



Assessment of Genetic Diversity and Traits Correlation Analysis in Lablab Bean Genotypes from Assam, North-Eastern India

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ABSTRACT

Background: *Lablab purpureus* (L.) Sweet is a widely cultivated legume vegetable for their seeds and pods. Assam has diverse cultivars of the genus and hence an excellent source of gene pool which needs to be utilised. The present study helps us in understanding the variation, correlation and principal components in the agronomically important traits, which can provide useful inputs on the breeding and improvement strategy of the crop. The study also aim to evaluate the genetic diversity among the selected genotypes of Lablab bean.

Methods: A total of 16 (sixteen) quantitative parameters from 16 (sixteen) different genotypes were studied during the period 2020-2023. The traits were accessed for their variation and correlation. Genotypic variance (σ_g^2), Phenotypic variance (σ_p^2), Environmental variance (σ_e^2), Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), were calculated based on standard method. Heritability in broad sense (h_b^2), Genetic Advance (GA) and Genetic Advance Percent of Mean (GAPM) were also estimated using the standard formula. Besides principal component of the traits and genetic divergence based on Mahalanobis distance were estimated.

Result: Variability and significant correlation were observed among sixteen studied traits of *Lablab* genotypes. The study depicts influence of genetic factors on the traits. Strong positive correlation among several traits, with perfect correlation between locule/pod and seeds/pod (1.00). Total variance of the traits 84.81% was explained by 5 (five) components. The genotypes clustered in 4 (four) different clusters, with maximum genotypes in cluster 1.

Key words: Correlation, Diversity, *Lablab*, Principal components analysis, Variability.

INTRODUCTION

Lablab is a very familiar genera of the family Leguminosae, cultivated and consumed primarily for the seeds and pods. The genera is monotypic containing a single species *Lablab purpureus* (L.) Sweet which further has two subspecies viz. *Lablab purpureus bengalensis* (Jacq.) Verdc. and *Lablab purpureus pupureus* (L.) Verdc. *Lablab* bean have immense potential due to their inherent ability of withstanding drought, soil acidity and tolerance against mineral toxicity such as Aluminium toxicity (Ansari *et al.*, 2019), besides they are also important as catch crops and herbage (Afsan and Roy, 2019). The genus is extremely diverse and about 3000 accessions of germplasm have been reported from the different regions of the world (Maass, 2010). The Indian sub-continent boasts of a large number of indigenous collections across the country (ICAR-NBPGR National Gene Bank). The north eastern region of India, Assam in particular is a remarkable natural gene repository with several indigenous germplasm traversing generations and their farmlands. In a study by Sarma *et al.* (2010) nine (9) landraces of *Lablab* has been reported from the different areas of Assam and Northeast.

Pods of *Lablab* beans are mostly consumed as vegetable (Dwivedi *et al.*, 2023), besides dried seeds are used as an alternative to common pulses and it has a great potential in overcoming problems related to malnutrition as it is nutritionally very rich (Deka and Sarkar, 1990). The improvement of this underutilised crop is

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important; however, the self-pollinating nature of the crop often poses as a hindrance in generating variability and selection is one of the ways to create variability. Hence it is imperative to understand the important traits for the improvement of the crop. *Lablab* has been an integral crop in the homesteads and farmlands in Assam, but these genotypes have not made itself to the core collection and are less utilised in crop improvement programmes. In this

regard Principal component analysis (PCA) or canonical root analysis serves as an important analytical tool which can help us to mark out certain traits that can be used for plant selection. Natural variations, their exploration and the extent of variation could be useful for genetic improvement of germplasm (Ullah *et al.*, 2022). Also, the selection of characters will be easier and more precise by understanding the correlation between the traits. The present study will be helpful in understanding the relationship among the traits and also in finding out the suitable genitors for further breeding programme.

MATERIALS AND METHODS

Collection and planting of plant material

Germplasm of 16 (sixteen) different genotypes were collected from the various locations of the six agro-climatic zones of Assam (Fig 1) and maintained in the departmental garden, Department of Botany, Cotton University, Assam from 2020 to 2023. The average weather parameters of the study site has been represented in the table (Table 1) (<https://mausam.imd.gov.in>). The experiments were laid in a randomized block design (RBD) with three (3) replications and 1 × 1 meter spacing. Quantitative characters as well as the stages of scoring are indicated in table (Table 2). Measurement of length and width was carried out using a

calibrated scale and vernier caliper. The individual traits were recorded in 3 (three) replicates and the parameters were observed in 4 (four) consecutive growing seasons.

Statistical analysis

The data were analysed using IBM SPSS Statistics v.28. Genotypic variance (σ_g^2), Phenotypic variance (σ_p^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_b^2), Genetic Advance (GA) and Genetic Advance Percent of Mean (GAPM) were estimated using the formula suggested by Lush (1949) and Johnson *et al.* (1955). The principal component and Eigen values for the individual data and the component scores for the various data were determined (Pearson, 1901; Hotelling, 1933). The linear correlation between the variables were determined at 5% level of significance (Pearson, 1896). The genetic divergence was measured using Mahalanobis D² statistics (Mahalanobis, 1936) and cluster analysis was carried out by Tocher's Method (Rao, 1952).

RESULTS AND DISCUSSION

Summary statistics for variables

Descriptive statistics were measured for sixteen (16) characters (Table 3) and the characters considered are

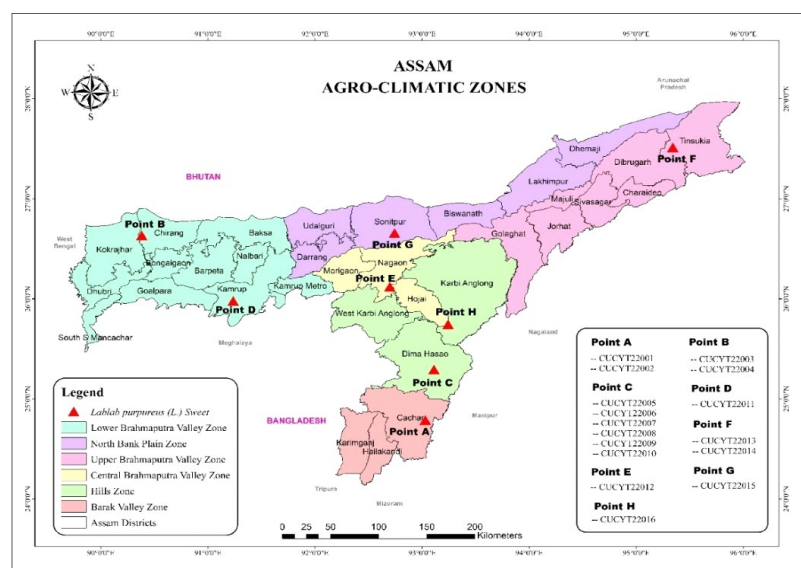


Fig 1: Map showing the collection site and the corresponding agroclimatic zones of Assam (Ingtpi and Rajkumari, 2023).

Table 1: Weather parameters of the study site during the study period.

Year	Average temperature (°F)		Relative humidity (%)	
	(Max±SD)	Min±SD)	Max±SD	Min±SD
2020	85.46±6.09	69.33±10.11	93.55±2.94	58.56±9.89
2021	86.58±5.70	69.31±9.61	95.31±2.42	59.42±10.72
2022	85.63±6.34	69.72±9.50	95.01±2.38	60.49±9.86
2023	86.70±5.52	70.84±9.49	94.80±1.88	59.17±8.03

shown in the Table 2. The highest variation was found for seed/plant with a CV of 55.45% and lowest was 5.69% for dal recovery.

Assessment of variability

The estimation of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, genetic advance are shown in Table 4. The mean sum of square (MS) is significant for most of the characters which revealed significant variations among the genotypes, except for the traits 100 seed (dry) weight and dal recovery. Lowest GCV and PCV was found for seed yield /plant and was recorded as 5.67 and 5.74 respectively. While, highest GCV and PCV was recorded as 52.97 and 56.14 for average pod (fresh) weight. The results indicate the influence of environment

on the traits. However, less difference between GCV and PCV indicates more influence of genetic component in phenotypic expression of the traits rather than environment. High GCV and PCV value for the traits except for leaf length (17.00 and 17.28), leaflet length (17.59 and 18.95), raceme/plant (17.45 and 17.49), 100 dry seed weight (10.16gm and 18.30 gm) and dal recovery (10.16 and 18.30) indicate high variability among the genotypes for the traits that provides scope for selection. Seed yield/plant showed low but significant GCV and PCV (5.67 and 6.74). Heritability insights the genetic basis of the traits of a population, thus provides scope for efficient selection of traits from diverse genotypes available. High heritability (>60) was recorded for most of the traits except dal recovery and pod/raceme (30.8%). Highest heritability was recorded for pods per plant (99.9%) followed closely by traits like seed yield/plant (99.6%) and days to first flowering (99.6%). Genetic advance (GA) and Genetic advance percentage of mean (GAPM) are related to prediction of the expected results of a selection or the advancement which a particular trait is likely to achieve. However, GA represents the absolute value and GAPM represents the relative value based on the population mean. High genetic advance (GA) for the traits under investigation was recorded for raceme/plant (27.32%) pod width (80.64%), average pod (Fresh) weight (244.43%), pod/raceme (53.13%) and pod/plant (21.87%) and that indicates presence of wide of genetic alleles which primarily control the traits with additive effect, thus provide advantage for selection. All other traits which exhibited low genetic advance may be due to the control of both additive and non-additive genes in combination over the traits. The values of GAPM were found to be high for 13 (thirteen) traits and only 3 (three) traits showed moderate GAPM, as proposed by Johnson *et al.* (1955). Highest GAPM was recorded for fresh average pod weight (102.94%) and the lowest was for the trait seed yield/plant (11.54%). None of

Table 2: Quantitative characters studied and stage of scoring in the 16 (sixteen) different genotypes.

Quantitative traits	Stages of scoring the traits
Leaf length	Fully grown leaf
Leaf width	
Leaflet length	
Raceme/Plant	At harvesting
Days to first flowering	Onset of flowering
Pod length	Mature pod
Pod width	
Fresh average pod weight	Post-harvest
Locule/Pod	
Seeds/Pod	
100 seeds wt. (Fresh)	
100 seeds wt. (Dry)	
Dal recovery (Saxena <i>et al.</i> , 1981)	
Pods per raceme	
Pods per plant	
Seed yield/plant	

Table 3: Descriptive statistics for quantitative characters of Lablab bean.

Characters	Minimum	Maximum	Mean	SD	CV (%)
Leaf length (cm)	14.30	27.30	21.33	3.5	16.41
Leaf width (cm)	5.10	12.00	8.08	1.82	22.52
Leaflet length (cm)	6.20	13.50	9.78	1.77	18.10
Raceme/Plant	6.00	24.00	16.83	3.91	23.23
Days to first flowering	52.00	111.00	76.13	13.29	17.46
Pods/Pant	72.00	198.00	119.83	41.5	34.63
Pods/Raceme	4.00	14.00	7.15	2.02	28.25
Pod length (cm)	4.00	14.30	8.46	2.96	34.99
Pod width (cm)	1.00	5.00	2.26	0.93	41.15
Fresh pod weight (gm)	1.30	13.90	5.82	2.89	49.66
Locule/Pod	3.00	7.00	4.67	0.64	13.70
Seeds/Pod	3.00	7.00	4.77	0.64	13.42
100 seeds wt. (fresh)	20.00	137.75	57.04	25.80	45.23
100 seeds wt. (dry)	20.09	65.50	37.43	10.65	28.45
Dal recovery %	75.90	95.77	84.21	4.79	5.69
Seed yield/Plant	103.84	680.00	232.7	129.04	55.45

the traits falls under the low GAPM category. Abundant diversity with high heritability and genetic advance in target germplasm is indispensable for breeding programme (Rasheed *et al.*, 2023). Influence of genetic factor on the traits, high heritability and genetic advance provide the scope for divergent parental line selection and heterozygosity advantage for the yield attributing traits in groundnut (Shekhawat *et al.*, 2023).

Pearson's correlation-coefficient analysis

Pearson's coefficient efficiently measures the strength and linear correlation relationship concerning two variables. In the present study (Table 5) strong positive significant correlation was seen for leaf width with leaflet length (0.898), pod length with fresh pod weight (0.709), fresh seed weight with dry seed weight (0.863), 100 fresh seed weight with seed yield/plant (0.807), dry seed weight with seed yield (0.806), pod/raceme with pod/plant (0.730). Similarly positive significant correlation was also seen for leaf length with leaf width (0.623), leaflet length with leaf length (0.661) and raceme/plant (0.604), pod length with 100 dry seed weight (0.633), pod weight with 100 dry and fresh seed weight (0.691 and 0.694). The locule/pod has shown perfect positive significant correlation with seeds/pod (1.000). Moderate correlation was seen for the characters raceme/plant with pod/plant (0.501), leaf width with pod width (0.506) and 100 seed weight with dal recovery (0.530). Pod/raceme, pod length, seed/pod, seed weight showed direct correlation on total yield of the plant. The study is in consent with the findings of Girgel *et al.* (2021) and Singh *et al.* (2018) who reported strong positive correlation among the yield attributing traits in *Phaseolus vulgaris* L. and *Carica papaya* L. respectively. Significant

positive correlation among the traits indicates the scope for selection and to improve multiple traits simultaneously.

Principal component analysis (PCA)

PCA is an important approach to find out the total variation in a population and interrelationship among the variables, thus plays an important role for selection of traits or germplasm for genetic improvement. The PCA under the present investigation was considered for the variables with Eigen values more than 1(one) as per Kaiser Rule (1961). The Eigen value, variability % and cumulative % values are indicated in the table (Table 6). Highest variability was shown by PC1 (32.95%) followed by PC2, PC3, PC4 and PC5 which represented 20.33%, 15.60%, 8.63%, and 7.30% respectively (Table 6). The total variance of 5 (five) components was recorded as 84.81%. Screw plot of Eigen value based on 16 traits has been represented in Fig 2. In PC1 all the characters except raceme/plant contributed positive loading value. The Scree plot shows that from the 11th PC (PC11) there was very little variance and the graph was more or less linear.

The positive and negative loadings of the various variable are represented in the Rotated Component Matrix (Table 7, Table 8) and PCA biplot (Fig 3). For traits located at narrow, wide and right angles the relationship was considered as positive, negative and no relationship respectively (Mohanlal *et al.*, 2023). The PCA biplot of the present study shows positive relationship between the traits like 100 seeds wt. (Fresh) and seed yield/plant, dal recovery and fresh average pod weight, pod width and leaf length, leaf width and leaflet length, locule/pod and seeds/pod.

In PC1 most of the yield attributing traits like 100 dry seeds wt., 100 Fresh seeds wt., seed yield/plant, fresh

Table 4: Estimates of variance components, broad sense heritability and genetic advance for quantitative characters of Lablab bean.

Characters	MS	σ_g^2	σ_e^2	σ_p^2	GCV	PCV	h_b^2	GA	GAPM
Leaf length	39.795**	13.12	0.43	13.55	17.00	17.28	91.6	7.34	34.47
Leaf width	9.904**	3.21	0.28	3.49	22.18	23.13	96.9	3.54	43.80
Leaflet length	9.355**	2.96	0.48	3.44	17.59	18.95	91.9	3.29	33.64
Raceme/Plant	530.261**	176.52	0.69	177.22	17.45	17.49	86.1	27.32	35.88
Days to first flowering	45.822**	14.93	1.03	15.96	22.96	23.73	99.6	7.70	45.74
Pod length	12.221**	3.89	0.55	4.44	27.60	29.49	93.6	3.80	53.22
Pod width	5174.578**	1673.44	154.26	1827.70	34.14	35.68	87.6	80.64	67.29
Fresh average pod weight	49406.525**	15817.61	1953.68	17771.30	52.97	56.14	91.6	244.43	102.94
Locule/Pod	26.337**	8.67	0.32	8.99	34.83	35.46	89.0	5.96	70.47
Seeds/Pod	2.610**	0.86	0.04	0.90	41.00	42.00	96.5	1.86	82.45
100 seeds wt. (Fresh)	25.10**	8.26	0.32	8.58	49.40	50.36	95.3	5.81	99.82
100 seeds wt. (Dry)	1.232 ^{NS}	0.23	0.53	0.76	10.16	18.30	96.2	0.55	11.61
Dal recovery	1.232 ^{NS}	0.23	0.53	0.76	10.16	18.30	30.8	0.55	11.61
Pods/Raceme	1997.071**	665.56	0.38	665.94	45.23	45.24	30.8	53.13	93.15
Pods/Plant	340.039**	113.18	0.51	113.69	28.42	28.49	99.9	21.87	58.42
Seed yield/Plant	68.904**	22.79	0.55	23.33	5.67	5.74	99.6	9.72	11.54

**= Significant at 1% level, σ_g^2 = Genotype variance, σ_e^2 = Environmental variance, σ_p^2 = Phenotype variance, GCV = Genotype coefficient of variation, PCV = Phenotype coefficient of variation, h_b^2 = Heritability in broad sense, GA= Genetic advance, GAPM= Genetic advance per cent of mean.

Table 5: Correlation matrix for sixteen (16) quantitative characters of Lablab bean.

Correlation	LL	LW	LFL	RP	DF	PL	PW	FPW	LPP	SPP	HSW (Fresh)	HSW (dry)	DR	PPR	PPP	SYP
LL	1.000															
LW	0.623	1.000														
LFL	0.661	0.898	1.000													
RP	0.604	0.372	0.358	1.000												
DF	-0.512	-0.171	-0.326	-0.272	1.000			-								
PL	0.037	0.319	0.410	-0.233	-0.001	1.000										
PW	0.259	0.506	0.473	-0.166	-0.196	0.304	1.000									
FPW	0.337	0.399	0.473	-0.023	-0.204	0.709	0.479	1.000								
LPP	0.262	0.474	0.488	-0.003	-0.198	0.407	0.321	0.237	1.000							
SPP	0.262	0.474	0.488	-0.003	-0.198	0.407	0.321	0.237	1.000	1.000						
HSW (Fresh)	0.193	0.077	0.132	-0.113	0.023	0.476	0.126	0.691	0.118	0.118	1.000					
HSW (Dry)	0.054	0.117	0.224	-0.156	0.100	0.633	0.122	0.694	0.160	0.160	0.863	1.000				
DR	0.241	0.321	0.435	0.231	-0.298	0.345	0.149	0.652	0.013	0.013	0.445	0.530	1.000			
PPR	-0.142	-0.438	-0.547	-0.108	0.021	-0.396	0.047	-0.051	-0.342	-0.342	0.274	-0.025	-0.161	1.000		
PPP	0.216	-0.204	-0.266	0.501	-0.123	-0.348	-0.106	-0.007	-0.285	-0.285	0.312	0.014	0.055	0.730	1.000	
SYP	0.168	0.063	0.160	0.194	-0.027	0.307	-0.001	0.484	0.076	0.076	0.807	0.806	0.493	0.195	0.422	1.000

**Correlation values marked bold are non-significant at 5% Level of significance.

LL- Leaf Length, LW- Leaf width, LFL- Leaflet length, RP-Raceme per plant, DF- Days to first flowering, PL- Pod Length, PW- Pod width, FPW- Fresh average pod weight.

LPP- Locule/Pod, SPP- Seeds/Pod, HSW (Fresh)-100 Seeds wt (fresh), HSW (dry)-100 Seeds wt (dry), DR- Dal recovery, PPR- Pods per race, PPP- Pods per plant, SYP- Seed yield/plant.

average pod weight, dal recovery, pod length, leaflet length, pods per plant and leaf width exert positive loadings but the trait raceme/plant showed negative relationship (Table 7). In PC2 positive contributions were made by leaf length (0.865), raceme/plant (0.818), leaflet length (0.700), leaf width (0.673), dal recovery (0.403), pods/ plant (0.288), fresh

average pod weight (0.233), pod width (0.220), locule/pod and seeds per pod (0.163), seed yield/plant (0.131). While negative contribution was seen for the traits like 100 seeds wt. (Fresh) (-0.024), pod length (-0.089), 100 seeds wt. (Dry) (-0.104), pods per raceme (-0.191), days to first flowering (-0.585).

Traits like pods/raceme (0.915), pods/plant (0.861), seed yield/plant (0.283), 100 seeds wt. (Fresh) (0.268), raceme/plant (0.132), leaf length (0.053) showed positive contribution in PC3. In case of PC4, strong positive effects were contributed by locule/pod and seeds/pod (0.942) followed by leaf width (0.299), pod length (0.284), leaflet length (0.278), pod width (0.198), leaf length (0.160), 100 seeds wt. (Fresh) [0.110], 100 seeds wt. (Dry) [0.098], seed yield/plant (0.074) and fresh average pod weight (0.039). Moreover strong negative contribution was found for some traits. In the PC5, traits like pod width (0.871), fresh average

Table 6: Eigen values, variability % and cumulative % for sixteen traits in *Lablab*.

Principal components	Eigen value	% of variability	Cumulative %
PC1	5.271	32.95	32.946
PC2	3.253	20.33	53.280
PC3	2.496	15.60	68.880
PC4	1.381	8.63	77.508
PC5	1.168	7.30	84.805

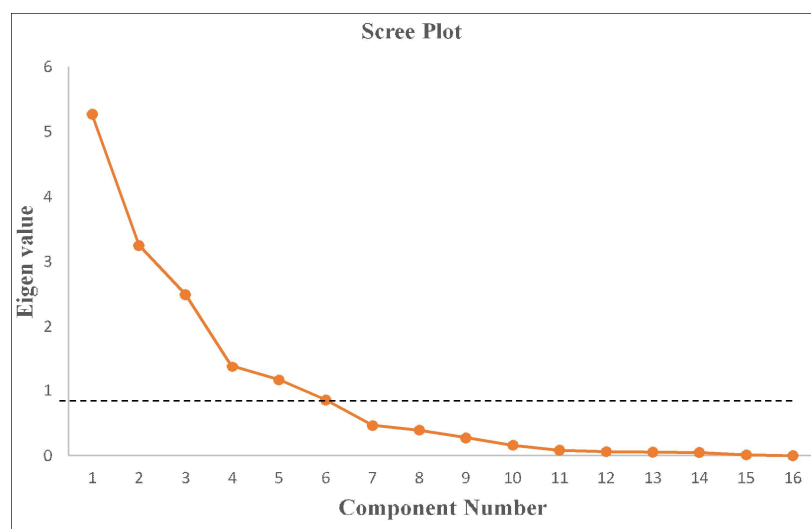


Fig 2: Scree plot diagram of Eigen values based on 16 (sixteen) quantitative traits.

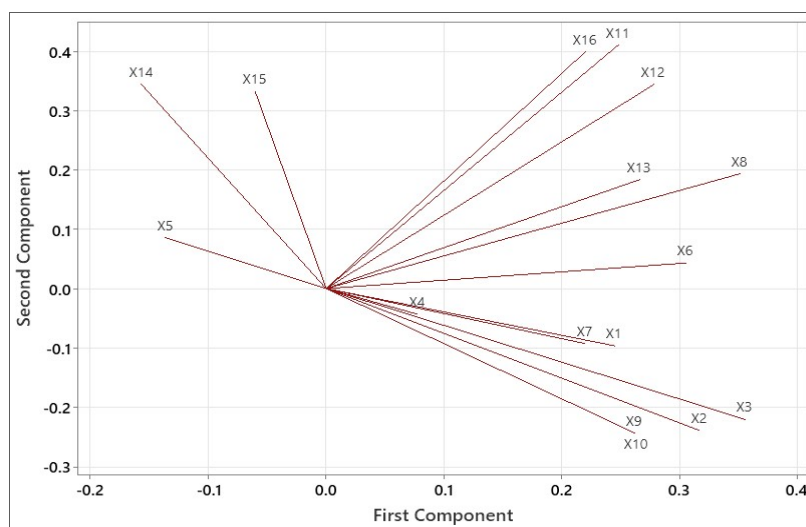


Fig 3: Biplot distribution of 16 studied traits depending on principal component axes PC1 and PC2.

pod weight (0.450), pod length (0.263), leaf width (0.261), leaflet length (0.236), Pods per raceme (0.181), locule/pod and seeds/pod (0.117), leaf length (0.085), dal recovery (0.083), 100 seeds wt. (Fresh) [0.069], 100 Seeds wt. (Dry) [0.007]. The proportion of variance decreases from PC1 to PC5. The study showed high percentage of variability *i.e.* 84.80% by the traits under PC1 to PC5. PC1 constitutes majority of variability accounting to 32.95% of the total variability. The significance of the characters in principal components has been reported for physiological and

biochemical parameters of rice cultivars by Chunthaburee *et al.* (2016) and the legume *Vigna radiata* (L.) Wilczek by John and Aravinth (2024). In the study most of the yield attributing traits are in PC1, showed high relationship among themselves (Fig 3) and may be considered for selection.

Genetic divergence and cluster analysis

The cluster analysis of genotypes revealed four (4) clusters. The first cluster is the largest comprising of 13 (Thirteen) genotypes *viz.* CUCYT22001, CUCYT22002, CU CYT2 2003,

Table 7: Rotated Component Matrix of sixteen (16) traits of *Lablab* genotypes.

Traits	PC1	PC2	PC3	PC4	PC5
Leaf Length	0.104	0.865	0.053	0.160	0.085
Leaf width	0.131	0.673	-0.402	0.299	0.261
Leaflet length	0.233	0.700	-0.479	0.278	0.236
Raceme/Plant	-0.043	0.818	0.132	-0.059	-0.452
Days to first flowering	0.047	-0.585	-0.127	-0.055	-0.263
Pod length	0.636	-0.089	-0.461	0.284	0.263
Pod width	0.100	0.220	-0.014	0.198	0.871
Fresh average pod weight	0.776	0.233	-0.129	0.039	0.450
Locule/Pod	0.091	0.163	-0.185	0.942	0.117
Seeds/Pod	0.091	0.163	-0.185	0.942	0.117
100 seeds wt. (Fresh)	0.908	-0.024	0.268	0.110	0.069
100 seeds wt. (Dry)	0.954	-0.104	-0.066	0.098	0.007
Dal recovery	0.655	0.403	-0.218	-0.265	0.083
Pods/Raceme	0.040	-0.191	0.915	-0.182	0.181
Pods/Plant	0.157	0.288	0.861	-0.171	-0.202
Seed yield/Plant	0.852	0.131	0.283	0.074	-0.225

Table 8: Rotated component matrix for 16 traits having maximum values in each PCs.

Characters	PC1	PC2	PC3	PC4	PC5
Days to first flowering		Leaf length	Pod/raceme	Locule/pod	Pod width
Pod length		Leaf width	Pod/plant	Seed/pod	
Fresh average pod weight		Leaflet length			
100 seed weight (fresh)		Raceme /plant			
Dal Recovery					
Seed yield/plant					

Table 9: Number of clusters and genotypes studied.

Cluster	Genotypes	Total nos
Cluster 1	CUCYT22001, CUCYT22002, CUCYT22003, CUCYT22004, CUCYT22005, CUCYT22008, CUCYT22009, CUCYT22010, CUCYT22011, CUCYT22012, CUCYT22013, CUCYT22014, CUCYT22015	13
Cluster 2	CUCYT22006	1
Cluster 3	CUCYT22007	1
Cluster 4	CUCYT22016	1

Table 10: Inter and intra-cluster among the genotypes.

Cluster number	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	952.508	4088.723	3670.571	3112.696
Cluster 2		0	7177.702	11283.130
Cluster 3			0	8624.409
Cluster 4				0

Table 11: D² distance among the different genotypes.

Genotypes	CUCYT22001	CUCYT22002	CUCYT22003	CUCYT22004	CUCYT22005	CUCYT22006	CUCYT22007	CUCYT22008	CUCYT22009	CUCYT22010	CUCYT22011	CUCYT22012	CUCYT22013	CUCYT22014	CUCYT22015	CUCYT22016
CUCYT22001	0.00	2811.34	1092.73	1494.93	1292.25	3226.85	1612.34	882.51	1039.47	1289.33	947.42	95.39	427.21	1235.91	403.13	4988.34
CUCYT22002		0.00	1289.71	976.35	900.66	6792.44	6728.04	773.57	1989.23	2590.24	1595.05	2552.08	1620.63	603.33	1541.98	813.70
CUCYT22003			0.00	1270.02	839.37	6278.08	2872.59	629.31	1649.26	2144.01	1711.51	1159.53	509.88	766.76	424.94	1863.60
CUCYT22004				0.00	737.02	4506.82	5176.79	297.13	779.90	1549.73	437.82	1297.52	1078.33	680.24	636.82	2452.08
CUCYT22005					0.00	5020.98	4187.72	485.59	559.30	1303.93	1157.64	1168.80	757.14	404.45	510.59	2160.43
CUCYT22006						0.00	7177.70	4414.43	2905.83	1981.08	2427.55	3175.31	3832.91	4291.75	4299.37	11283.13
CUCYT22007							0.00	3709.76	3863.46	4075.51	4482.09	1864.24	2518.05	4207.78	2419.06	8624.41
CUCYT22008								0.00	720.04	1167.39	433.74	701.35	455.39	231.22	236.13	2121.45
CUCYT22009									0.00	407.60	655.59	907.62	888.51	747.34	626.13	4193.48
CUCYT22010										0.00	820.86	1220.19	1269.50	870.50	1110.69	5085.54
CUCYT22011											0.00	788.53	872.50	691.90	726.09	3961.78
CUCYT22012												0.00	373.07	1098.49	367.25	4691.28
CUCYT22013													0.00	710.63	281.97	3232.31
CUCYT22014														0.00	524.39	1988.17
CUCYT22015															0.00	2912.89
CUCYT22016																0.00

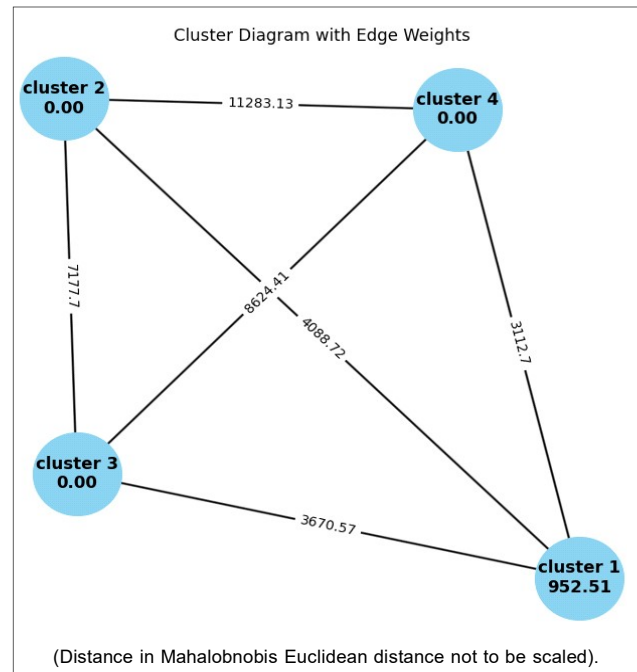


Fig 4: Intra and inter cluster distance among 4 (four) clusters in the genotypes studied.

CUCYT22004, CUCYT22005, CUCYT22008, CUCYT22009, CUCYT22010, CUCYT22011, CUCYT22012, CUCYT22013, CUCYT22014, CUCYT22015 (Table 9). The other three clusters include only one genotype each i.e. CUCYT22006, CUCYT22007 and CUCYT22016 in the second, third and fourth cluster respectively (Table 9). The maximum inter-cluster distance was observed between cluster 2 and cluster 4 with a distance of 11283.13 and minimum was between cluster 1 and cluster 4 with a distance of 3112.670 (Table 10 and 11; Fig 4). The occurrence of larger inter-cluster distance is indicative of the occurrence of larger genetic diversity. Intra-cluster distance, the maximum was recorded for cluster 1 (952.51) indicates the relatedness of traits. The occurrence of rich genetic diversity was highlighted by Prasanna *et al.* (2023) in *Vigna mungo* (L.) Hepper using distance analysis. Genetic diversity in a population is the prime requirement for the plant improvement program (Appalaswamy and Reddy, 2004) that can ensure food security.

CONCLUSION

The current scenario for attaining food security necessitates the utilisation of the existing genetic diversity. Under the present investigation, less difference between PCV and GCV indicates the influence of genetic factor on the phenotypic expression of the certain traits. Heritability determines the population structure and transmissibility of the traits. High heritability and high genetic advance for certain traits signifies the variability among the traits is due to genetic factor rather than the environment. High genetic advance for the traits favours for effective selection for

substantial improvement of germplasm. Significant positive correlation among the traits under Pearson's Correlation-coefficient analysis indicates the scope for selection and to improve multiple traits simultaneously. On the other hand, negative correlation for certain traits reflects adverse effect towards selection.

The understanding of the correlation among the traits can help in accentuating a particular trait and thereby help in the proper selection of the agronomically significant trait. *Lablab* has high potential as a futuristic crop though highly underrated; hence high correlation among yield and yield attributing variables observed in the study significantly indicates the advantage for targeted selection. From the study it can be concluded that traits like fresh average pod weight, 100 seeds weight (fresh), pods per raceme, seeds per pod, locule per pod, pod width and pod length may contribute in making *Lablab* adaptable to diverse environment, generating variability and subsequent genetic gain. The segregation of genotypes into different clusters indicates the diversity existing among the genotypes of Assam, which needs to be harnessed before it cease to exist. However, the differential expression of the traits in the different genotypes need to be ascertained by analysis of expression pattern of the genes. This can further be supplemented by the analysis of the differential expression of the traits as per the edaphic and climatic conditions to develop a climate smart crop.

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Informed consent

Not applicable.

Conflict of interest

I, on behalf of all the authors of the manuscript do hereby declare that all the authors have no conflict of interest to declare. All co-authors have seen and agreed 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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