

Agro-morphological characterization of 100 pigeonpea [*Cajanus cajan* (L.) Millsp.] accessions of Indian National Gene Bank and assessment of diversity present for efficient utilization in pigeonpea improvement programs

Anchal Mishra

mishraanchal85@gmail.com

Indira Gandhi Krishi Vishwavidyalaya

Padmavati Gore

ICAR- National Bureau of Plant Genetic Resources

Mayuri Sahu

Indira Gandhi Krishi Vishwavidyalaya

Research Article

Keywords: DUS characterization, Cluster analysis, Diversity, Germplasm, Pigeonpea

Posted Date: June 19th, 2024

DOI: <https://doi.org/10.21203/rs.3.rs-4516057/v1>

License: © ⓘ This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Additional Declarations: No competing interests reported.

Agro-morphological characterization of 100 pigeonpea [*Cajanus cajan* (L.) Millsp.] accessions of Indian National Gene Bank and assessment of diversity present for efficient utilization in pigeonpea improvement programs.

Anchal Mishra¹, Padmavati Gore² and Mayuri Sahu³

^{1,3}*Department Of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgrah, India. 492012.*

²*ICAR- National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi, India. 110012*

Abstract:

Altogether 100 genotypes of pigeonpea including 6 checks viz; KRG- 33, PT-0012, UPAS-120, CORG-9701, BDN-716, C.G ARHAR-2 were evaluated in Augmented Block Design. Characterization and grouping of genotypes for yield specific traits were carried out with the help of descriptor of pigeonpea suggested by PPV&FRA. The knowledge of nature and extent of genetic variation are available in the pigeonpea genotypes, collection, conservation and characterization of genotype is the backbone of any crop improvement program which in turn depends on the extent of genetic diversity in gene pool. Diversity in plant genotypes provides opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both preferred traits viz. earliness and yield attributing traits. In the present study assessment of genetic diversity is done with the help of D² Analysis. 100 accessions were grouped into 6 clusters. The intra cluster distance varied from 0 to 1713.60 and the inter cluster varied from 2235.09 to 9750.48 it clearly demonstrated considerable amount of genetic divergence present in material study.

Keywords : DUS characterization, Cluster analysis, Diversity, Germplasm, Pigeonpea.

Email Address of Corresponding Author – mishraanchal85@gmail.com

Introduction:

As a highly proteinaceous crop, pigeonpea has established its prominence across the globe. Its seed can be cooked as 'dal' and in many other forms it is consumed in different parts of world. It has 62.78 g of Carbohydrate, fat content is only 1.49 g and protein content is 21.7g/100. Generally, the amount of crude protein ranges from 18-29 % which is three times the value of protein content found in cereals (Techale *et al.* 2013). It is a valuable source of vegetarian protein, especially in underdeveloped nations where the bulk of people rely on low-cost vegetarian options. In Indian scenario, Pigeonpea is second most prominent pulse crop after Chickpea (Vijayalakshmi *et al.* 2013). India is the largest pigeon pea producer across the globe, accounting for 90 per cent of the world production (Rangare *et al.* 2013). The world's largest pigeonpea producing areas include India, Eastern Africa, Central and South America, the Caribbean, and the West Indies. (Vijayalakshmi *et al.* 2013).

The Pigeonpea germplasm provide information on the nature and degree of genetic diversity, which is much required for any plant breeding project. Germplasm handling activities like collection, conservation and characterization of accessions is the backbone of any crop improvement program because any such program depends on the amount of variability and diversity present in gene pool. Diversity in plant genotypes allows plant breeders to create new and improved cultivars with desired traits. From the very beginning of agriculture, natural genetic variability has been exploited within crop species to meet subsistence food requirements, and now it is being focused on surplus food production in order to fulfill the requirements of increasing populations. So, the current study is aimed to describe and group one hundred genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp] in order to isolate a suitable line that might be employed as a parent in future breeding programs.

Material and Method :

100 genotypes (Table 1.1) of pigeonpea including 6 checks viz; KRG- 33, PT-0012, UPAS-120, CORG-9701, BDN-716, C.G. ARHAR-2 were evaluated in Augmented Block Design during *kharif* season 2022-23 at experimental area of pigeonpea, IGKV Research farm and specific traits were again recorded and verified in next *kharif* 2023-24 in the same Augmented block design. 11 morphological traits were recorded in both seasons along with 9 biometrical traits for the assessment of variability and diversity present in germplasm.

Table 1.1 List of 100 Accessions which were used in experiment.

S.No.	Accessions	S.No.	Accessions	S.No.	Accessions	S.No.	Accessions	S.No.	Accessions
1	KRG-33	21	IC-15707	41	IC-22511	61	IC-28194	81	IC-261382
2	PT-0012	22	IC-16206	42	IC-22531	62	IC-28195	82	IC-267493
3	UPAS-120	23	IC-25053	43	IC-22532	63	IC-28196	83	IC-268203
4	CORG-9701	24	IC-28193	44	IC-22533	64	IC-28198	84	IC-329116
5	BDN-716	25	EC-843234	45	IC-22534	65	IC-28199	85	IC-323307
6	C.G. ARHAR-2	26	EC-843247	46	IC-22535	66	IC-245477	86	IC-347516
7	RPS 2015-49	27	EC-843254	47	IC-22536	67	IC-245478	87	IC-349776
8	RPS 2015-51	28	EC-843277	48	IC-22555	68	IC-245479	88	IC-385887
9	RPS 2015-4	29	EC-843278	49	IC-23672	69	IC-245482	89	IC-393694
10	RPS 2015-40	30	EC-8362	50	IC-23679	70	IC-245519	90	IC-424779
11	RPS 2015-1	31	IC-11011	51	IC-23683	71	IC-245520	91	IC-468174
12	RPS 2014-32	32	IC-14992	52	IC-23685	72	IC-245522	92	IC-468334
13	RPS 2014-34	33	IC-15710	53	IC-25050	73	IC-245525	93	IC-468590
14	RPS 2014-6	34	IC-16194	54	IC-25054	74	IC-245534	94	IC-468591
15	RPS 2014-21	35	IC-16195	55	IC-25055	75	IC-245539	95	IC-521410
16	RPS 2014-19	36	IC-16203	56	IC-25056	76	IC-245550	96	IC-523150
17	RP-1	37	IC-16210	57	IC-25059	77	IC-245560	97	IC-634397
18	IPAD-5	38	IC-22501	58	IC-25060	78	IC-259318	98	IC-634438
19	EC-14995	39	IC-22502	59	IC-26114	79	IC-259319	99	C.G. ARHAR-1
20	IC-15706	40	IC-22510	60	IC-28192	80	IC-261355	100	Rajeevlochan

Table 1.2 Morphological traits which were defined is defined by PPV&FRA.

S.No.	Trait	Category	Notation	Stage for observation
1	Epicotyl Anthocyani colouration	Present	1	At seedling stage when primary leaves are completely unfolded.
		Absent	9	

2	Growth Habit	Determinate	1	At full flowering stage.
		Indeterminate	9	
3	Stem Anthocyanin colour	Absent	1	At full flowering stage.
		Present	9	
4	Leaflet shape	Oblong	1	At full flowering stage.
		Obovate	2	
		Lanceolate	3	
5.	Pod pubescence	Absent	1	At green pod stage.
		Present	9	
6	Base colour of petal	Yellow	3	At full flowering stage.
		Red	9	
		Purple	7	
7	Pattern of streaks on petal	Absent	1	At full flowering stage.
		Sparse	3	
		Medium	5	
		Dense	7	
8	Pod colour	Green	1	Observed at full podding stage
		Green with brown streaks	3	
		Green with purple streaks	5	
		Purple	7	
9	Pod constriction	Prominent	1	Observed at green pod stage
		Slight	9	
10	Seed shape	Oval	3	1 month after harvest
		Elongate	7	
		Globular	5	
11	Seed colour	Cream	1	1 month after harvest
		Grey	4	
		Brown	2	
		Dark Brown	3	
		Purple	5	

Along with it 9 biometrical traits were included for diversity in yield aspect which are- 1.Plant height, 2. Number of Primary branches, 3. Number of pods/plant, 4. Pod length (cm), 5. Seeds/pod, 6. Days to first flowering ,7. Days to fifty %flowering, 8. Days to maturity. 9. 100 seed weight.

Result And Discussion

1. Morphological Characterization

1. Epicotyl Anthocyanin Pigmentation:

The 100 genotypes were classified under this trait out of which 96% were having anthocyanin pigmentation and rest 4% were devoid of it, which indicates the anthocyanin colouration of hypocotyls can be seen in most of the pigeonpea accessions studied. Muniswamy *et al.*(2014) and Metkar and Gawande (2014) Reported that the presence anthocyanin colouration is more prominent in pigeonpea. This trait will be useful in breeding programs for differentiation of genotypes and also in maintenance breeding [Fig. 1(a), 1(b) and 1(c)]

2. Growth Habit:

For growth habit, 23 out of 100 genotypes were found to be determinate and rest 77 were found to be of indeterminate growth habit [Fig. 2(a), 2(b) and 2(c)]. Gumber and Singh (1997) have confirmed that the presence of two genes Dt₁ and Dt₂ controlling growth habit in pigeonpea and indeterminate growth habit is found to be dominant

over determinate growth habit, Similar results were reported earlier by Ranjani and Jaymani (2021), Padma Priya *et al.* (2022) and Upadhyaya *et al.* (2007)

3. Stem Anthocyanin Pigmentation:

When pigmentation in stem was recorded, 22 out of 100 were found to be pigmented and 78 were having clear green stem [Fig. 3(a), 3(b) and 3(c)] Naphade *et al.* (1980) and Singh and Srivastava (1981) reported monogenic recessive inheritance of green stem colour with dominance of purple stem colour. Vanniarajan *et al.* (2023), Sujit *et al.* (2022) and Ranjani and Jaymani (2021) reported similar result.

4. Leaflet shape:

D'cruz *et al.* (1973) reported three allelic genes Llt, lltr, llt are involved in lanceolate, ovate and obovate leaflet shapes. Out of 100 genotypes 84 were oblong, 8 were obovate and rest 8 genotypes were lanceolate. [Fig. 4(a), 4(b), 4(c) and 4(d)]. Leaf characteristics are useful for the identification of varieties and categorizing genotypes into different groups. Ranjani and Jayamani (2021) and Padma Priya *et al.* (2022) found oblong leaflet shape to be predominant.

5. Base Petal Colour:

This trait is important in entomological point of view as it has been found that *Helicoverpa armigera* laid more eggs on genotypes with yellow base petal than those with red base petal (Kumari *et al.* 2006 and Lakshmipathi, 2000) When colour of base petal was observed at full flowering stage, 11 were found to be of red coloured and 89 were of yellow base petal. [Fig. 5(a), 5(b), 5(c)]. Similar results were obtained by Vanniarajan *et al.* (2023).

6. Pattern of streaks on petal:

At full flowering stage, pattern of streaks was observed and 68 out of 100 were found to be sparse streaked, 15 medium, 13 dense and in only 4, no streaks were recorded. [Fig. 6(a), 6(b) and 6(c)]

7. Pod Colour:

Singh *et al.* (1994) found purple pod colour to be controlled by dominant genes but codominance gene actions were found predominant in population giving green pod with brown streaks. Machanwar and Bantewad (2019) reported green coloured pod brown streaks showed less infestation of *helicoverpa*. When at green pod stage, colour was observed, 77 out of 100 were found to be green with brown streaks, 13 were found to green with purple streaks, 6 were pure green without any streaks and 4 were pure purple coloured. [Fig. 7(a), 7(b) and 7(c)]

8. Pod Constriction:

Out of 100, 25 were found to be with prominent pod constriction and rest 75 were having slight constriction. [Fig. 8(a), 8(b) and 8(c)]

9. Pod Pubescence:

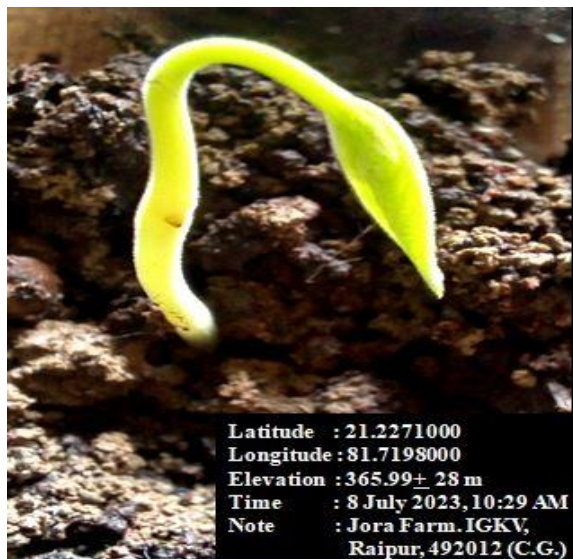
Aruna *et al.* (2005) reported association of this trait with resistance to *Helicoverpa armigera*. At physiological maturity (Raw pod stage), Pod's surface is observed for presence of pubescence was found in 7 accessions which are - RP-1, EC-14995, IC-16206, IC-22533, IC-16194, IC-245478, IC-245525.

10. Seed shape:

After one month of harvesting seed shape was recorded for which 87 accessions out of 100 came out to be oval shaped, 10 were globular and rest 3 were found to be of elongate shape.

11. Seed Colour:

71 out of 100 genotypes were having brown seeds, 13 grey, 6 cream coloured, 6 dark brown and 4 were found to be purple seeded.



ANTHOCYANIN PIGMENTATION ABSENT IN EPICOTYL

Fig. 1(a)



ANTHOCYANIN PIGMENTATION PRESENT IN EPICOTYL

Fig. 1(b)

Epicotyl Anthocyanin Pigmentation

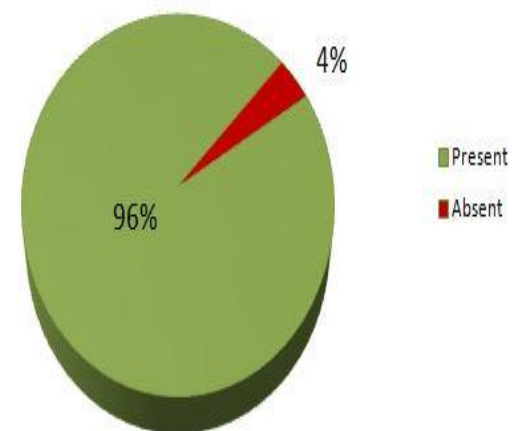


Fig. 1(c)



Determinate type

Fig. 2(a)



Indeterminate Type

Fig. 2(b)

Plant Growth Habit

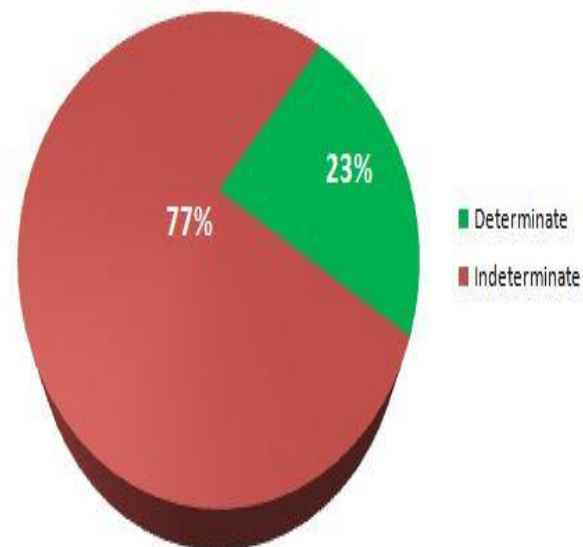


Fig. 2(c)



GREEN STEM COLOUR

Fig. 3(a)



PURPLE STEM COLOUR

Fig. 3(b)

Stem Anthocyanin Pigmentation

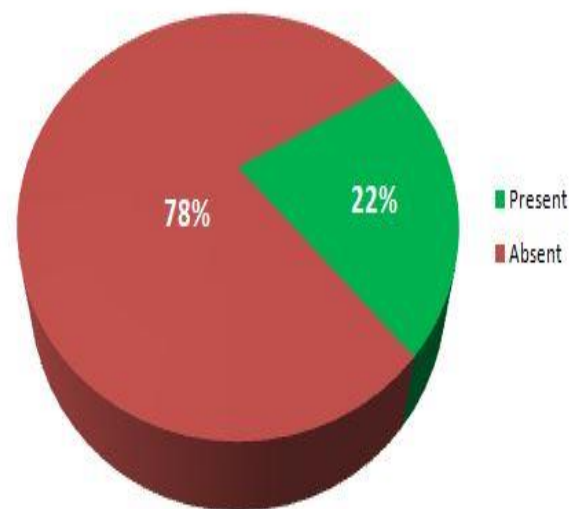


Fig. 3(c)



Lanceolate

Fig. 4(a)



Oblong

Fig. 4(b)



Obovate

Fig. 4(c)

Leaflet shape

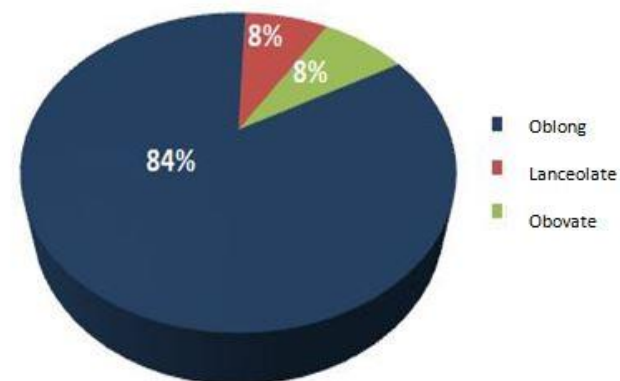


Fig. 4(d)

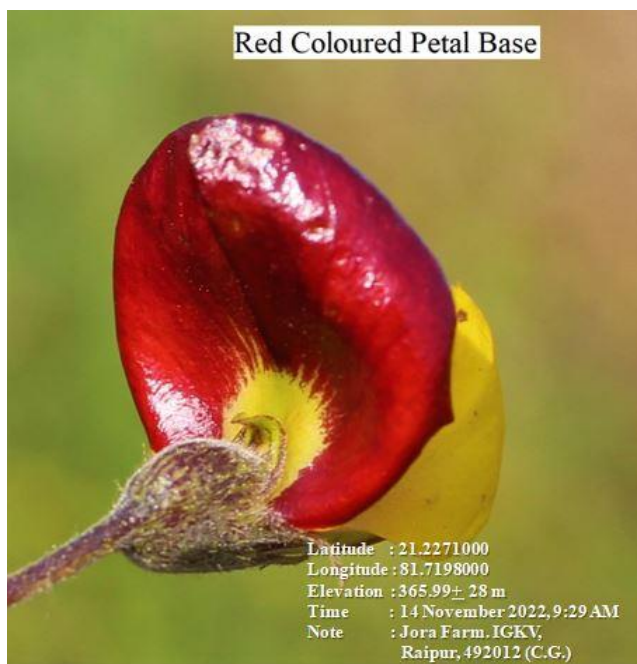


Fig. 5(a)



Fig. 5(b)

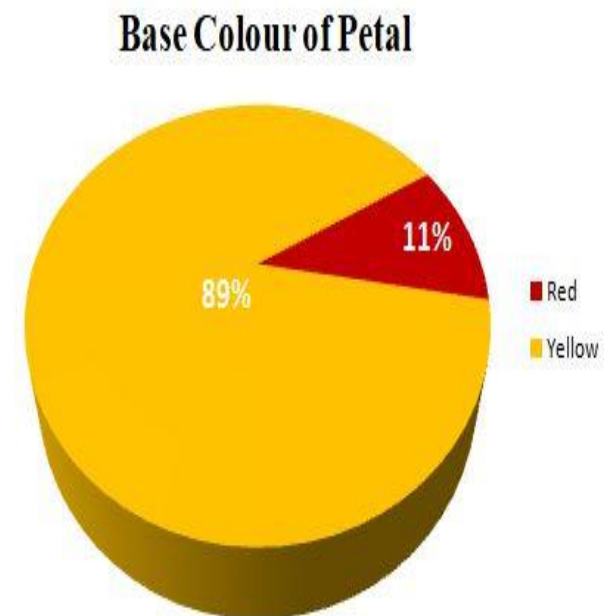


Fig. 5(c)



Streaks Absent

Fig. 6(a)



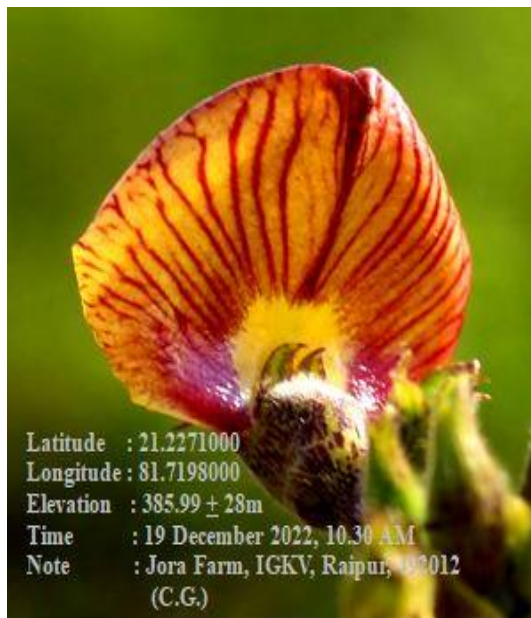
Sparse

Fig. 6(b)



Medium

Fig. 6(c)



Dense Streaks

Fig. 6(d)

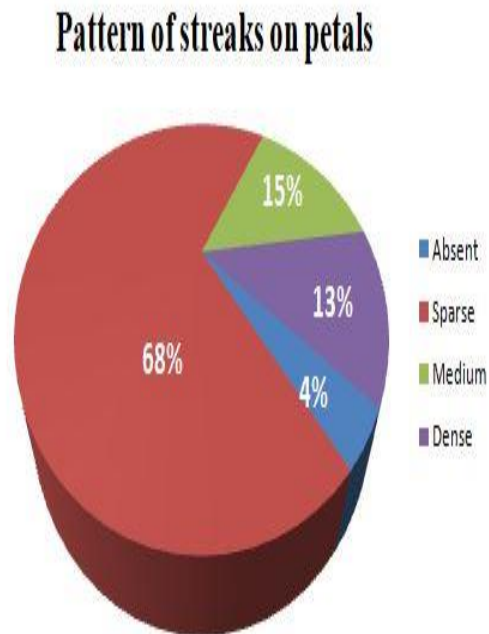


Fig. 6(e)



Green Pod

Fig. 7(a)



Green Pod with Brown Streak

Fig. 7(b)



Green Pod with Purple Streak

Fig. 7(c)



Purple Pod

Fig. 7(d)

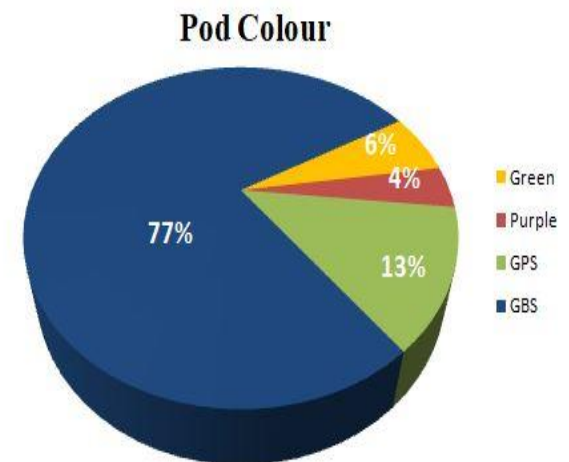
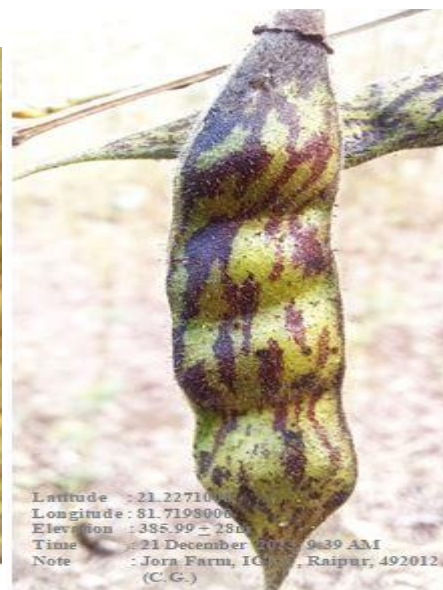


Fig.(7e)



Prominent

Fig. 8(a)



Slight Constriction

Fig. 8(b)

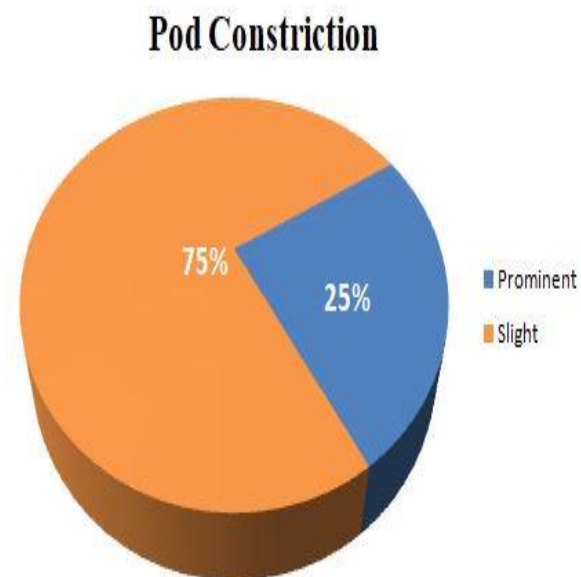


Fig. 8(c)



Presence of Pod Pubescence

Fig. 9(a)

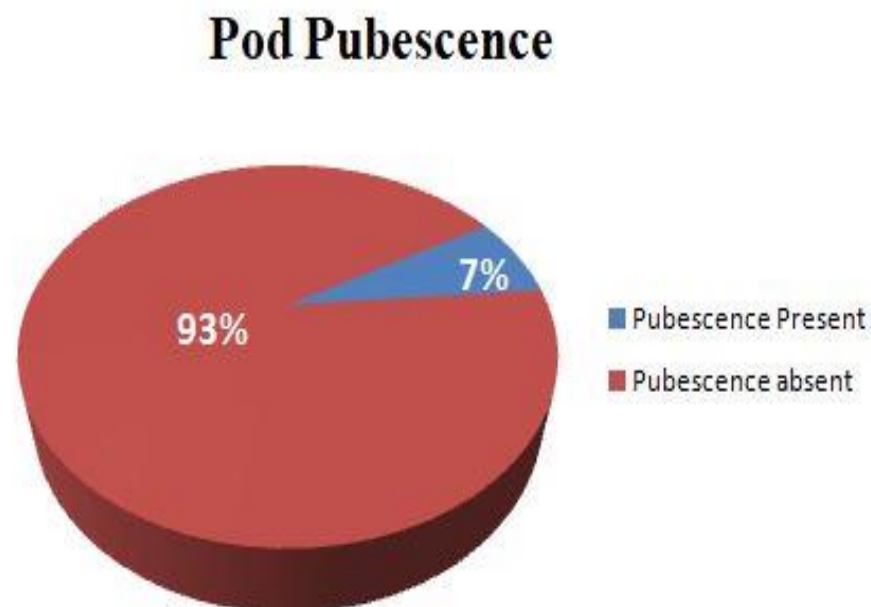
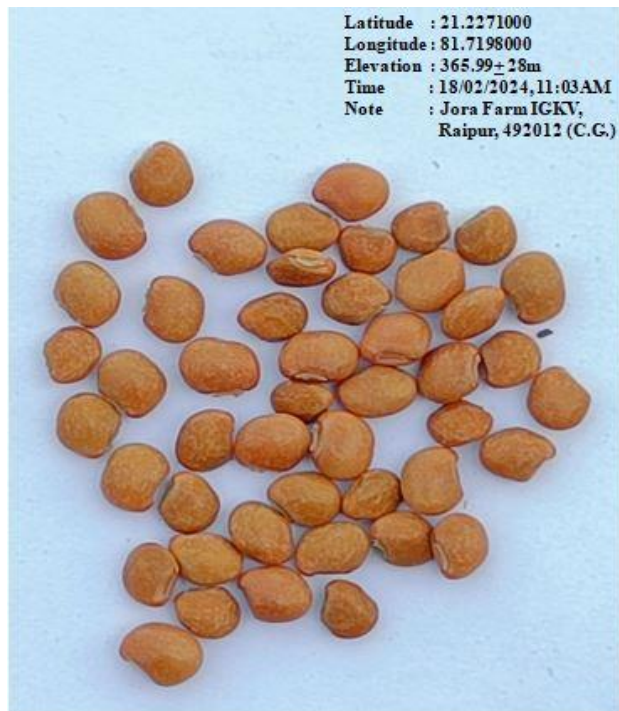
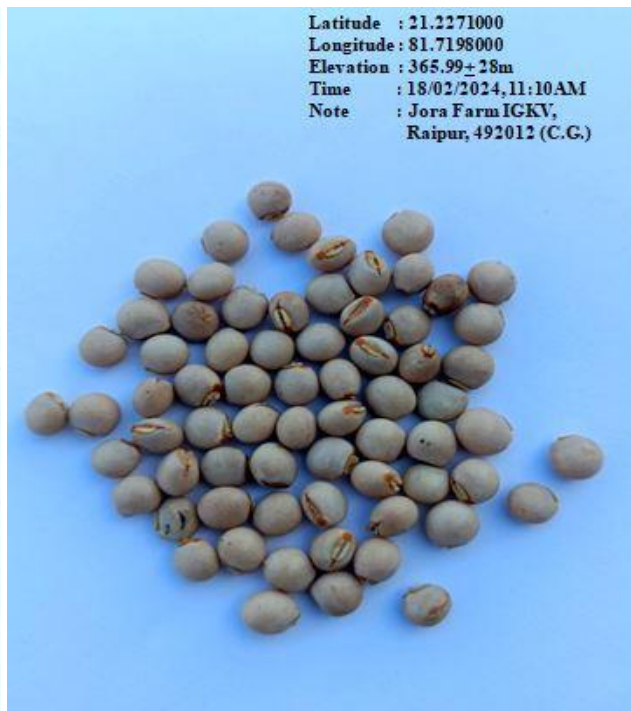


Fig. 9(b)



Elongate Seed

Fig. 10(a)



Globular Seed

Fig. 10(b)



Oval Seed

Fig. 10(c)

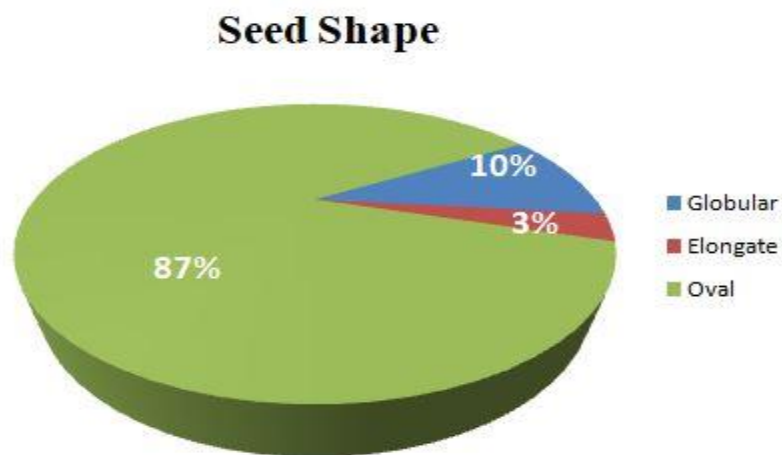


Fig. 10 (d)



Cream coloured Seed

Fig. 11(a)



Brown coloured Seed

Fig. 11(b)



Dark Brown coloured Seed

Fig. 11(c)



Purple coloured Seed

Fig. 11 (d)

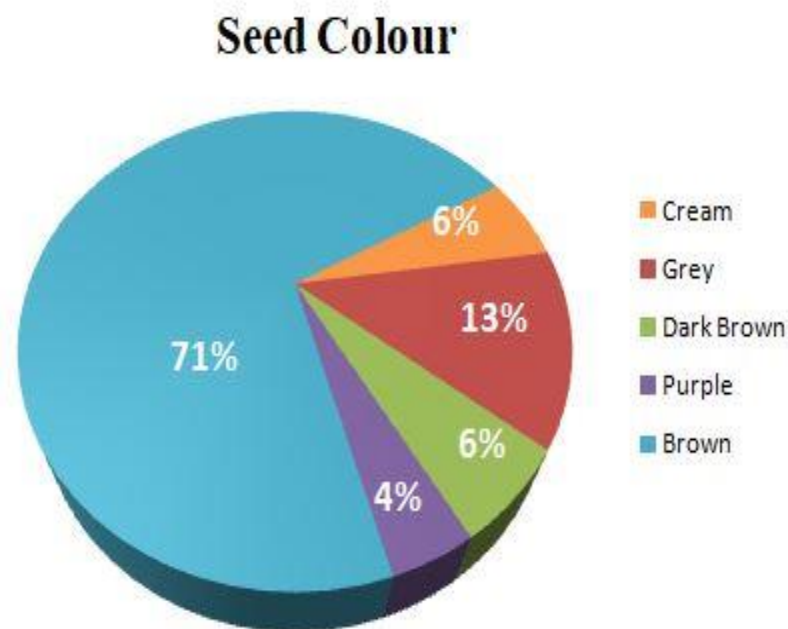


Fig. 11(e)

Table 1.3 Categorization of accessions into different trait.

S.No.	Trait	Category	Notation	Frequency (%)	Name of accessions
1	Epicotyl anthocyanin pigmentation	Present	1	4%	IPAD-5, IC-22533, IC-25056 and IC-245539
		Absent	9	96%	Rest all 96 out of 100 were found to lack epicotyl pigmentation.
2	Plant growth habit	Determinate	1	23%	UPAS- 120, RPS 2015-4, RPS 2014-32, RPS 2014-34, EC-14995, IC-15706, IC-15707, IC-28193, IC-16210, IC-22531, IC-22535, IC-23685, IC-25050, IC-25055, IC-25060, IC-28194, IC- 28196, IC-245479, IC-245519, IC-245534, IC-468174, IC-523150, IC-634397.
		Indeterminate	9	77%	Rest all 77 out of 100 were found to be of indeterminate type.
3	Stem anthocyanin colour	Present	9	22%	RPS 2014-32, RPS 2014-19, IC-16206, EC-843278, IC-15710, IC-16195, IC-25050, IC-25055, IC-25056, IC-25059, IC-26114, IC-28194, IC-28196, IC-245522, IC-245534, IC-268203, IC-329116, IC-424779, IC-468591.
		Absent	1	78%	IC-521410, C.G. Arhar-1, Rajeevlochan.
4	Leaflet shape	Lanceolate	3	8%	Rests 78 out of 100 were found to have clear green stem.
		Obovate	2	8%	RPS 2014-34, RPS 2014-19, IC-15706, IC-23672, IC-23679, IC-28194, IC-245525, IC-329116
		Oblong	1	84%	IC-634397, IC-259319, IC-245520, IC-28192, IC-22531, IC-14992, EC-843278, EC-843247
		Red	9	11%	Rest all 84 out of 100 were found to have oblong leaflet
5	Base Petal Colour	Red	9	11%	RPS 2015-51, RPS 2015-4, IC-16195, IC-16210, IC-23683, IC-25053, EC-843254, IC-22510, IC-22534, IC-22535 and IC-25059.
		Yellow	3	89%	Rest all 89 out of 100 genotypes were found to have Yellow colored base petal.
6	Pattern of streaks on petals	Absent	1	4%	BDN-716, RPS 2015-51, EC-843278 and IC- 16210
		Medium	5	15%	IC- 11011, IC-22510, IC-22533, IC-22534, IC-22535, IC-28194, IC-28196, IC-245522, IC-245534, IC-268203, IC-329116
		Dense	7	13%	IC-634397, IC-16210, IC-14992, RPS 2014-19, IC-16206, EC-843278, IC-15710, IC-16195, IC-25050, IC-25055, IC-25056, IC-25059, IC-26114,
		Sparse	3	68%	Rest all 68 were found to be Sparse.
7	Pod Colour	Green	1	6%	EC-14995, IC-28193, IC-22533, IC-23685, IC-634438, IC-523150
		Green with brown streaks	3	77%	Rest all 77 were found to have green pod with brown streaks
		Green with purple streaks	5	13%	RPS 2014-34, RPS 2014-21, IC-15706, IC-15707, IC-16206, EC-843247, EC-843254, EC-8362, IC-11011, IC-14992, IC-15710, IC-16194, IC-16210
		Purple	7	4%	IC-22501, IC-23683, IC-245478, IC-245479
		Prominent	1	25%	RPS 2014-19, IC-16206, EC-843278, IC-15710, IC-16195, IC-25050, IC-25055, IC-22531, IC-14992, EC-843279, EC-843247, IC-22531, IC-14992, EC-843278, EC-843247 IC-25050, IC-25055, IC-25056, IC-25059, IC-26114, IC-28194, IC-28196, IC-245522, IC-245534, IC-268203
8.	Pod Constriction	Slight	9	75%	Rest all were having slight constriction
		Present	1	7%	RP-1, EC-14995, .IC-16206, IC-22533, IC-16194, IC-245478, IC-245525
9	Pod Pubescence	Absent	9	93%	Rest all were not having any pod pubescence
		Elongated	7	3%	IC-28196, IC-245479, IC-245479
10.	Seed Shape				

		Globular	3	10%	C.G Arhar- 2, KRG-33, CORG-9701, RPS 2015-49, RPS 2014-21, IC-16206, EC-843277, IC-22531, IC-23683, IC-25054
11	Seed colour	Oval	5	87%	Rest all 87 were found to have oval seed shape.
		Cream	1	6%	IC-11011, IC-16194, IC-16195, IC-16203, IC-22501, IC-634438
		Grey	4	13%	RPS 2014-19, IC-16206, EC-843278, IC-15710, IC-16195, IC-25050, IC-25055, IC-22531, IC-14992, EC-843279, EC-843247, IC-22531, IC-14992
		Brown	2	71%	Rest all 71 were found to have brown seed shape.
		Dark Brown	3	6%	IC-22510, IC-22533, IC-22534, IC-22535, IC-28194, IC-28196
		Purple	5	4%	IC-26114, IC-28194, IC-28196, IC-245522

2. Descriptive Statistics for grain yield and its contributing traits:

Descriptive statistics are fundamental tools used throughout the plant breeding process to summarize and understand data about plant traits. In present investigation the results obtained are presented under following heads:

2.1 Range and mean performance of Pigeonpea Germplasm

2.2 Skewness and Kurtosis

2.1 Range and mean performance of Pigeonpea Germplasm

Range and mean performance, standard deviation, standard error and coefficient of variation of 100 genotype were observed for 9 different characters are presented in Table 2. Performance of individual character is described as follows:

1. Plant height

Plant height ranged from 66.4 on to 180.20 cm with mean of 134.28 cm. S.D. of this character recorded 24.06 S.E. was 2.42 and CV was observed 18%.

2. Number of primary branches/plant

Number of primary branches ranged from 3.70 to 9.80 with mean of 6.74 S.D. of this character recorded 1.26, S.E. was 0.13 and CV was observed 19%.

3. Number of Pods/Plant

Number of pods /plant ranged from 21.90 on to 139.60 with mean of 80.38 S.D. of this character recorded 26.72, S.E. was 2.69 and CV was observed 33%.

4. Pod length (cm)

Length of pod ranged from 3.810 cm to 5.80 cm with mean of 4.85 cm. S.D. of this character recorded 0.45, S.E. was 0.05 and CV was observed 9%.

5. Number of Seeds/pod

Number of seeds/plant ranged from 2.90 to with mean of 4.5. S.D. of this character recorded 0.30, S.E. was 0.03 and CV was observed 8%.

6. Days to First flowering

Days to first flowering ranged from 74 DAS to 87 DAS with mean of 77.43 S.D. of this character recorded 2.60, S.E. was 0.26 and CV was observed 3%.

7. Days to 50% flowering

Days to 50% flowering ranged from 102 DAS to 147.03 cm with mean of 151 DAS. S.D. of this character recorded 10.90, S.E. was 1.10 and CV was observed 9%.

8. Days to maturity

Days to maturity ranged from 130 DAS to 203 DAS with mean of 174.03. S.D. of this character recorded 15.75, S.E. was 1.58 and CV was observed 9%.

9. 100 Seed weight

100 Seed weight ranged from 4.606 to 12.06 with mean of 6.95. S.D. of this character recorded 1.65, S.E. was 0.17 and CV was observed 24%.

2.2 Skewness and Kurtosis

Skewness and kurtosis indicate relative mean performance and nature of distribution of traits. Skewness represents the asymmetry of a data distributed in normal distribution curve. It is a distortion of symmetry. If value ranges from -0.5 to 0.5 then the data is normally distributed i.e., symmetrical. Kurtosis indicates the peak ness or flatness of a tail of a curve. If the value is near ($\beta = 3$) then the data is normally distributed (mesokurtic). Kurtosis ($\beta < 3$) indicates the flatness of the curve i.e., platykurtic and if it is ($\beta > 3$) then it indicates the peak ness of a curve i.e., leptokurtic (Misra et al. 2008). Positive skewness i.e., longer tailed to the right shows dominant and complementary gene action where negative skewness i.e., longer tailed to the left is associated with dominant and duplicate gene action (Pooni et al. 1977). Leptokurtic (positive kurtosis) indicates that traits are governed by fewer number of genes and platykurtic (negative kurtosis) shows that traits are governed by large number of genes (Kapur et al. 1981).

Plant height

For plant height the value of skewness observed was -0.54 which shows slightly negative skewness indicating presence of dominant and duplicate gene action. Along side the value of kurtosis was recorded to be -0.05 indicating leptokurtic curve showing that this trait is governed by fewer number of genes.

Number of primary branches/plant

The value of skewness for number of primary branches/plant was recorded -0.21 which indicated normal distribution. The value of kurtosis was recorded -0.12 indicating leptokurtic curve suggesting that fewer number of genes are controlling this trait.

Number of pods/plant

For this trait the value of skewness was 0.14 suggesting normal distribution of population alongside a leptokurtic curve (kurtosis value -0.31) indicating the trait is governed by fewer genes.

Pod length

The value of skewness recorded for Pod length is 0.04 suggesting a normal distribution and the value of kurtosis is -0.48 suggesting it to be leptokurtic curve

Number of seeds/pod

Value of skewness recorded for this trait is -0.10 suggesting the population to be normally distributed for this trait. The value of kurtosis was recorded to be 0.10 which is suggesting a leptokurtic curve and control of fewer genes over traits

Days to First Flowering

The value of skewness recorded for days to first flowering was 0.88 which indicates positive skewness suggesting dominant and complementary gene actions working for this trait. Alongside the value of kurtosis was recorded to be 0.83 suggesting a leptokurtic curve and indicating that this trait is governed by fewer genes.

Days to 50% flowering

For days to 50% flowering the value of skewness was 0.07 suggesting a normal distribution and the value of kurtosis was recorded to be -0.42 indicating a leptokurtic curve and involvement of fewer genes in expression of trait.

Days to Maturity

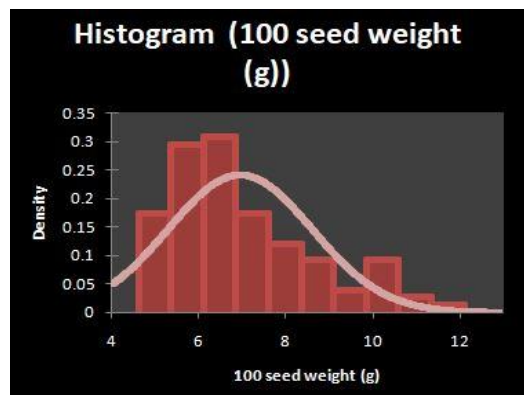
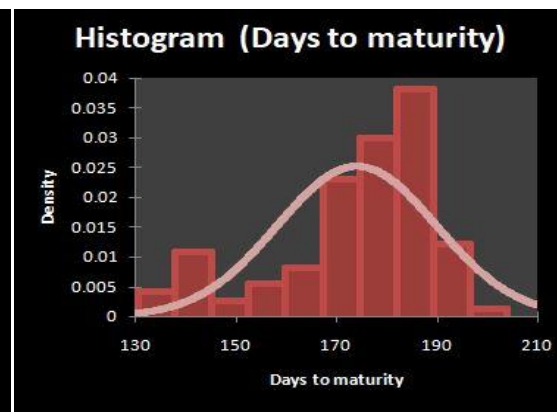
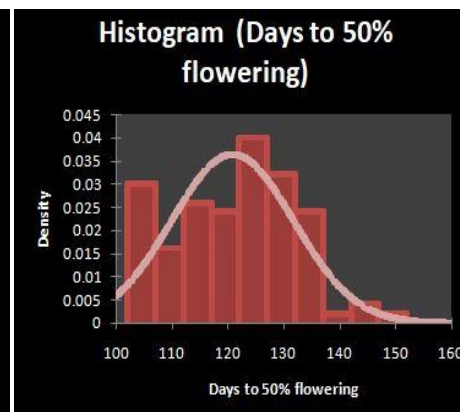
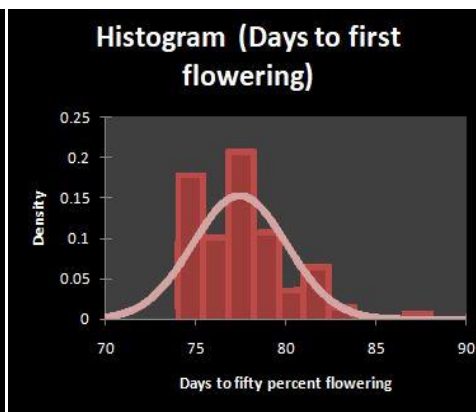
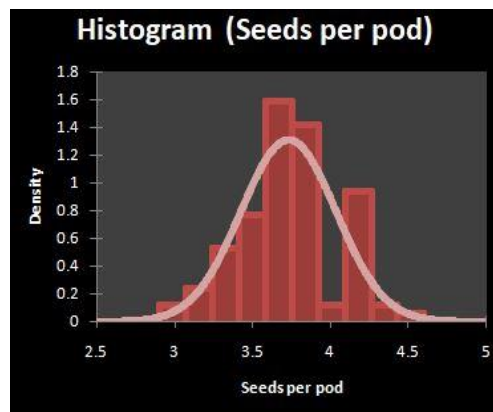
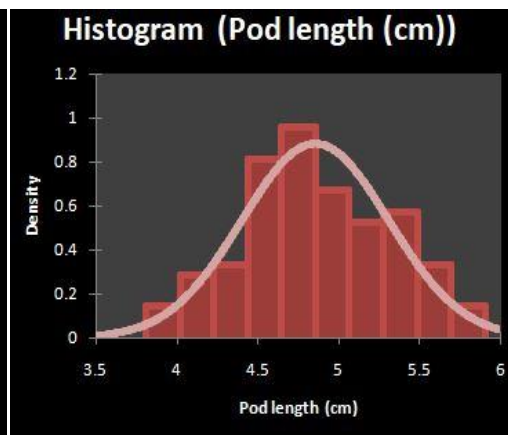
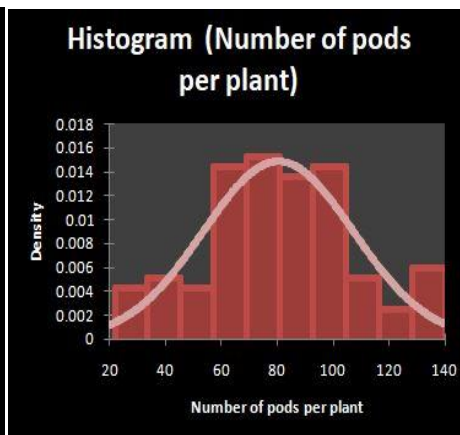
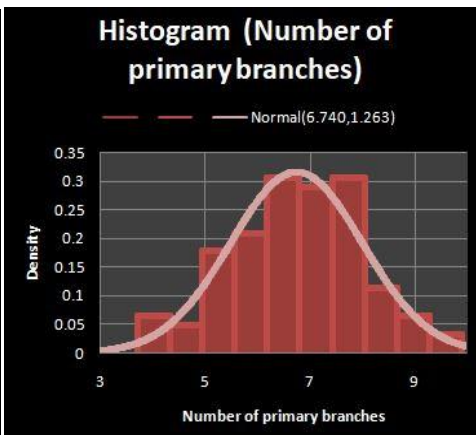
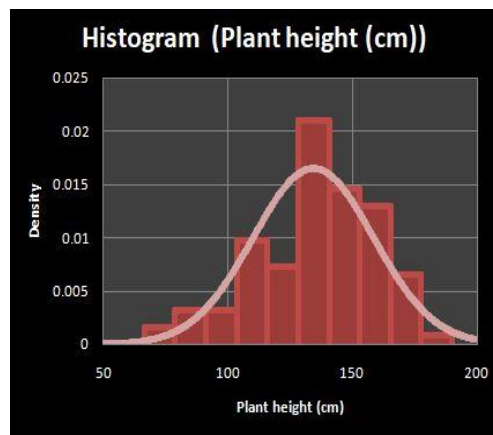
The value of skewness recorded for days to maturity was -1.07 showing negative skewness which is associated with dominant and duplicate gene action and the value of kurtosis was found to be 0.53 indicating negative kurtosis suggesting the trait to be controlled by few genes.

100 Seed weight

For 100 seed weight skewness was recorded to be 0.95 which shows positive skewness suggesting dominant and complementary gene actions also the kurtosis value (0.29) indicates leptokurtic curve.

Table 2 Descriptive statistics for 9 biometrical traits in pigeonpea germplasm

Traits	Minimum	Maximum	Mean	Variance (n)	Standard deviation (n)	Standard error of the mean	Variation coefficient (n)	Skewness (Fisher)	Kurtosis (Fisher)
Plant height (cm)	66.400	180.200	134.28	578.82	24.06	2.42	0.18	-0.54	-0.05
Number of primary branches	3.700	9.800	6.74	1.58	1.26	0.13	0.19	-0.21	-0.12
Number of pods per plant	21.900	139.600	80.38	714.11	26.72	2.69	0.33	0.14	-0.31
Pod length (cm)	3.810	5.800	4.85	0.20	0.45	0.05	0.09	0.04	-0.48
Seeds per pod	2.900	4.500	3.73	0.09	0.30	0.03	0.08	-0.10	0.10
Days to fifty percent flowering	74.000	87.000	77.43	6.76	2.60	0.26	0.03	0.88	0.83
Days to 50% flowering	102.000	151.500	120.79	118.90	10.90	1.10	0.09	0.07	-0.42
Days to maturity	130.500	203.500	174.03	248.20	15.75	1.58	0.09	-1.07	0.53
100 seed weight (g)	4.606	12.061	6.95	2.72	1.65	0.17	0.24	0.95	0.29



Graphical representations of distribution of population for different traits.

3. Study of genetic divergence

A clear understanding of the extent of variability prevalent for each character in germplasm would simply for improving characters through selection. Hybridization program where selection of genetically diverged parent is important to get wide array of recombination, the knowledge of genetic diversity among the accessions of germplasm is necessary.

3.1 D² statistic

Result of cluster analysis has been presented in table 3.1, 3.2 and 3.3. The derivations on plant height (cm), number of primary branches per plant, length of primary branch, number of pods per plant, pod length, number of seeds per pod, 100 seed weight (g), days to first flowering, days to 50% flowering, days to maturity, traits of 100 genotypes were used to obtain D² value which grouped these genotype into 6 cluster (Table no. 3.1) by using D² value in such a way that genotypes within a cluster D² values than those of in between the clusters.

Cluster I include 45 genotypes whereas cluster II, III, IV, V and VI included 10, 17, 18, 19 and 1 genotypes, respectively. The clustering pattern showed that genotypes collected from the same geographic region were found to be distributed in several clusters; similarly genotypes called from the different place were accommodated in the same cluster. Thus the distribution of genotypes into different cluster was not associated with their geographic origin. The cluster mean of green forage yield and its attributing characters in given in Table 3.2.

The highest cluster mean for plant height was obtained in cluster III(162.19) and lowest in cluster IV (99.17). The cluster mean for number of primary branch was highest for cluster III (7.66) and lowest for cluster VI (5.50).

Number of pods per plant had the highest cluster mean was obtained in cluster II (130.86) and lowest in cluster 5 (40.09). Lowest cluster mean values for Pod length were recorded in cluster II and IV (4.70) and highest in cluster III (5.32).

For seeds/pod highest cluster mean value was recorded in cluster II (3.6) and lowest in cluster IV (3.28). Cluster II (8.54) had the highest cluster mean for 100 seed weight whereas, the lowest value was obtained in cluster III and IV (6.18). For days to first flowering the highest cluster mean was recorded by cluster IV (54.27) and lowest in cluster V (49.33). Cluster II (69) had the highest cluster mean value for days to 50% flowering whereas, the lowest value exhibited in clusters I (59.73). For days to maturity the highest cluster mean value was registered by cluster II (107) and lowest cluster in VI (102.33).

On the basis of earlier reports, heterosis and better recombinants were obtained by crossing parents between clusters of high and low means (Kumari and Prasad, 2005). Cluster mean values showed a wide range among the characters studied which indicated presence of variation among the genotypes studied.

The intra cluster distance varied from 0 to 1713.60. It indicated wide range of diversity in term of genetic distance (D²). The high intra cluster distance shown by cluster IV (1713.60) having 18 genotypes namely, IC-25054, IC-26114, IC-25060, IC-245479, IC-424779, IC-393694, IC-245520, IC-245534, IC-15710, IC-245478, IC-245560, IC-245525, IC-22502, IC-245519, IC-245539, IC-

245550,IC-28198 and IPAD-5 indicated the presence of wide genetic diversity among the genotypes in this cluster followed by cluster III (1540.50) having 17 genotypes namely *viz.*, RPS 2015-51,Rajeevochan,C.G. ARHAR-1,RPS 2015-40,RPS 2014-21,RP-1,BDN-716,RPS 2014-6,KRG-33,RPS 2014- 19,UPAS-120,RPS 2015-4,C.G. ARHAR-2,RPS 2014-34,RPS 2015-49,IC-468591 and EC-843247. The D² analysis indicated the presence of appreciable genetic diversity in the material. The inter cluster varied from 2235.09 to 9750.48 it clearly demonstrated considerable amount of genetic divergence present in material study. The highest inter cluster distance between II and cluster V has been reflected in the relatively higher mean value for traits *viz.*,plant height, length of primary branch, number of pods/ plant, days to maturity, 100SW, GMY (Table no. 3.3)

Plant height, length of primary branch, number of pods/ plant, days to maturity, 100SW, GMY are most important in diversity point of view and in Pigeonpea.

Table 3.1 Catagorization of Accession into different clusters.

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	45	IC-11011,IC-16194,IC-16195,IC-16206,IC-22501,IC-22534,IC-385887,IC-15710,IC-468334,IC-468590,EC-8362,IC-15706,EC-843278,EC-843234,CORG-9701,EC-843277,IC-16210,EC-843254,IC-25059,IC-22535,IC-28192,IC-22510,IC-28199,IC-25050,IC-23685,IC-25053,IC-28194,IC-28193,IC-25056,IC-25055,IC-259318,IC-28195,IC-23679,IC-22555,IC-22511,PT-0012,IC-23672,IC-468174,IC-634397,IC-634438,IC-349776,IC-22531,IC-14992,IC-22533 and IC-23683
2 Cluster	10	EC-14995,IC-245482,IC-16203,IC-22536,IC-22532,IC-521410,IC-245522,IC-268203,RPS 2014-32 and RPS 2015-1
3 Cluster	17	RPS 2015-51,Rajeevchan,C.G. ARHAR-1,RPS 2015-40,RPS 2014-21,RP-1,BDN-716,RPS 2014- 6,KRG-33,RPS 2014-19,UPAS-120,RPS 2015-4,C.G. ARHAR-2,RPS 2014-34,RPS 2015-49,IC-468591 and EC-843247
4 Cluster	18	IC-25054,IC-26114,IC-25060,IC-245479,IC-424779,IC-393694,IC-245520,IC-245534,IC-15710,IC-245478,IC-245560,IC-245525,IC-22502,IC-245519,IC-245539,IC-245550 ,IC-28198 and IPAD-5
5 Cluster	9	IC-259319,IC-261382,IC-347516,IC-261355,IC-28196,IC-323307,IC-267493,IC-329116 and IPAD-5
6 Cluster	1	IC-245477

Table 3.2 Cluster means for 9 biometrical traits.

Cluster Means : Tocher Method									
	Plant height (cm)	Number of primary branches	Number of pods per plant	Pod length (cm)	Seeds per pod	Days to 50% flowering	Days to flowering	Days to maturity	100 seed weight (g)
Cluster 1	133.75	6.72	85.21	4.79	3.68	77.03	121.37	178.70	6.73
Cluster 2	134.71	6.73	130.86	4.70	3.72	78.55	122.70	177.80	6.66
Cluster 3	162.19	7.66	77.01	5.32	3.91	77.38	106.94	147.29	7.41
Cluster 4	99.17	5.91	62.64	4.70	3.70	77.75	126.14	180.78	6.70
Cluster 5	153.39	6.90	40.09	4.76	3.67	77.39	127.83	180.17	7.60

Cluster 6	139.70	5.50	97.40	5.08	3.90	79.50	151.50	203.50	10.10
-----------	--------	------	-------	------	------	-------	--------	--------	-------

Table 3.3 Inter and intra cluster distances.

Cluster Distances						
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6
Cluster 1	1041.18	3140.66	3306.49	3051.36	3561.38	2235.09
Cluster 2	3140.66	1204.45	6104.38	7289.15	9750.48	3190.85
Cluster 3	3306.49	6104.38	1540.50	7206.17	4269.63	6807.64
Cluster 4	3051.36	7289.15	7206.17	1713.60	4848.35	4834.13
Cluster 5	3561.38	9750.48	4269.63	4848.35	1318.02	5175.14
Cluster 6	2235.09	3190.85	6807.64	4834.13	5175.14	0.00

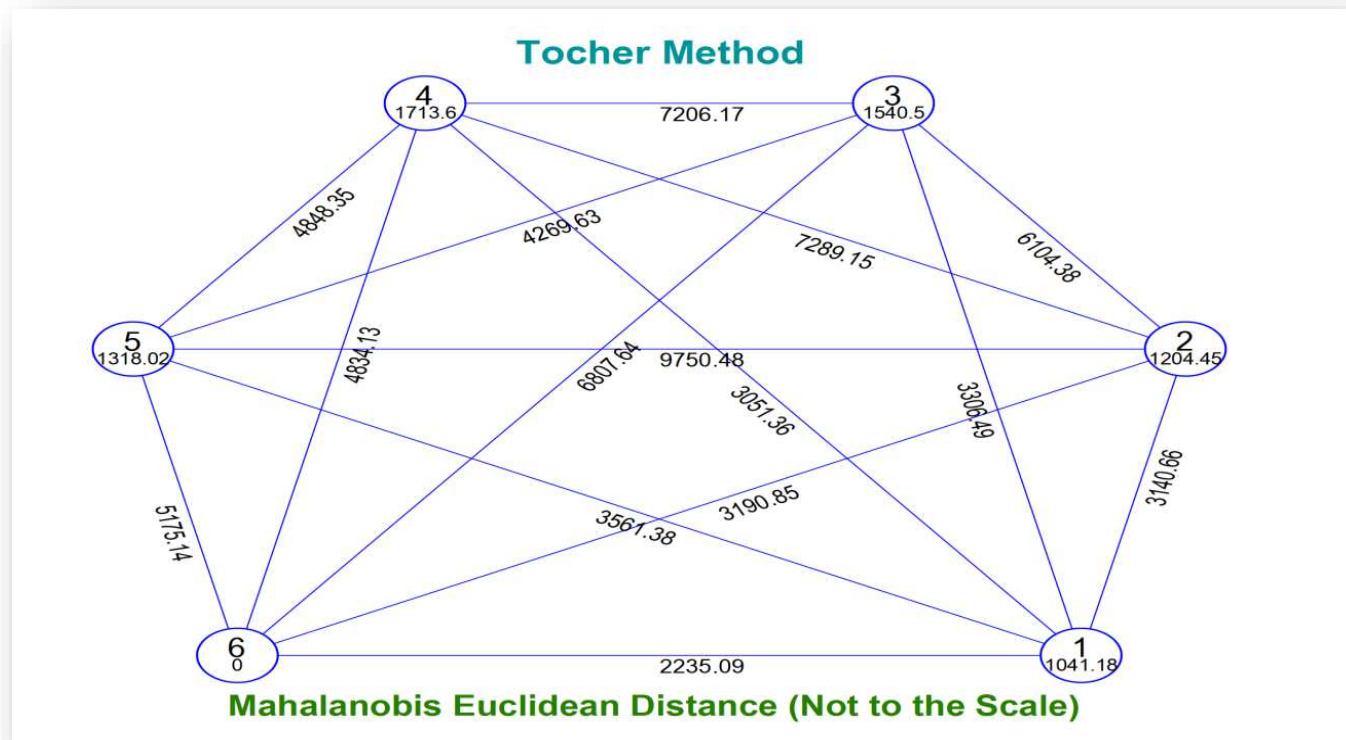
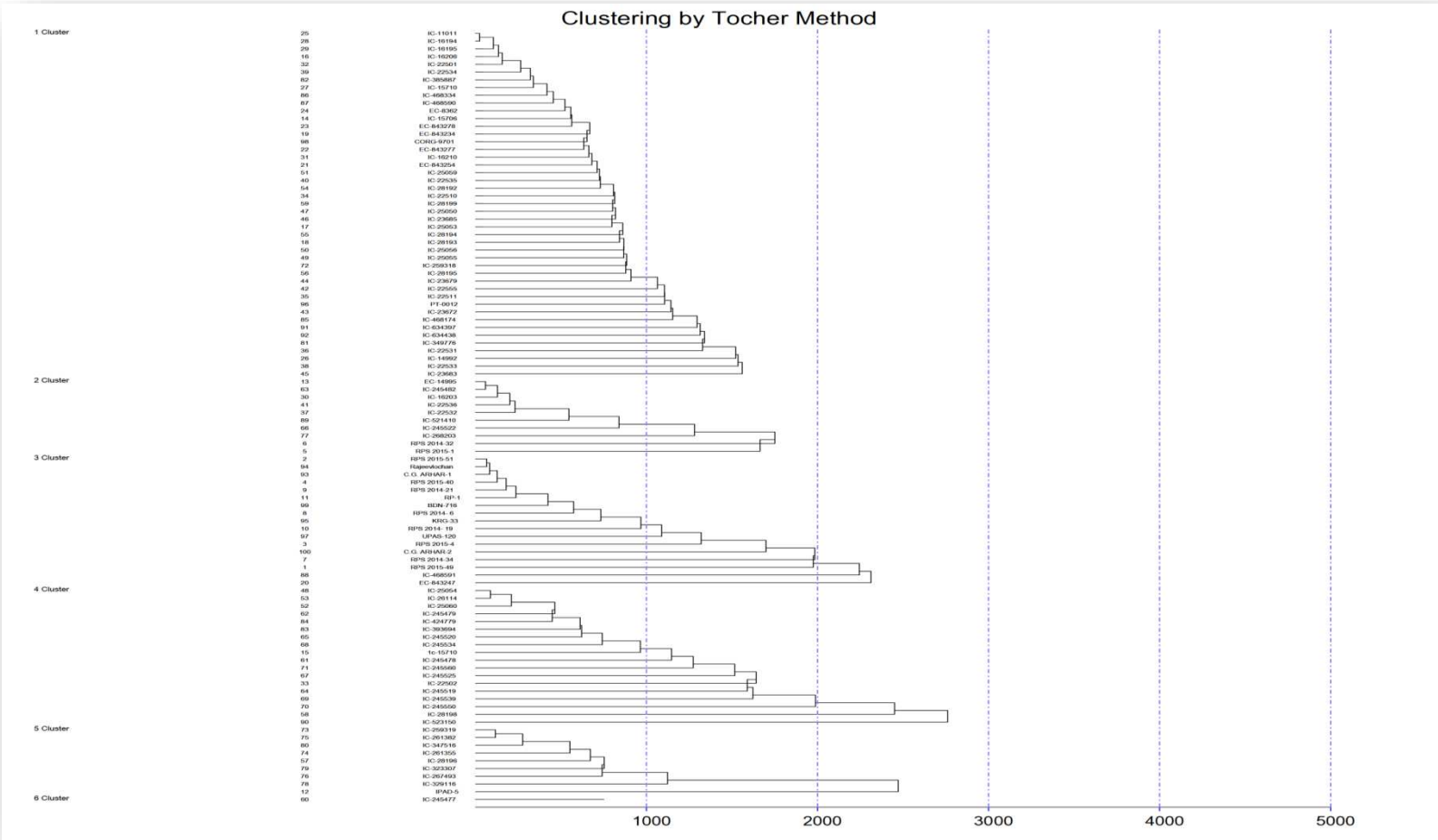


Fig. 3.1 Diagrammatic representation of inter and intra cluster distances

Fig. 3.2 Dendrogram (Clustering by Tocher Method)



Conclusion:

- Morphological characterization some genotypes with unique characters like presence of pod pubescence and pod constriction which are traits for natural resistance towards pod borer. So genotypes RP-1, EC-14995, IC-16206, IC-22533, IC-16194, IC-245478, IC-245525, RPS 2014-19, IC-16206, EC-843278, IC-15710, IC-16195, IC-25050, IC-25055, IC-22531, IC-14992, EC-843279, EC-843247, IC-22531, IC-14992, EC-843278, EC-843247 IC-25050, IC-25055, IC-25056, IC-25059, IC-26114, IC-28194, IC-28196, IC-245522, IC-245534, IC-268203 can be used in crop improvement program against pod borer complex. Also, distinctiveness of accessions were recorded for easy identification and use in breeding program.
- Highest coefficient of variation was recorded in –Number of pods/plant (33%), 100 seed weight (24%), Number of primary branch (19%) and plant height (18%) indicating high degree of untapped variability which can be used in further breeding programs. Lowest coefficient of variation was recorded in days to first flowering.
- Normal distribution of population was observed for most of the traits except plant height (Negative skewness, -0.54), Days to first flowering (Positive skewness, 0.88), Days to maturity (Negative skewness, -1.07), 100 seed weight (positive skewness, 0.95) and leptokurtic curve was observed for all the traits suggesting that traits are governed by fewer number of genes.
- From results we can conclude that variability among the genotypes for the mentioned characters existed in ample amount and there is sufficient scope for improvement of genotypes.
- On the basis of earlier reports, heterosis and better recombinants were obtained by crossing parents between cluster of high and low means (Kumari and Prasad, 2005) So for yield related traits such as 100 seed weight cluster 6 and cluster 2 have highest and lowest cluster mean 10.10 and 6.66 respectively, so, best recombinants can be obtained by crossing them. Similarly for obtaining best recombinants for number of pods/plant, cluster 2 (130.86) and cluster 5 (40.09). For obtaining best recombinants for number of seeds per pod cluster 3 (3.91) and cluster 5 (3.67).
- Diversity analysis revealed that the genetic diversity is present in ample amount in germplasm. Cluster 2 and cluster 5 showed highest inter cluster distance. Superior recombinants can be obtained by hybridization between these two clusters which can be used in further breeding programs.
- Major Findings of this result is for 100 seed weight (g) highest yield is recorded in genotypes, IC-245477, RP -1, IC-259319, IC-261382, IC-347516, IC-261355, IC-28196, IC-323307, IC-267493, IC-329116 and IPAD-5.

References:

- Aruna, R., Rao, D.M., Reddy, L.J. (2005). Inheritance of trichomes and resistance to pod borer (*Helicoverpa armigera*) and their association in interspecific crosses between cultivated pigeonpea (*Cajanus cajan*) and its wild relative *C. scarabaeoides*. *Euphytica*; **145**, 247–257.
- D'Cruz, R., Patil, P.S. and Deokar, A.B. (1973). Genetic studies in pigeonpea XIII. Poona Agricultural College iMagazine, 62, 23-26.
- Gumber, R., Singh, S.(1997). Genetics of flowering patterns in pigeonpea: further evidence for two gene control. *Euphytica*, **96**, 233–236
- Machanwar, Sukanya and Bantewad, Sanjeev. (2019). Assessment of pigeonpea restorers on morphological basis of host plant resistance against ppod boarers. *International Journal of Current Microbiology and applied sciences*, 8(12), 1016-1025.
- Metkar, A. P. and V. L. Gawande. (2014). Genetic variability and morphological characterization studies in CMS lines of pigeonpea derived from *Cajanus*. *PKV Research Journal*; 38(2), 15-25.
- Muniswamy S, Lokesha R, Dharmaraj PS, Yamanura and Diwan JR. (2014). Morphological characterization and assessment of genetic diversity in minicore collection of pigeonpea (*Cajanus Cajan* (L.) Millsp) *European Journal of Pharmaceutics and Biopharmaceutics*, 5(2),179-186.
- Padma Priya, M., Gnanamalar, R.P., Kartibha, L. and Thanga Hemavathy, A. (2022). Morphological characterization of early duration pigeonpea genotypes. *Electronic Journal of plant Breeding*; 13(2), 679-689.
- Rangare NR, Reddy GE, Kumar SR. (2013). Study of heritability, genetic advance and variability for yield contributing characters in pigeonpea (*Cajanus cajan* L. Millspaugh). *Trends in Biosciences*, 6(5), 660-662.
- Ranjani, S. M. and Jayamani, P. (2021). Characterization of pigeonpea genotypes based on DUS traits. *International Journal of Plant and Soil Science*, 33(23), 289 – 297.
- Singh, I.P., D.P. Srivastava & N.P. Singh, (2000). Inheritance of certain morphological characters in interspecific crosses of *Cajanus* species. *Indian Journal of Agricultural Science*, 70, 667–670.
- Sujit.,Singh, M.K., Belsariya, Neha., Rana, Luchika., Konreddy, Sathish and Pandey, Vipin kumar. (2022). Studies on morphological characterization in pigeonpea [*Cajanus cajan* (L.) Millsp] germplasm of Chhattisgarh. *The Pharma Innovation Journal* 2022, 11(11), 323-331.
- Techale B, Mekonen., Habatamu, Zeleke Uta., Ayana, Amsalu and Teka, Abera Tilahun. (2013). Genetic Variability, heritability and genetic advance in early maturing pigeon pea (*Cajanus Cajan* L.) genotypes. *World Journal of Agricultural Sciences*, 1(7), 241-247.
- Upadhyaya HD, Reddy, KN, Gowda CLL, Silim SN. (2007). Patterns of diversity in pigeon pea (*Cajanus cajan* (L.) Millsp.) germplasm collected from different elevations in Kenya. *Genetic Resources and Crop Evolution*, 54, 1787-1795.
- Vanniarajan, C., Magudeeswari, P., Gowthami, R., Indhu, S.M., Ramya, K.R., Monisha, K., Pillai, M.A., Verma, N., Yasin, J.K. and Jayapradhachandran (2023). Assessment of Genetic Variability and Traits Association in Pigeonpea [*Cajanus cajan* (L.) Millsp.] Germplasm. *Legume Research*, 46(10), 1280- 1287.
- Vijaylakshmi P, Anuradha CH, Pavan Kumar D, Sreelaxmi A, Anuradha G. (2013). Path Coefficient and Correlation response for yield Attributes in Pigeon Pea (*Cajanus Cajan* L). *International Journal of Scientific and Research*; 3(4), 2250-3153.