The results from variance analysis for dry matter and seed yield are shown in Table 7. For dry matter yield year, location, year-location interaction, genotype, and genotype-location interaction were highly significant ($p < 0.001$) however, the year-genotype interaction and year-location-genotype interaction were not significant ($p > 0.05$). On the other hand, year, location and year-location interaction were significant ($p < 0.001$) and also year-genotype and location-genotype were significant ($p < 0.05$) but genotype and location-genotype-year interaction were not significant ($p > 0.05$) for seed yield (Table 7). For dry matter and seed yield, the second order interactions (location*genotype*year) was not significant ($p > 0.05$). This indicates that each location in each year could be treated as combined environment for both traits.

Table 7
Analysis of variances for dry matter and seed yields of lablab genotypes

Source of variation	Dry matter yield				Seed yield		
	Df	SS	MS	F-Value	SS	MS	F-Value
Year (Y)	1	63.336	63.336	23.08***	238	2383	166.9***
Location (L)	2	1245.592	622.796	226.95***	4127	2063	14.5***
Y*L	2	219.912	109.956	40.07***	7587	3793	26.6***
Replication	2	38.695	6.449	2.35*	1831	9156	6.4**
Genotype (G)	12	382.837	31.903	11.63***	2261	1884	1.3ns
Y*G	12	16.153	1.346	0.49ns	3247	2397	1.9*
L*G	24	197.021	8.209	2.99***	5754	2397	1.7*
L*G*Y	24	19.397	0.809	0.29ns	5344	2226	1.6ns
Error	154	411.634	2.744		2198	1427	
Total	233	2594.58			7597		

***, **, * and ns Significant at p (0.001, 0.01, 0.05) and non-significant respectively.

Dry matter and seed yield stability

An analysis of variance revealed that genotype environment interactions were highly statistically significant ($p < 0.001$) for dry matter yield (Table 4) and regression coefficient ranged from 0.02 to 1.6 for dry matter yield (Table 7). This large variation in regression coefficients reflects the difference response of difference genotype to environmental changes. With respect to dry matter yield genotypes like 6528 and 11612 showed poor and average adaptability to all environment respectively ($b_i>1$ and $x_i>x$). The genotypes that obtained the highest dry matter yield were 11615, 14459 and 11619. Due to their small bi values, they were having better adaptability to unfavorable environmental condition ($b_i<1$ and $x_i>x$). These genotypes were relatively averagely adapted to unfavorable environmental condition and insensitive to environmental changes. Genotypes 11613 and 10953 were better adaptable to all environments and better adaptable to unfavorable environment respectively with ($b_i=1$ and $x_i>x$). Therefore, the cultivation of such genotypes under a given environments can be recommended with respect to their dry matter yield.

The genotype represents relatively adaptable to all environment in average value of seed yield and ($b_i= 0.8$ and $x_i>x$) was 10953 while 11613 was better yielder for all environmental conditions with ($b_i= 1$ and $x_i>x$). Even though, according to Eberhart and Russel (1966) the larger values of deviation from regression mean square, genotypes have lower in stability so that seed yield would not stable across the study locations in the present study relative to the dry matter yield obtained (Table 7, Fig. 1 and Fig. 2).

Table 7
Stability parameters of lablab purpureus genotypes for dry matter and seed yield

Genotypes	Dry matter yield					Seed yield				
	X_i (t/ha)	b_i	S^2d_i	A	R^2	Xi (kg/ha)	b_i	S^2d_i	a	R^2
11615	7.3	0.4	23.2	-1.6	0.52	777.3	-0.83	8.1	987.5	0.48
14459	7.8	0.08	52	-3.2	0.65	1062	0.23	3.2	782.8	0.51
6528	8.2	1.3	3.4	0.8	0.58	780.4	-0.68	1.8	908.7	0.51
11612	7.8	1.2	4.6	3.1	0.81	972.7	-0.43	1.6	879.3	55.2
14417	7.4	0.02	26.1	2.4	0.59	919.4	1.65	1.2	912.5	0.5
11613	10.5	1	66.9	3.8	0.81	1080	0.95	2.2	948	0.63
14425	7.4	0.04	32.3	2.1	0.55	1013	0.32	2.3	882	0.49
10953	9.9	0.8	11.4	5.7	0.71	970.5	0.91	1.4	926	0.61
14435	6	0.5	3.3	3.1	0.51	933.1	0.43	1.6	932	0.49
11619	7.8	0.25	4.6	3.2	0.75	1075.9	0.12	1.1	903.5	0.53
14445	7.7	1.6	5.2	1.5	0.61	938.8	0.06	1.01	906.6	0.52
11614	6	1.26	37	-1.2	0.52	836.7	0.15	1.3	911.6	0.62
Gebisa	6.1	0.09	25.2	1.3	0.49	891.5	-0.7	2.5	913.2	0.52
Average	7.7	0.6				942.4	0.17			

X_i= yield mean, b_i= regression coefficient, s^2d_i = regression deviation mean square, a = regression line intercept, R^2 = coefficient of determination

Chemical composition and In-vitro dry matter digestibility

The combined analysis of variances showed that crud protein (CP), crud protein yield (CPY), neutral detergent fiber (NDF) and neutral detergent fiber yield (NDFY) have significant ($p < 0.01$) however, IVDMD was significant ($p < 0.001$) among the lablab genotypes (Table 8).

The highest and lowest CP content recorded 25.9 for T5 and 21.3 for T9 with 23.4 mean values whereas CPY scored maximum of 2.2 for T6 and minimum 1.9 for T9 with 1.7 mean values. Hector and Jody (2002) reported higher CP content of lablab forage with in a range of 15–30%. On the other hand lower range value of 14.8 to 21.0% was reported by Murphy and Colucci (1999). In general, the crude protein values observed in this study could satisfactorily supply the crude protein acquirement of ruminant animals. Therefore, lablab has high CP value which can supplement low quality roughages which couldn't attain CP requirement of ruminant livestock like natural pasture, rehodes grass, Teff straw, Maize Stover and Finger millet straw with very low CP value of 5.5, 7.1, 4.2, 2.84 and 4.1 respectively (Abebe et al., 2015) and Bracheria (6.70) (Wassie *et al.*, 2018) and also desho grass (8.4) (Asmare et al., 2017).

The IVDMD recorded 62.4 (T4) and 58.6 (T9) as maximum and minimum values with mean of 61.7% in dry matter bases (Table 8). The result of IVDMD obtained in the current study was above the previous report for that of lablab foliage about 55% digestibility (Hector and Jody, 2002).

Table 8
Chemical composition, in-vitro dry matter digestibility and crude protein in DM% bases of lablab genotypes during 2019 cropping season at Tepi, Bechi and Kite testing sites

Genotype	DM	CP	CPY	NDF	ADL	IVDMD	ADF	Ash
11615	91.7^{a}	23.5^{bc}	1.7^{bcd}	48.3^{ab}	6.9^{ab}	61.5^{ab}	34.5	14.4^{abc}
14459	91.7^{a}	23.2^{bc}	2.0^{ab}	47.7^{ab}	6.5^{bcd}	62.2^{ab}	33.1	14.3^{abc}
6528	91.7^{a}	23.4^{bc}	1.8^{abc}	48.7^{a}	6.9^{abc}	61.6^{ab}	34.9	14.5^{abc}
11612	91.6^{a}	24.1^{ab}	1.8^{abc}	46.6^{abc}	6.8^{abc}	61.8^{ab}	34.6	14.2^{bc}
14417	91.8^{a}	25.9^{a}	1.7^{bcd}	44.5^{c}	6.5^{bcd}	62.4^{a}	32.5	14.3^{abc}
11613	91.1^{b}	23.6^{bc}	2.2^{a}	47.6^{ab}	6.3^{cd}	62.1^{ab}	33	15.7^{a}
14425	91.7^{a}	23.8^{b}	1.7^{bc}	45.6^{c}	6.4^{bcd}	62.1^{ab}	32.5	15.0^{ab}
10953	91.9^{a}	23.5^{bc}	2.1^{ab}	47.9^{ab}	7.0^{ab}	61.7^{ab}	34.1	14.9^{abc}
14435	91.7^{a}	21.3^{d}	1.2^{e}	49.3^{a}	7.3^{a}	58.6^{c}	36	14.8^{abc}
11619	91.7^{a}	23.2^{bc}	2.0^{abc}	49.0^{a}	6.9^{ab}	61.8^{ab}	34.9	14.1^{bcd}
14445	91.1^{b}	23.5^{bc}	1.8^{abc}	49.2^{a}	6.8^{abc}	61.6^{ab}	33	12.7^{d}
11614	91.7^{a}	24.1^{ab}	1.6^{cde}	47.3^{abc}	6.0^{d}	62.1^{ab}	34.3	14.7^{abc}
Gebisa	91.6^{a}	22.1^{cd}	1.3^{de}	49.3^{a}	6.7^{abc}	60.9^{b}	35.7	13.5^{cd}
Mean	**91.6**	**23.4**	**1.7**	**47.8**	**6.7**	**61.7**	**34.1**	**14.4**
LSD	**0.3**	**1.6**	**0.8**	**4.7**	**0.7**	**1.4**	**3.8**	**1.5**
CV (%)	**12.5**	**7.1**	**13.6**	**7.2**	**6.2**	**2.4**	**8.5**	**6.2**
P-value	**	**	**	**	*	***	NS	**

Means followed by different letters within a column are significantly different (P ≤ 0.05). ***, **, *, and NS are significant at p 0.001, 0.01, 0.05 and non-significant respectively. DM = dry matter, CP = crud protein, CPY = crud protein yield, NDF = neutral detergent fiber, ADL = acid detergent lignin, IVDMD = in-vitro dry matter digestibility and ADF = acid detergent fiber.

Crud protein and in-vitro dry matter digestibility across location

The variation across location for CP and IVDMD across three location in the first cropping season were significant ($p < 0.01$) and ($p < 0.001$) respectively (Table 9). The highest CP and IVDMD content were showed in location 1 with maximum of 25.2 and 64.6 and minimum of 22.1 and 60.1% in dry matter bases respectively. Previous reports summarized, chemical composition of forages varies due to differences in temperature, precipitation and soil characteristics (Daniel, 1996).

Table 9
Mean, maximum and minimum value of crude protein and in-vitro dry matter digestibility of lablab genotypes during 2019 cropping season at Tepi, Bechi and Kite testing sites

Location	Cropping season	Location	Crude protein content (%)			IVDMD (%)		
			Mean**	Maxi	Mini	Mean***	Maxi	Mini
L1	2018–2019	Tepi	24.0[a]	25.2	22.1	63.1[a]	64.6	60.1
L2	2018–2019	Bechi	23.6[a]	24.5	21.6	60.8[b]	63.2	59.2
L3	2018–2019	Kite	23.4[b]	23.4	21.1	60.8[b]	62.6	58.4

Means followed by different letters within a column are significantly different ($P \leq 0.05$). ** and *** significant ($p < 0.01$) and ($p < 0.001$) respectively.

Conclusion And Recommendations

The two genotypes like 11613 and 10953 were recorded higher as 10.5 t/ha and 9.9 t/ha dry matter yield and obtained seed yield 1080 kg/ha and 970.5 kg/ha respectively. Those genotypes were also have higher yield advantage up to 72.1% and 62.2% for genotype 11613 and 10953 for dry matter yield and 21.1% and 8.9% for seed yield over the standard check (Gebisa) respectively. While the CP yield advantage of thus genotypes are 6.8% and 6.3% respectively.

The stable genotypes were identified by using mean yield, regression coefficient and regression deviation from mean square. Thus indicated genotypes were relatively stable across the study location. These undermined to evaluate the nutritional effect of the selected lablab genotypes on live animal feeding trials. Thus genotypes also need to be evaluating intercropping with cereals and grass and also plant spacing were need to identifying to attain better production and productivities.

Declarations

Data Availability

The datasets used during the current study are available from the author on reasonable request.

Conflicts of Interest

The authors declared there is no conflict of interests.

Contribution of the authors

The first three writers each contributed equally by gathering data, entering it, analyzing it, and producing the paper. The final draft was being revised and commented on by the last two of them, who ensured that it had the most accurate information possible.

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Figures

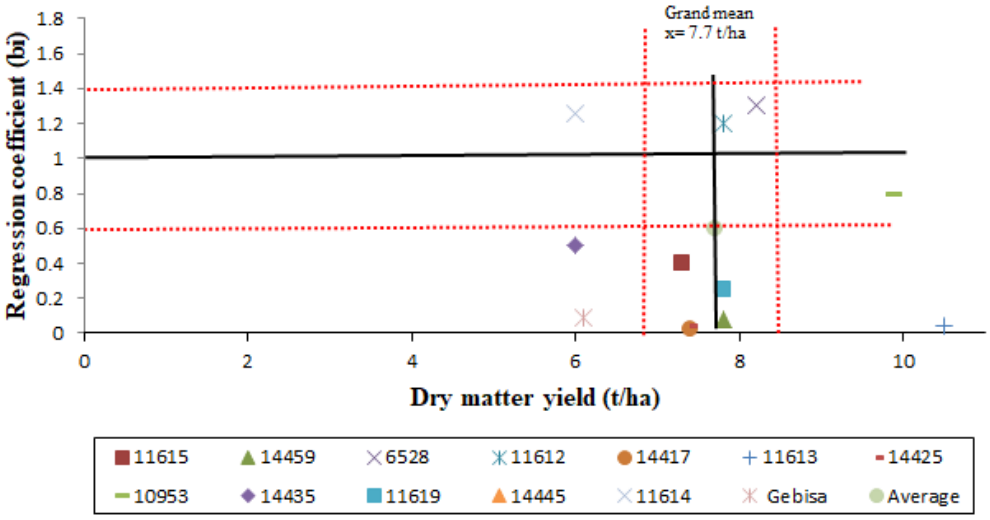

Figure 1

The relationship between the regression coefficient and mean dry matter yield (t/ha) for lablab purpureus genotypes

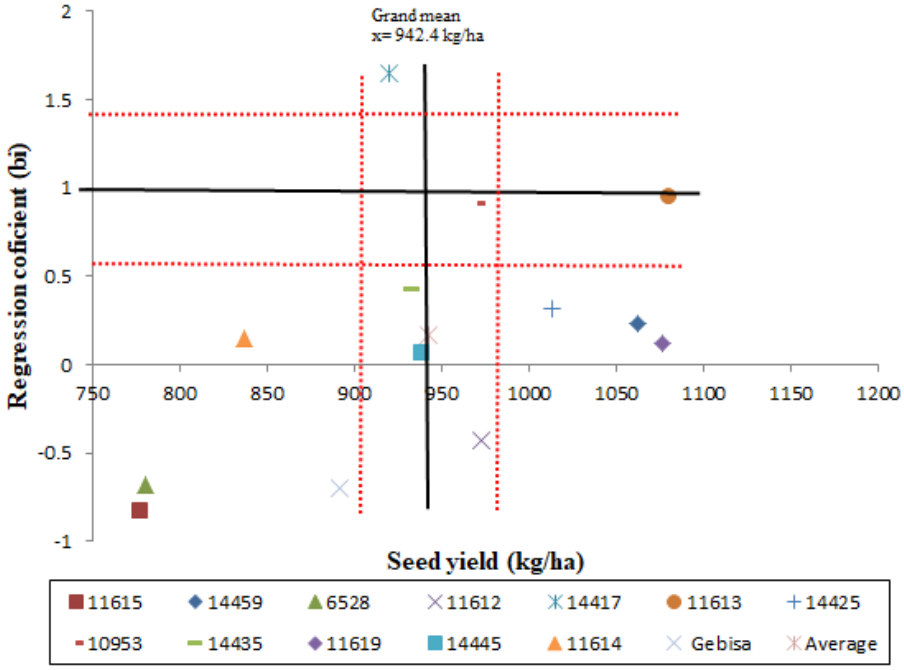

Figure 2

The relationship between the regression coefficient and mean seed yield (kg/ha) for lablab genotypes