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Variability and Correlation-coefficient Analysis for Some Proximate Components of *Lablab purpureus* (L.) Sweet Genotypes of Assam

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ABSTRACT

Background: *Lablab purpureus* (L.) Sweet is an important and primarily consumed vegetable crop in Assam. Large number of genotypes of *Lablab purpureus* (L.) Sweet are available in Assam, India, which are prosperous source of the gene pool. However, there has been limited understanding of the genetic background of the various proximate components of *Lablab*, although we primarily use the crop for these proximate components. The present study helps us understand the genetic background of the various proximate components so that they can be efficiently utilized to further improve the genotypes.

Methods: Sixteen (16) genotypes of *Lablab purpureus* (L.) Sweet of Assam were collected from the 6 (six) Agro-climatic zones of Assam, their genetic variability were assessed and correlation analysis with respect to their proximate components during the period 2020-2023. The various proximate components that were analyzed includes moisture, ash, fibre, fat, crude protein content and total carbohydrate content. Various genetic parametres were also determined which included heritability, genotypic and phenotypic coefficient of variance (GCV and PCV) and genetic advance percentage of mean (GAPM).

Result: Significant differences were found among the genotypes in all studied traits in the study. GCV and PCV revealed variability and less influence of the environment that supports the influence of heritable components on traits. High heritability and genetic advance for all the traits indicated action of additive genes. Heritability along with GAPM is a positive indicator of expected progress through selection. The study will help us in understanding the genetic parameters associated with the various proximate components.

Key words: Character association, Genetic variability, *Lablab purpureus* (L.) Sweet, Proximate component.

INTRODUCTION

Lablab purpureus (L.) Sweet belonging to the family Leguminosae is a widely cultivated legume crop of Assam for their adaptability, high productivity, minimum maintenance requirement and acceptability as a vegetable crop. It is a climber showing pole type and bush type habit, with tri-pinnate leaf and mostly pink and white flowers showing vexillary aestivation. Delineating a cosmopolitan distribution, a total of about 3000 accessions of *Lablab purpureus* (L.) Sweet has been reported worldwide (Maass, 2010). In the context of the Indian sub-continent, large numbers of indigenous collections have been reported (ICAR- NBPGR National Gene Bank). Asati and Yadav (2004) reported twelve (12) cultivars of *Lablab purpureus* (L.) Sweet along with two (2) wild-related species from North East India. Sarma *et al.* (2010) reported nine (9) landraces of *Lablab purpureus* (L.) Sweet from Assam which grows widely in diverse agro-climatic zones of Assam. The crop has multidimensional uses, which includes their use as forage, cover crop and addressing several geomorphological effects of erosion and weed control (Afsan and Roy, 2019). Despite these large recognised benefits, this legume has not been explored or promoted and many are marginally known.

In this regard, extensive study on identification of potential genotypes, agricultural management and their proper utilization is required so that these crops further can be a readily available and affordable alternative source of food and can be a promising source of protein and minerals for human and livestock consumption. Genetic variability of germplasm is the prerequisite for any crop improvement program and useful for the development of new genotypes. However, variability can be aptly used if they are heritable. Heritability of trait determines the structure of a population as it reflects the degree of transmissibility of traits (Ahmad *et al.,* 2015).

Correlation analysis is important in finding relationship among the traits and selecting desirable genotypes. On the

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other hand, correlation coefficient analysis determines the nature of relationship between response variable and its contributing components (Yahaya *et al.,* 2021). The present study focuses on genetic variability of sixteen (16) genotypes of *Lablab purpureus* (L.) Sweet genotypes of Assam and correlation analysis of various nutrient components to highlight their importance for future utilization. The relationship between the proximate parameters and the underlying genetic parameters will be helpful in explaining the interrelationships among the parameters and also to single out suitable parameter. The knowledge of genetic parameters with variability serves as the basis of selection in the different crop improvement programs (Baranidharan *et al.,* 2023). The understanding of correlation of proximate components and genetic parameters will help in the development of nutrient-fortified varieties from the underutilised indigenous varieties.

MATERIALS AND METHODS

Sixteen (16) genotypes of *Lablab purpureus* (L.) Sweet were collected from six agro-climatic zones of Assam (Table 1). The collected genotypes were planted in the Department of Botany, Cotton University, Assam, India during 2020-23. The experimental sample (air-dried, matured seeds) were considered for proximate component analysis. The moisture, dietary fibre, ash, protein, carbohydrate and fat content were analysed by following standard protocols. For analyses, the air-dried samples were powdered and stored in screw-capped bottles at room temperature. Each sample was analysed in triplicates and the data were subjected to statistical analysis.

Analysis of proximate components

Moisture content of seed was determined by oven drying method. The samples were kept in oven at 105°C ±1°C temperature.

$$\text{Moisture content (\%)} = \frac{\text{Weight loss on drying}}{\text{weight of the sample}} \times 100$$

The ash content of the seeds was determined by the method described in AOAC (2005).

$$\text{Ash content (\%)} = \frac{\text{Weight of ash}}{\text{Weight of sample}} \times 100$$

Dietary fibre content of seed was estimated as per the method of Sadasivam and Manikam (1992).

$$\text{\% Fibre} = \frac{\text{(wt. of crucible with dry residues- - wt. of the crucible with ash)}}{\text{Weight of sample}} \times 100$$

Crude Fat of seed was determined by Soxhlet extraction method (AOAC 2005). Crude fat was extracted with petroleum ether and crude fat content was calculated.

$$\text{\% fat} = \frac{\text{Weight of ether extract}}{\text{Weight of the sample}} \times \frac{100}{1}$$

Crude protein content

To determine total nitrogen, the Kjeldahl digestion method (Thiex *et al.,* 2002) was used and from that the seed's crude protein content was determined using protein correction factor 5.95 (Jones 1941).

Total carbohydrate content

Total Carbohydrate content of seeds were determined by Anthrone method (Thimmaiah 1999).

Table 1: List of coordinates of germplasm collection site and the corresponding Agroclimatic zones of Assam (Ingtipi and Rajkumari, 2023).

Germplasm Id	Coordinates		Name of the agroclimatic zones
	Latitude	Longitude	
CUCYT22001	24.78852°N	93.02961°E	Barak Valley Zone
CUCYT22002	24.78852°N	93.02961°E	Barak Valley Zone
CUCYT22003	26.63563°N	90.38114°E	Lower Brahmaputra Valley Zone
CUCYT22004	26.63563°N	90.38114°E	Lower Brahmaputra Valley Zone
CUCYT22005	25.29430°N	93.11121°E	Hills Zone
CUCYT22006	25.29430°N	93.11121°E	Hills Zone
CUCYT22007	25.29430°N	93.11121°E	Hills Zone
CUCYT22008	25.29430°N	93.11121°E	Hills Zone
CUCYT22009	25.29430°N	93.11121°E	Hills Zone
CUCYT22010	25.29430°N	93.11121°E	Hills Zone
CUCYT22011	25.97996°N	91.23510°E	Lower Brahmaputra Valley Zone
CUCYT22012	26.12102°N	92.69759°E	Upper Brahmaputra Valley Zone
CUCYT22013	27.51477°N	95.34160°E	Upper Brahmaputra Valley Zone
CUCYT22014	27.51477°N	95.34160°E	Central Brahmaputra Valley
CUCYT22015	26.658312	92.742131	North Bank Plain Zone
CUCYT22016	25.74648°N	93.24242°E	Hills Zone

Statistical analysis

The analysis of variance for individual character was carried out using R software version 4.2.2 [R Core Team 2021]. Genetic parameters such as Genotypic variance(σ_e^2), Phenotypic variance (σ_e^2), Environmental variance (σ_e^2), Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), were calculated based on method by Burton and Devane (1953). Heritability in broad sense (h^2_b), Genetic Advance (GA) and Genetic Advance Percentage of Mean (GAPM) were estimated for different characters using the formula suggested by Lush (1949) and Johnson *et al.* (1955). Genotypic and phenotypic correlation coefficients were measured with the formula suggested by Johnson *et al.* (1955) and later on adopted by Hanson *et al.* (1956).

RESULTS AND DISCUSSION

Proximate components of sixteen (16) *Lablab purpureus* (L.) Sweet genotypes of Assam is presented in Table 2. The mean moisture content was highest in CUCYT22004 and the lowest in CUCYT22003 and was recorded as 7.87% and 4.04%, respectively. Hossain *et al.* (2016) reported 8.47% moisture content in seeds of *Lablab purpureus* (L.) Sweet. The present study revealed low moisture content compared with the moisture content of some legume seeds (4.40% to 11%) as reported by some other workers (Thakur *et al.,* 2005 and Aremu *et al.,* 2006). Moisture content predicts the shelf-life of seeds and less moisture content of the seeds under the present investigation showed advantage for storage.

Total dietary fibre showed the highest mean value (4.62%) in CUCYT22001 and recorded the lowest (2.52%) in CUCYT22010. The maximum ash content was recorded as 4.79% in CUCYT22011 followed by CUCYT22012 (4.29%) and minimum ash value was in CUCY22009 (2.89%). All sixteen (16) genotypes showed noticeably high value of ash content which signifies the presence of high contents of minerals and organic compounds. Among the genotypes, highest protein content (26.39%) was found in CUCYT22001 and lowest (15.63%) was in CUCYT22010. CUCYT22008 exhibited lowest carbohydrate content 56.58% and highest 63.19% was by CUCYT22001. Highest fat content (2.83%) was found in CUCYT22012, followed by CUCYT22016 (2.82%), while the lowest value (1.91%) was recorded in CUCYT22001.

Table 2: Proximate components of 16 (Sixteen) genotypes of *Lablab purpureus* (L.) Sweet of Assam.

Germplasm Id	Moisture content (%)	D. Fibre content (%)	Ash content (%)	Protein content (%)	Carbohydrate content (%)	Fat content (%)
CUCYT22001	7.33±0.04	4.62±0.25	3.19±0.03	26.39±0.02	63.19±0.03	1.91±0.02
CUCYT22002	4.16±0.03	3.70±0.09	3.68±0.07	19.35±0.02	59.74±0.02	2.11±0.12
CUCYT22003	4.04±0.02	3.45±0.02	4.01±0.05	17.82±0.01	61.72±0.05	2.19±0.04
CUCYT22004	7.87±0.04	3.52±0.08	3.44±0.26	18.99±0.02	60.52±0.01	2.38±0.03
CUCYT22005	5.85±0.06	2.95±0.05	3.80±0.04	20.64±0.03	58.53±0.02	2.35±0.06
CUCYT22006	7.63±0.02	4.27±0.10	4.04±0.08	25.15±0.03	61.12±0.04	2.71±0.04
CUCYT22007	5.57±0.01	3.11±0.07	3.79±0.02	26.13±0.02	56.68±0.04	2.48±0.13
CUCYT22008	5.48±0.03	4.24±0.05	4.17±0.07	21.24±0.05	56.58±0.04	2.37±0.01
CUCYT22009	5.25±0.01	4.18±0.05	2.89±0.12	24.92±0.03	59.69±0.03	2.47±0.01
CUCYT22010	6.51±0.04	2.52±0.62	3.81±0.07	15.63±0.01	62.62±0.07	2.21±0.05
CUCYT22011	7.71±0.01	3.74±0.02	4.79±0.07	20.07±0.02	58.91±0.01	1.97±0.03
CUCYT22012	5.28±0.04	3.77±0.05	4.29±0.06	19.17±0.05	57.33±0.03	2.83±0.02
CUCYT22013	6.19±0.02	3.58±0.08	3.57±0.04	16.76±0.02	61.87±0.03	2.48±0.05
CUCYT22014	6.88±0.03	3.16±0.02	3.62±0.05	23.39±0.02	61.78±0.01	2.50±0.01
CUCYT22015	7.31±0.03	2.81±0.04	3.30±0.11	22.86±0.02	60.94±0.05	2.76±0.04
CUCYT22016	4.18±0.03	3.53±0.06	4.02±0.10	26.25±0.03	62.27±0.02	2.82±0.02

Table 3: Genetic parameters for proximate components of *Lablab purpureus* (L.) Sweet of Assam.

Characters	Range	MS	ó^{2}g	ó^{2}e	ó^{2}p	GCV	PCV	h^{2}b	GA	GAPM
Moisture	4.04-7.87	5.118**	1.70	0.010	1.71	21.46	21.58	98.9	2.67	43.95
Dietary Fibre	2.52-4.62	0.991**	0.98	0.030	1.01	15.86	16.55	91.81	1.12	31.30
Ash	2.89-4.79	0.638**	0.64	0.010	0.65	12.16	12.32	97.37	0.93	24.72
Carbohydrate	56.58-63.19	13.355**	13.35	0.002	13.36	3.50	3.52	99.96	4.35	7.22
Protein	15.63-26.39	37.393**	37.28	0.330	37.61	16.32	16.53	97.42	7.15	33.18
Fat content	1.91-2.83	0.244**	0.081	0.002	0.08	11.79	11.94	97.48	0.58	23.98

**Significant at 1% level.

Table 4: Correlation coefficient for proximate components of *Lablab purpureus* (L.) Sweet of Assam.

Characters		D.Fiber	Ash	Carbohydrate	Protein	Fat
Moisture	rg	0.023	- 0.077	0.193	0.068	-0.109
	rp	0.019	- 0.074	0.192	0.066	- 0.110
Fibre	rg		- 0.028	- 0.066	0.386**	- 0.179
	rp		- 0.027	- 0.063	0.370**	- 0.173
Ash	rg			- 0.372**	- 0.265	- 0.020
	rp			- 0.367**	- 0.255	- 0.015
Carbohydrate	rg				- 0.029	- 0.137
	rp				- 0.029	- 0.136
Protein	rg					0.257
	rp					0.256

** = Significant at 1% level.

Estimation of Variability parameters

Variability parameters are presented in Table 3. The results showed significant difference among the genotypes for all the traits**.** Under the present study highest genotypic and phenotypic variance was found for protein content which was 37.28 and 37.61 respectively and lowest for fat content (0.081 and 0.083). High and moderate variability was recorded for most of the nutritional traits. Low GCV and PCV was observed only for carbohydrate content. Higher and moderate GCV and PCV for the traits reveals higher magnitude of variance for those traits and indicates scope for improvement of these traits through selection and hybridization. For all the proximate components studied PCV showed greater value than GCV reveals the influence of environment on phenotypic expression of the traits. However, less difference between GCV and PCV indicates less influence of environment on the traits and supports the more influence of heritable component in expression of traits. Heritability estimate predicts the reliability of phenotypic value and high value of heritability is useful in effective selection of traits. Heritability (broad sense) in all traits ranged from 91.81% - 99.96% (Table 3) indicates minimal environmental influence on the traits, hence selection will be effective. Genetic advance (GA) indicates the expected progress for phenotypic trait selection and is used to measure the type of gene action in quantitative traits. High genetic advance percentage of mean (GAPM) was recorded from 23.98% - 43.95%, except for carbohydrates which was recorded as 7.22%. Heritability along with GAPM gives good impression of expected progress through selection. High heritability associated with high GAPM was observed for moisture, fibre, ash, protein and fat content, which indicates less influence of environment, action of additive genes for the traits and also indicates the possibilities of getting a response through phenotypic selection due to their high transmissibility. Breeding programmes can only be successfully adopted if heritability, genetic advance and variability are abundant in the target germplasm (Mandal *et al.,* 2022).

Character association

Correlation analysis is presented in Table 4. Moisture showed insignificant positive correlation with fibre (0.023, 0.019), carbohydrate (0.193, 0.192) and protein (0.068, 0.066) at genotypic and phenotypic level, while insignificant negative correlation with ash (-0.077, -0.074) and fat (-0.109, -0.110) at both the level. The positive correlation of moisture with fibre, protein and carbohydrate indicates that the seeds with high amount of fibre, carbohydrate and protein retain more moisture. Fibre showed a significant positive correlation with protein (0.386, 0.370) and insignificant negative correlation with ash, carbohydrate and fat at genotypic and phenotypic level.

Ash exhibited significant negative correlation with carbohydrate (-0.372, -0.367) both at genotypic and phenotypic level which indicates that increasing carbohydrate content of seeds decreases ash value significantly. Ash and carbohydrates show insignificant negative correlation with protein and fat. On the other hand, protein showed positive correlation with fat content. Genotypic and phenotypic correlation coefficients among various yield-attributing characteristics of lablab beans had been reported by Salim *et al.* (2013) and stated a significant positive correlation for certain traits. The positive correlation among the useful parameters will indeed be advantageous as both will be in tandem under different set of environmental conditions.

CONCLUSION

Evaluation of plant genotypes by genetic analysis is the basic requirement of plant improvement program and to select the parental lines for their further utilization. The present study showed adequate variability among the genotypes of *Lablab purpureus* (L.) Sweet of Assam. Less difference between phenotypic variance with their corresponding genotypic variance gives clear indication of minimum influence of the environment and genetic components has played a significant role in the expression of traits. Heritability estimates determines the selection response and indicator of genotypes potential genetic ability, which can be used as selection tools. High heritability and genetic advance estimates were found for all the traits which indicates predominance of additive gene action and scope for selection of the traits for improving yield potential of the genotypes.

Conflict of interest

I, on behalf of all the authors of the manuscript, do hereby declare that all the authors have no conflicts of interest to declare. All co-authors have seen and agree with the contents of the manuscript and there is no financial interest to report or involvement in any organization or entity with any financial interest while carrying out the work.

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