



Exploring genetic diversity in vegetable type pigeonpea

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Abstract

Twelve morphological and phenological characteristics were used in principal component analysis to identify the pattern of genetic variability in 33 vegetable type pigeonpea genotypes. The largest variation was observed for number of pods per plant with coefficient of variation of 80.05 % followed by single plant yield (67.21), leaf width (37.69). The least variation was observed in days to maturity with coefficient of variation of 2.33%. Principal component analysis extracted five components contributing to around 79.99% of total variability among twelve characters. Principal component 1 had the contribution from the traits such as pod length, no. of seeds per pod and leaf length which accounted to 27.30 % of the total variability. The principal component 2 explained 18.50 % of total variability from number of pods per pod, single plant yield and days to maturity. Thus the results of principal component analysis used in the study had revealed the high level of genetic variation and the traits controlling for the variation were identified. Hence, these entries can be utilized for trait improvement in breeding programs for the traits contributing for major variation. The biplot analysis indicated days to 50% flowering, days to maturity, and hundred seed weight showed positive associations due to acute angle between them. Zero correlation was noticed between number of pods per plant and number of seeds per pod due to angle between the traits is 90°. Cluster analysis acknowledged one major cluster with single genotype ICP15269 for lowest hundred seed weight.

Keywords: Vegetable pigeonpea, Diversity, Principal Component Analysis (PCA), Cluster analysis

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] having diploid chromosome number of $2n=22$ with genome size of 858 Mbp. It is often cross-pollinated crop 35% out crossing. Pigeonpea is mainly grown for its rich edible protein in developing countries like Asia and Africa. India rank first in area (81 %) and production (79 %) at global level covering 4.9 million hectares with 4.22 million tones of production (<http://dpd.gov.in> - 2024). Myanmar stands second position in area (4.47 %) followed by Malawi (2.63 %). India is a key market for pigeon pea in the world due to its high consumption in the country. It is a main protein sources next to chickpea and people consumed as dry dehulled split seed. The people of the vegan consumed pigeonpea as a main source of protein because its seed have 20-22% protein and complement the rice and wheat rations. Pigeonpea also consumed as immature green seed as green vegetable. Vegetable pigeonpea is characterized by large pods, big seed size with easy shelling and good organoleptic properties. Vegetable pigeonpea act as alternative to green peas (*Pisum sativum*) due to its good source of protein, vitamins, minerals and dietary fiber, Vegetable pigeonpea immature seeds are available in the market as canned food in western countries. In southern and eastern Africa, southern America, and the Caribbean islands pigeonpea immature fresh seeds are available as seasonal vegetable. In India in the state of Karnataka, Gujarat and Tamilnadu the

use of vegetable type pigeonpea immature shelled seeds is very accepted. Hence, this study aimed to identify vegetable pigeonpea with large pod, big attractive white seed, good in appearance, sweet in taste, multiple harvesting of pods, easy shelling, good organoleptic properties, long shelf life of green pods and shelled grains in order to obtain consumer acceptance and to get good price in the market.

Materials and Methods

A total of thirty-three vegetable type pigeonpea germplasm accessions (Table 1) were evaluated at ARS Virinjipuram (Latitude: 12° 93'N and Longitude: 79° 01' E) Vellore district Tamilnadu state during Kharif 2022. Each genotype was raised with inter row spacing of 150 cm and within the row plant to plant spacing of 30 cm was adopted. Healthy crop was maintained by following standard agronomic package and practices and plant protection measures. Measurement of morphological and phenological characters for particular traits was documented from five plants in the row. The following phenological characters such as days to 50% flowering, days to maturity and morphological traits such as plant height (cm), no. of branches/plant, no. of pods/plant, pod length (cm), pod width (cm), no. of seeds/pod, hundred seed weight (g) leaf length, leaf width and single plant yield (g) were assessed for all entries. The observed data were subjected to basic statistics and principal component analysis (PCA) using Statistical Tool for

Agricultural Research (STAR) soft ware. Clustering NTSYS software was used for cluster analysis.

Result and Discussion

The basic statistics events i.e., minimum, maximum, mean, standard deviation (sd) and coefficient of variation (CV) for observed characters are exhibited in the Table 2. The days to 50% flowering for the germplasm accessions is minimum of 115 days and maximum of 130 days with mean of 124 days. The number of days for maturity ranged from 180 days to 190 days and mean of 185 days. Days to maturity had observed with as early as of 180 days and as late as of 190 days after sowing with mean of 185 days. The plant height noticed as short as from 126 cm to as height as 277 cm with average height of 197.27 cm. Number of branches in a plant diverged from 2.4 to 9.2 with a mean of 5.65. The number of pods per plant minimum value is 5.0 and maximum value is 699 with mean of 179.73. The mean value for pod length is 8.01 cm and revealed minimum of 5.4 cm and maximum of 10.7 cm. The minimum and maximum value for the pod width is 1.0 cm and 1.9 cm respectively with mean value of 1.33 cm. Number of seeds per pod displayed mean value of 5.71 with minimum value of 4.4 and maximum of 7.4. Hundred seed weight of 33 collected vegetable pigeonpea showed as high as 23.4 g and as low as of 9.7 g with mean of 18.52 g. The leaf length ranged from 4.3 cm to 11.6 cm with mean of 8.72 cm. leaf width varied from 2.0 cm to 7.9 cm with a mean of 3.68. The single plant yield revealed a broad range from 5 g to 439 g with a mean of 152.48 g. The number of pods per plant recorded largest variation with CV of 85.05 goes behind by seed yield per plant (67.21) leaf width (37.69) number of branches (29.4), plant height (21.03). Days to maturity recorded the least variation with CV of 2.33. The highest deviation from the population mean (152.86) was observed in number of pods per plant followed by other traits for instance seed yield per plant (102.48), plant height (41.48), days to maturity (4.32) and days to fifty percent flowering (3.78). Study on skewness clarifies the extent of deviation from a normal distribution and provides insights into the nature of gene actions that influence a particular trait. Kurtosis offers details regarding the flatness or peakedness of a distribution and estimates the number of genes that contribute to the expression of a trait. (Ajay *et al.*, 2016) [1]. While the frequency distribution is asymmetrical, it indicates the distribution is skewed and it designate the trait is controlled by non-additive gene action and may be persuaded by environmental variables. A skewed distribution of certain traits suggests the influence of dominant gene action, with positive skewness indicating complementary gene interactions and negative skewness reflecting duplicate gene interactions [Naveena, *et al.*, 2024] [5]. The frequency distribution of thirty-three vegetable type pigeonpea accessions for twelve traits revealed different distribution patterns as shown on (Fig 1). No one trait had shown normal distribution. The traits number of branches, number of pods per plant, pod width, number of seeds per pod, leaf width and single plant yield were positively skewed denote complementary gene interaction. Negative skewness was detected in days to 50% flowering, days to maturity, plant height; pod length, hundred seed weight and leaf length attest duplicate gene interaction. The identification of leptokurtic and platykurtic curves is based on positive and negative kurtosis values, respectively. Positive kurtosis signifies the presence of gene interactions,

whereas negative kurtosis indicates their absence. Traits exhibiting a leptokurtic distribution are typically regulated by a limited number of genes, while those with a platykurtic distribution are influenced by a larger number of genes. The traits such as number of pods per plant, pod width, number of seeds per pod, 100 seed weight, leaf width and single plant yield were leptokurtic while days to 50% flowering, days to maturity, plant height, number of branches, pod length and leaf length were platykurtic.

1. Principal component analysis

To assess the genetic diversity among various vegetable-type pigeonpea entries, principal component analysis (PCA) was conducted. PCA evaluates the significance and independent effect of specific traits on the overall variance, while the coefficient of proper vectors indicates the extent to which a variable contributes to a principal component (Sanni, *et al* 2012) [7]. The total variance in each principal axis is determined by the number of variables taken into account. Higher coefficients, irrespective of their sign, enhance the ability to effectively differentiate between accessions (Islam, *et al.*, 2016) [4]. In the study PCA has pull out five principal components having eigen value above 1.0 and exhibited total variance of 79.99 (Fig.2, Table 3). The largest contribution to the total variation in the population is from principal component 1 (27.30 %) followed by component 2 (18.50%), component 3 (15.08 %) component 4 (10.68 %) and component 5 (8.42 %). All the collected vegetable type pigeonpea entries were widely scattered across different quarters (Fig 3).

Principal Component 1 has revealed 27.30 % of the total variability make available from pod length (-0.4819), number of seeds per pod (-0.4337) and leaf length (-0.4047). The Principal Component 2 is related number of pod per plant (0.5750), single plant yield (0.5130), days to maturity (-0.3005) and days to 50% flowering (-0.2985) that elucidated 18.50% of total variability. The Principal Component 3 accounted 15.08% of total variability contributed from days to maturity (0.4281), single plant yield (0.4165), 100 seed weight (0.3490) and days to 50% flowering (0.3395). The Principal Component 4 has 10.68% of total variability from Plant height (-0.5266), Leaf length (-0.4648), number of branches (-0.4376). Principal component 5 has put in 8.42% of total variation donated from 100 seed weight (-0.5379), days to 50% flowering (0.4614), leaf width (0.4132) and plant height (0.3947). The five principal components accounted a cumulative variation of 79.99% from the 12 characters as explicated by the first five axes in a genetic diversity analysis of vegetable type pigeonpea.

2. Biplot analysis

A genotype by trait biplot serves as a tool to analyze the relationships between traits and their corresponding genotypes. The cosine of the angle formed between traits illustrates their relationship: A positive correlation was obtained between traits when angle is less than 90° and an angle greater than 90° signifies a negative correlation. An angle of exactly 90° denotes no correlation between traits. (Weikai & Judith 2018) [10].

The biplot ordination indicated positive associations of days to 50% flowering, days to maturity, and hundred seed weight due to acute angle (less than 90°) among them. Similarly, number of pods per plant and single plant yield

showed positive associations and acute angles. In the same way leaf length, plant height, number of seeds per pod, pod length, pod width and leaf width reveal positive associations and acute angles. Number of branches having an obtuse angle (greater than 90°) with leaf width, pod width, pod length, number of seeds per pod, plant height and leaf length and showed negative association with these traits. Number of branches and single plant yield showed zero correlation. Likewise number of pods per plant and number of seeds per pod explained zero correlation due to angle between the traits is 90°.

The angle formed between a genotype and a trait reflects the relative level of the genotype concerning that trait. An acute angle, measuring less than 90°, specifies to the genotype is exceeding average for the trait, while an obtuse angle, above 90°, signifies that the genotype is under average. A right angle, measuring exactly 90°, denotes that genotype is average to the trait. Vectors lengthen from the origin to each trait represent the degree of variation associated with that trait (Shushay, *et al.*, 2023) [9]. A greater vector length corresponds to increased variation, whereas a shorter length indicates reduced variation. In this study, the number of pods per plant, single plant yield, pod length, and leaf length were thoroughly examined, revealing a significant degree of variability. (Fig 3).

The cluster formation using NTSYs software reveals the dendrogram drawn out of UPGMA give a picture of two major clusters A and B (Rana & Bhat, 2005) [6]. Major cluster A had no sub cluster and had one genotype ICP15269 stand for lowest hundred seed weight. Major

clusters B containing 32 genotypes. Cluster B is again subdivided into two sub clusters, b1 and b2, of which b1 had 28 genotypes and b2 had 2 genotypes. In b2 sub cluster ICP15195 and ICP13107 are placed which has highest pod number among 33 genotypes. In b1 sub cluster ICP11441 and ICP 8000 formed separate group which has highest leaf width among all genotype analyzed. The genotypes ICP14085, ICP13831 and ICP13828 formed one group and recorded highest number of seed per pod. Similarly the genotypes ICP13524 and ICP13526 formed one group and recorded lowest number of seed per pod. More closely associated cultivars are recognized by cluster analysis.

Conclusion

PCA analysis revealed pod length, number of seeds per pod and leaf length, number of branches and plant height contributed most to the variation in principal component. Thus, the results will be exploited to identify parents for improving various morphological traits analyzed in this study. Cluster analysis revealed to facilitate hybridization of vegetable type pigeonpea among distant clusters could lead to higher heterosis levels. A crossing of pigeon peas ICP15269 with 12746 and Kaadaikannu will produce higher heterosis in F₁ and better segregation in the F₂ generation related to 100 seed weight. Making crossing between high number of pods per plant genotypes ICP15195, ICP13107 with highest hundred seed weight genotypes ICP12746 and Kaadai kannu will offer superior segregants for high yield and high hundred seed weight with big seed size of consumer attraction.

Table 1: Germplasm used for diversity analysis

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	ICP15195	10	ICP13414	19	ICP7035	28	Varusanadu
2	ICP14085	11	ICP13413	20	ICP15222	29	Vathalmalai
3	ICP13831	12	ICP13107	21	ICP15269	30	TKK1
4	ICP13828	13	ICP12807	22	BRG1	31	TKK2
5	ICP13599	14	ICP12746	23	BRG2	32	TKK3
6	ICP13526	15	ICP12184	24	BRG3	33	Kaadaikannu
7	ICP13524	16	ICP11441	25	BSR1		
8	ICP13442	17	ICP8000	26	Gudalore		
9	ICP13438	18	ICP7088	27	KPN		

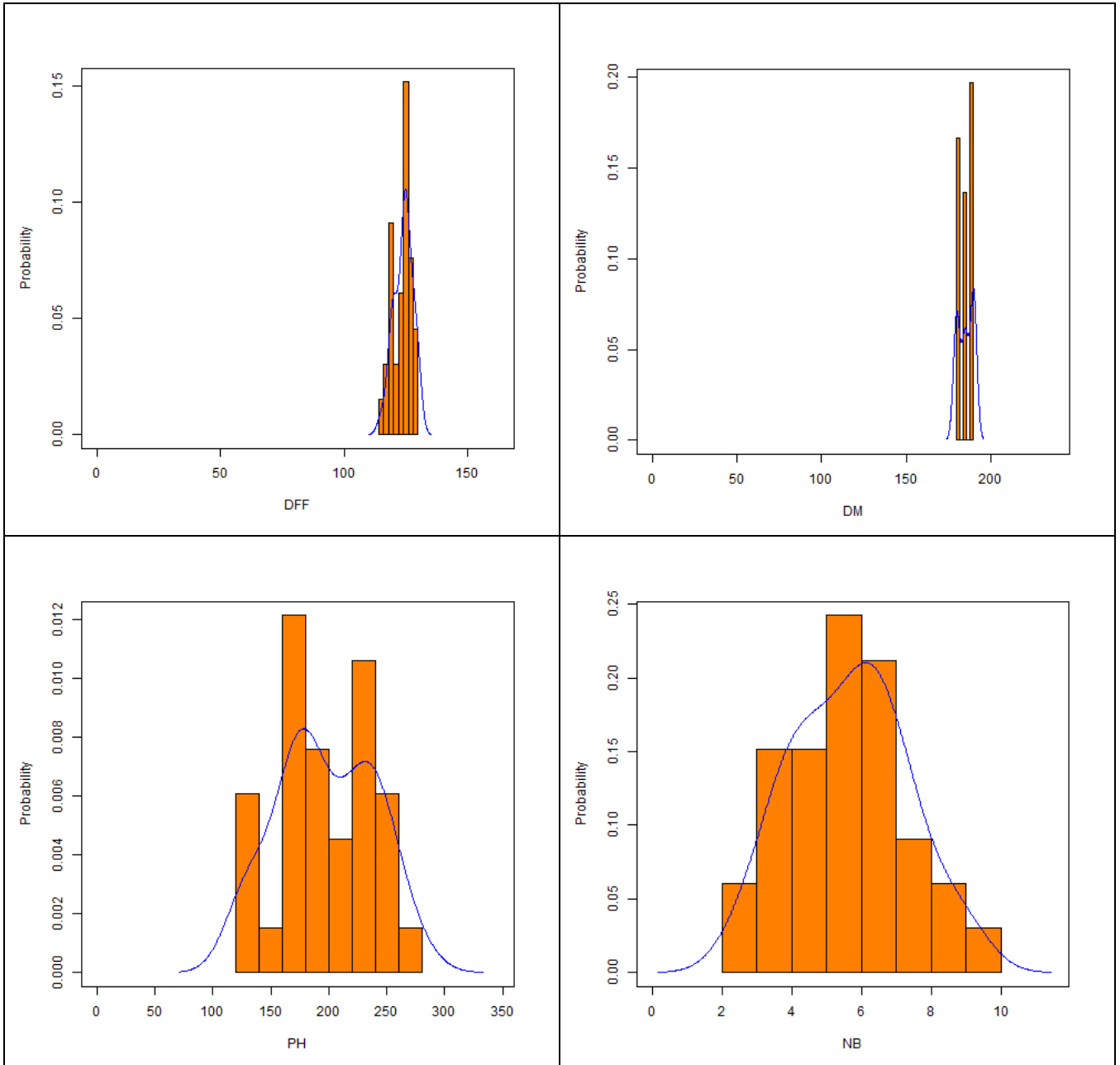
Table 2: Descriptive analysis for 12 traits of 33 vegetable type pigeonpea

Traits	Min	Max	Mean	Std Dev.	CV	Skewness	Kurtosis
DFF	115	130	124	3.78	3.05	-0.35	-0.37
DM	180	190	185	4.32	2.33	-0.12	-1.68
PH	126	277	197.27	41.48	21.03	-0.03	-0.92
NB	2.4	9.2	5.65	1.66	29.4	0.1	-0.51
NPP	5	699	179.73	152.86	85.05	2.07	5.4
PL	5.4	10.7	8.01	1.67	20.89	-0.04	-1.37
PW	1	1.9	1.33	0.19	14.25	0.76	1.14
NSP	4.4	7.4	5.71	0.7	12.26	0.48	0.7
X100SW	9.7	23.4	18.52	2.57	13.87	-1.14	3.38
LL	4.3	11.6	8.72	1.9	21.76	-0.54	-0.61
LW	2	7.9	3.68	1.39	37.69	1.44	2.8
SPY	5	439	152.48	102.48	67.21	0.79	0.61

Table 3: Five principal components and their eigen value, percent of total variation and component matrix

Principal Components	PC1	PC2	PC3	PC4	PC5
EigenValues	3.28	2.22	1.81	1.28	1.01
% of Variance	0.2730	0.1850	0.1508	0.1068	0.0842
Cumulative %	0.2730	0.4581	0.6089	0.7157	0.7999
Component matrix					
Days to 50 % Flowering	0.1940	-0.2985	0.3395	-0.0468	0.4614

Days to Maturity	0.1006	-0.3005	0.4281	-0.0838	0.1445
Plant Height	-0.3434	0.0788	-0.0563	-0.5266	0.3947
Number of Branches	0.3542	0.0406	0.2787	-0.4376	0.0475
Number of Pods per Plant	0.0044	0.5750	0.2693	0.2130	0.2098
Pod Length	-0.4819	-0.1242	0.0876	0.0418	0.0880
Pod Width	-0.2132	-0.1254	0.0876	0.1958	-0.0210
Number of Seeds per Pod	-0.4337	-0.0448	0.1093	0.0387	-0.3084
100 Seed Weight	-0.0463	-0.2827	0.3490	-0.1072	-0.5379
Leaf length	-0.4047	0.1695	0.0464	-0.4648	-0.0102
Leaf Width	-0.2725	-0.2776	-0.0744	0.4175	0.4132
Single Plant Yield	-0.0544	0.5130	0.4165	0.1823	-0.0267



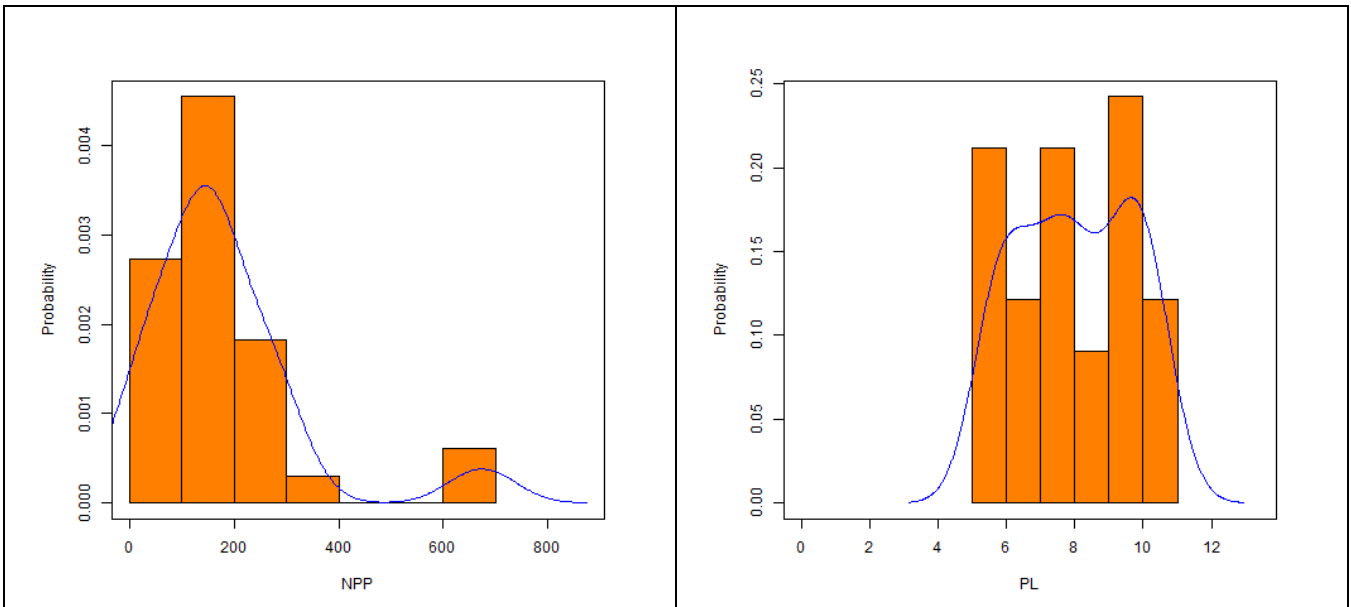
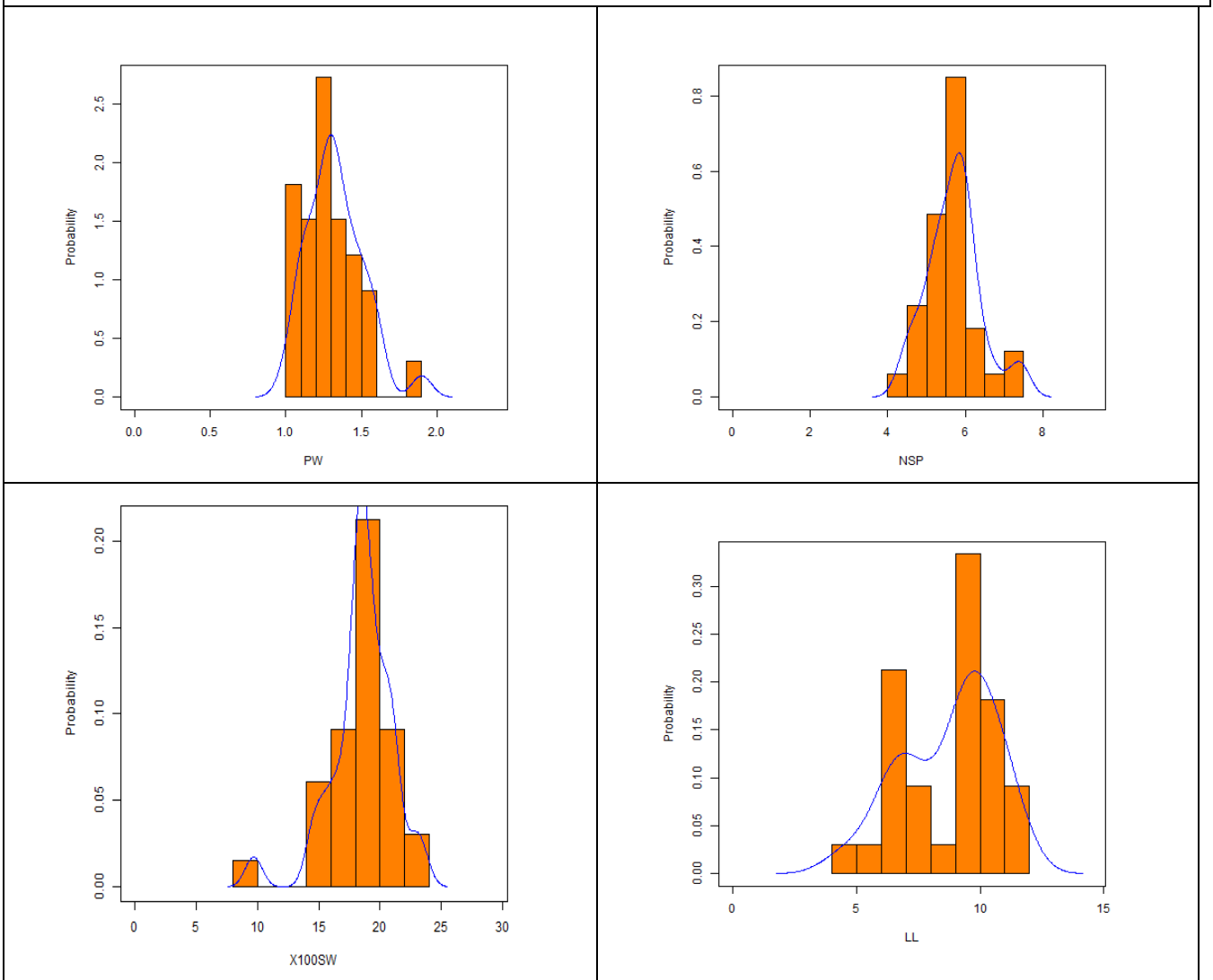


Fig 1: The frequency distribution of thirty-three vegetable type pigeonpea accessions for twelve traits



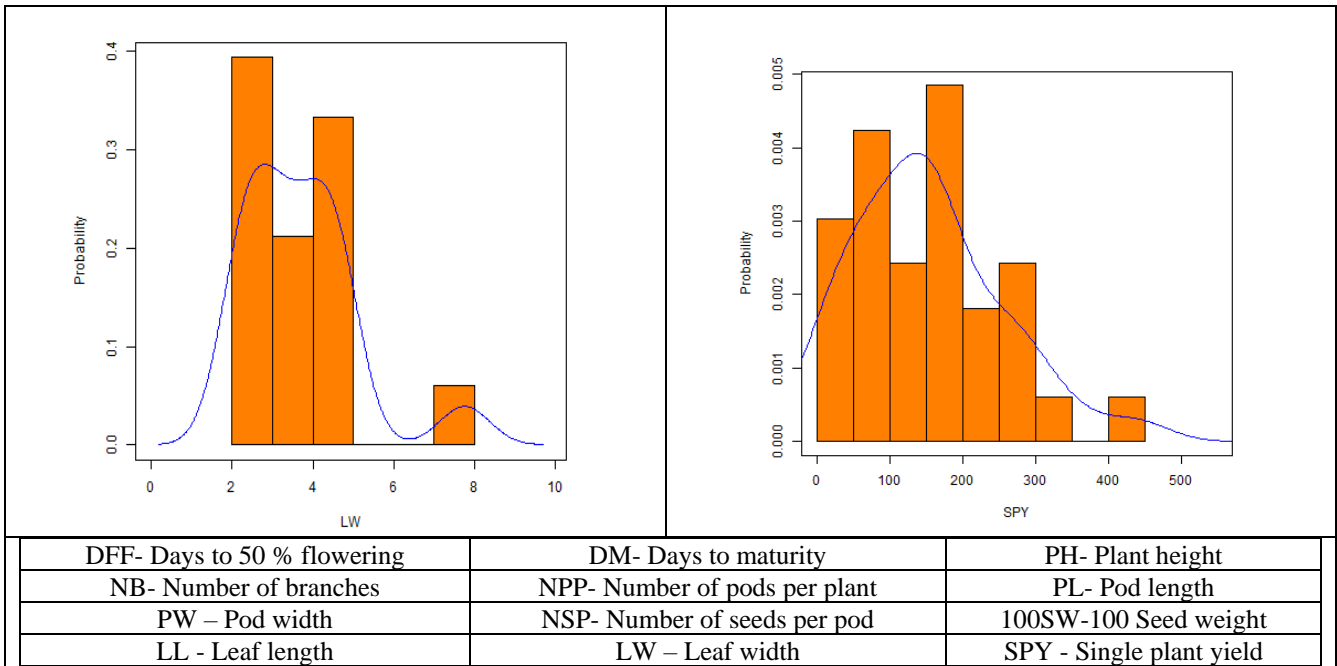


Fig 2: Scree plot diagram of eign values constructed on 12 traits recorded in 33 vegetable type pigeonpea germplasm.

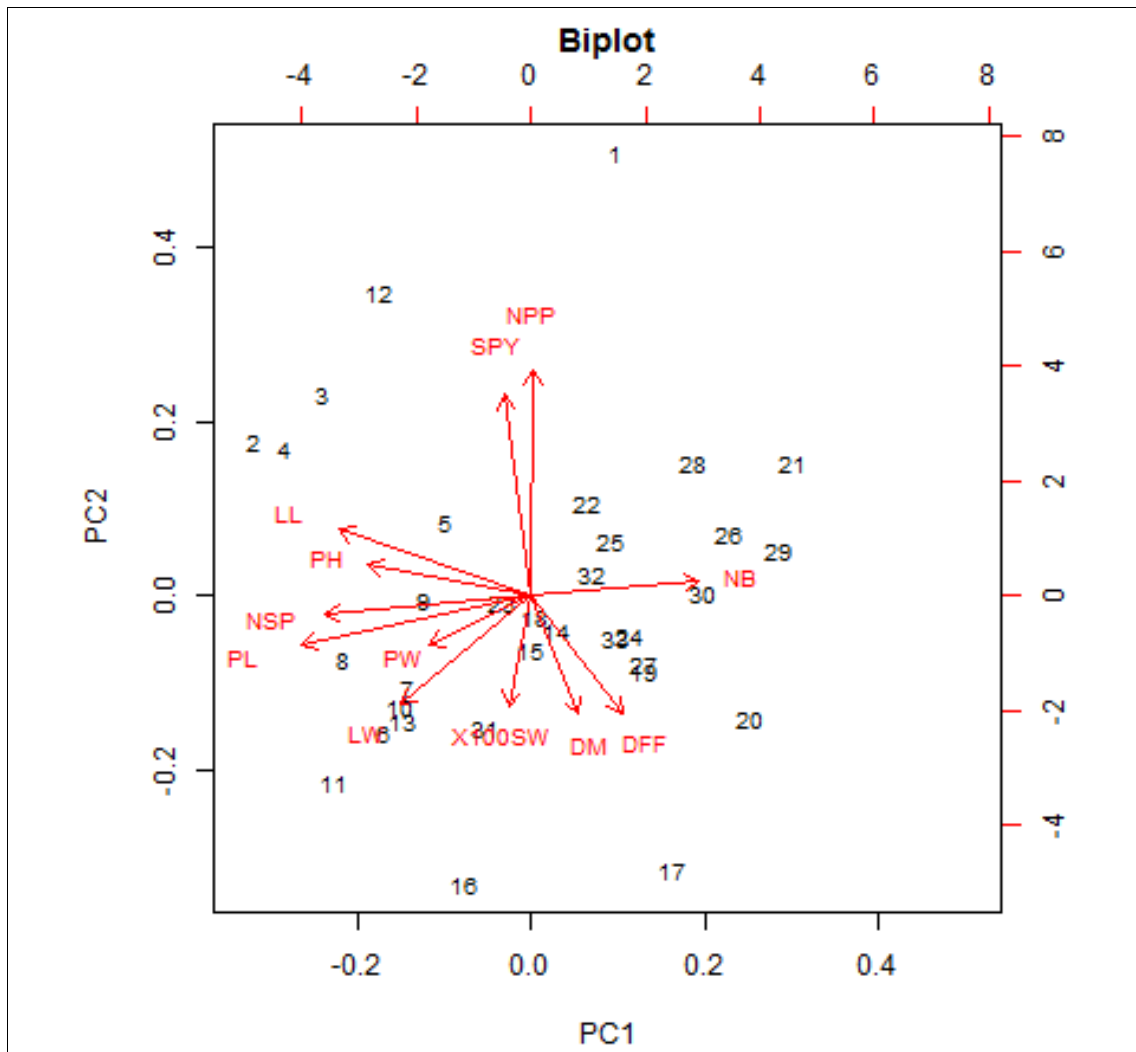


Fig 3: Biplot of trait relationship of 33 vegetable type pigeonpea

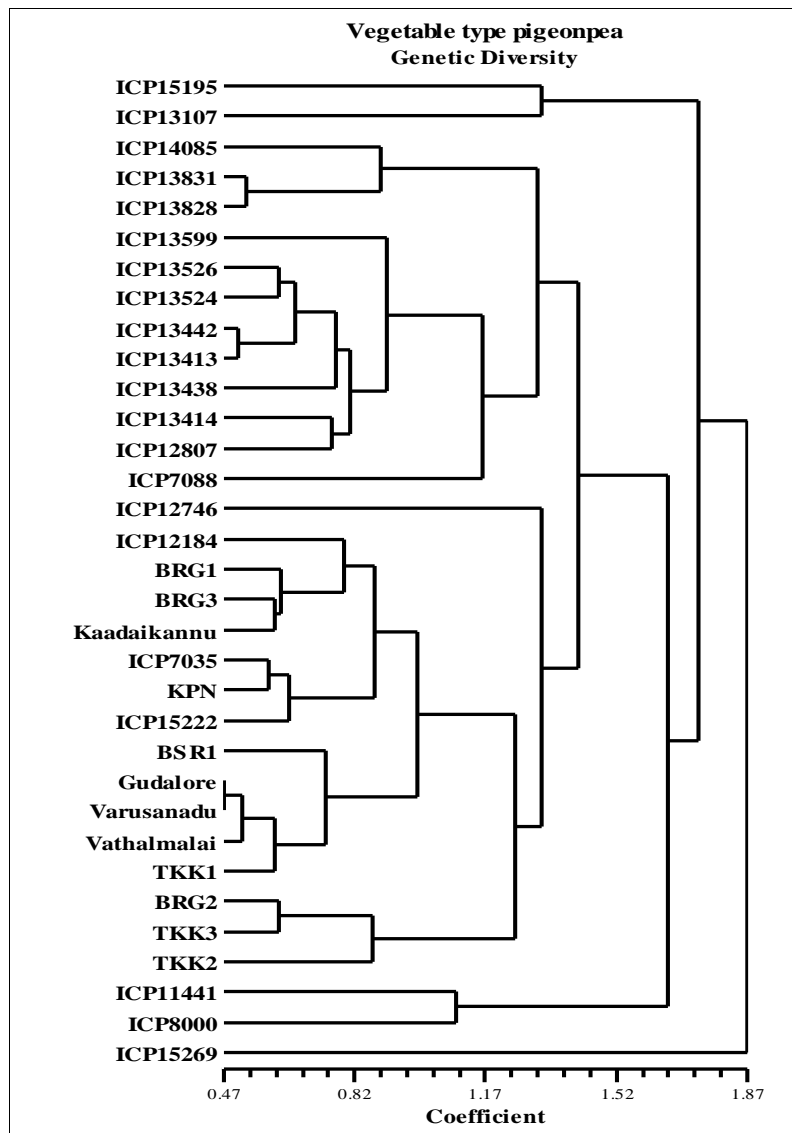


Fig 4: UPGMA cluster analysis-based dendrogram depicting genetic relationships among 33 vegetable type pigeonpea.

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