



Research Article

GENETIC DIVERSITY IN PIGEONPEA [*Cajanus Cajan* L. Millsp.]

SATANKAR NAVNEET*, SIKARWAR R.S., SINGH A.K. AND RAI ANIL KUMAR

Department of Plant Breeding and Genetics, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishva Vidyalyaya Gwalior, 474 002, Madhya Pradesh

*Corresponding Author: Email-navneet.satankar83@gmail.com

Received: March 22, 2017; Revised: April 03, 2017; Accepted: April 04, 2017; Published: April 18, 2017

Abstract- A set of 30 pigeonpea genotypes were evaluated during kharif season 2013-14 at Research farm, College of Agriculture, Gwalior, Madhya Pradesh, to assess the genetic diversity. The study revealed that there was wide range of genetic diversity among genotypes for all 11 yield and its attributing characters. D² analysis grouped 30 genotypes into 5 clusters. Cluster III was largest consisting of 15 genotypes, followed by cluster I and IV both containing 6 genotypes, cluster V had 2 genotypes and the cluster II was solitary. The inter cluster D² values indicated that most diverse clusters were cluster II and V (641.98) followed by Cluster I and V (636.22), cluster I and II (632.00) and cluster I and III (479.77). The highest intra-cluster distance was observed in cluster V (247.40) followed by cluster IV (223.67) and cluster III (140.23) which indicated maximum variability within the cluster. Cluster V showed highest mean for most of the characters viz. length of pod (7.23), number of seeds per pod (5.28), days to maturity (256.50), 100 seed weight (10.24), seed yield per plant (166.42) and seed yield per hectare (1325.72), while cluster I showed lowest mean for most of the characters viz. number of primary branches per plant (13.60), number of pods per plant (285.36), plant height (141.50), seed yield per plant (84.04) and seed yield per hectare (701.50). Cluster II showed high mean for number of pods per plant (470.20), while lowest mean for days to 50% flowering (91.50), days to maturity (185.98) and 100 seed weight (8.12). Cluster III showed high mean for days to 50% flowering (113.83) and number of primary branches per plant (18.36). Cluster IV showed high mean for pod bearing length of plant (138.35) and plant height (18.36). The contribution of characters towards genetic divergence was highest in seed yield per plant (16.65%) followed by seed yield per ha (16.53%), number of pods per plant (13.58) and number of primary branches per plant (11.99). The characters such as seed yield per plant, seed yield per ha, number of pod per plant and number of primary branches per plant had potential variability which can be used as parameters while selecting diverse parents in the hybridization programme for further improvement of yield and its contributing characters in pigeonpea.

Keywords- Genetic diversity, Cluster analysis, Pigeonpea.

Citation: Satankar Navneet, et al., (2017) Genetic Diversity in Pigeonpea [*Cajanus cajan* L. Millsp.]. International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 9, Issue 18, pp.-4177-4179.

Copyright: Copyright©2017 Satankar Navneet, et al., This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

Academic Editor / Reviewer: Basant Kachouli

Introduction

Pigeonpea [*Cajanus cajan* L. Millsp.] is an important food legume crop mostly cultivated in tropical and subtropical regions of the world. It has been recognized as a good source of vegetarian protein particularly in the developing countries where majority of the population depends on the low priced vegetarian food. It is consumed in combination with cereals, it makes well-balanced human diet. It is a rich source of protein, carbohydrate, vitamins, lipids and certain minerals. Split pigeonpea (Tur Dal) is quite common in India. It has diversified uses such as food (dried peas, flour, or green vegetable peas), feed, fodder and fuel. Being a legume crop, the pigeonpea enriches soil fertility through symbiotic nitrogen fixation. The plants are drought resistant and can be grown in areas with less than 650 mm annual rainfall. The productivity of pigeonpea in India is still very low and there are several reasons responsible for it. The use of higher productive genotypes is the most important measure for increasing the productivity in a sustainable manner.

Genetic diversity is the total number of genetic characteristics in the genetic makeup of a species. Darwin, 1859 used the expression of divergence in characters to denote variation in genera, species and varieties [1]. In any crop improvement programme, genetic diversity is an essential prerequisite for hybridization. Genetically diverse parents are preferred for use in hybridization programme because crosses involving divergent parents have been found to provide greater possibility for obtaining desirable segregants in segregating

generations. The multivariate analysis by means of D² statistics has been found useful in selecting genetically divergent parents for hybridization [4]. Therefore in this study D² statistics is used to identify the extent of genetic diversity.

Materials and Methods

The experiment was conducted at Research farm, College of Agriculture, Rajmata Vijayaraje Scindia Krishi Vishva Vidyalyaya, Gwalior, Madhya Pradesh. Thirty diverse genotypes of pigeonpea were sown in Randomized Block Design with three replications during Kharif season of 2013-14. Each entry was sown in single row of 2 meter length adopting 60 cm Row to Row and 20 cm Plant to Plant distance. From each accession, five competitive plants were selected randomly for collection of data on eleven yield and its component traits viz., days to 50% flowering, number of primary branches per plant, pod bearing length of plant (cm), number of pod per plant, length of pod (cm), number of seed per pod, plant height (cm), days to maturity, 100-seed weight (g), seed yield per plant (g) and seed yield per hectare (kg). Genetic diversity was estimated by [4], clustering was done as per method [8] used for cluster formation. Average intra and inter cluster distances were estimated as per the procedure outlined by [14].

Results and Discussion

D² statistics and cluster analysis grouped 30 pigeonpea germplasm in to 5 clusters

[Table-1]. This indicated existence of high degree of genetic diversity in the germplasm evaluated in this study. Therefore, these germplasm would serve as valuable source for selection of diverse parent. Cluster pattern revealed that, cluster III was largest consisting of 15 genotypes, followed by cluster I and IV both containing 6 genotypes, cluster V had 2 genotypes and the cluster II was solitary. The discrimination of germplasm lines into many discrete clusters indicated presence of substantial diversity in the material evaluated. Earlier researcher [16,3,13] have also reported existence of high degree of genetic diversity in the pigeonpea material evaluated by them.

Table-1 Grouping of 30 genotypes of pigeonpea into different clusters.

Cluster	No. of genotypes	Genotypes
I	6	NPS819, JKPR-2005-2, WRG-75, ICPR-3933, JKM-186 and ICPL-7035
II	1	UPAS120
III	15	TAT9804, TAT9629, JSA-59, ICPR-3381, ICPR-3497, ICPR-3462, ICPR-3762, ICPR-3464, JKE-114, JKT-115(E), BAHAR, JKM-189, TJT-501 and GRG-295-1,
IV	6	ICPR-2740, ICPR-3491, ICPR-2671, CEAP1144, CEAT-1162 and BRG-05-11
V	2	K.L.S. and Asha

The intra and inter-cluster distance among different clusters has been given in [Table-2]. The inter-cluster distances were greater than intra-cluster distances, revealing that considerable amount of genetic diversity existed among the genotypes. Maximum differences among the genotypes within the same cluster (intra cluster) were shown by cluster V (247.40) followed by cluster IV (223.67) and cluster III (140.23) which indicated maximum variability within the cluster. While the minimum intra cluster distance were observed in cluster II which had no i.e. zero intra cluster distance followed by cluster I (77.15), indicated that genotypes of these clusters could be closely related in their evolutionary process and passed through similar evolutionary factors, hence selection will be ineffective. The similar findings were also reported by [17, 16, 2, 10]. Inter-cluster distance is the main criterion for selection of genotypes using D^2 analysis. The maximum inter cluster distance was recorded between cluster II and V (641.98) followed by Cluster I and V (636.22), cluster I and II (632.00) and cluster I and III (479.77). Genotypes belonging to the clusters with maximum inter-cluster distance are genetically more divergent and hybridization between genotypes of divergent clusters would be useful to improve the yield potential in pigeonpea. Singh *et al.*, 2015 also suggested that crossing between genotypes from diverse cluster may provide a wide spectrum of genetic variability into progenies with superior combination of different traits viz., early maturity, short plant stature and higher grain yield. Minimum inter-cluster distance was observed between cluster II and IV

(49.48) followed by Cluster IV and V (74.97), which indicated close relationship between genotypes of these clusters, which would not provide any significant diversity similar findings were also reported by [13,6].

Table-2 Estimates of average intra and inter-cluster distance D^2 values for 5 clusters constructed from 30 genotypes of pigeonpea

cluster	I	II	III	IV	V
I	77.15	632.00	479.77	103.69	636.22
II		0.00	155.11	49.48	641.98
III			140.23	165.34	176.95
IV				223.67	74.97
V					247.40

Bold figures represent intra-cluster distance.

The mean performance of all the characters in different cluster is presented in [Table-3]. Cluster II showed high mean for number of pods per plant (470.20), while lowest mean for days to 50% flowering (91.50), days to maturity (185.98) and 100 seed weight (8.12). Cluster III showed high mean for days to 50% flowering (113.83) and number of primary branches per plant (18.36) while low mean for length of pod (5.45) and number of seeds per pod (3.82). Cluster IV showed high mean for pod bearing length of plant (138.35) and plant height (169.15). Cluster V showed highest mean for most of the characters viz. length of pod (7.23), number of seeds per pod (5.28), days to maturity (256.50), 100 seed weight (10.24), seed yield per plant (166.42) and seed yield per hectare (1325.72), while lowest mean for pod bearing length of plant (113.45) therefore genotypes could be selected from this cluster for improvement in the yield contributing characters. Cluster I showed lowest mean for most of the characters viz. number of primary branches per plant (13.60), number of pods per plant (285.36), plant height (141.50), seed yield per plant (84.04) and seed yield per hectare (701.50). The similar findings were also reported by [7, 11].

The utility of D^2 statistics is enhanced by its applicability to estimate relative contribution of various characters towards genetic divergence [Table-3]. Relative contribution of seed yield per plant (16.65%) has maximum contribution in divergence followed by seed yield per ha (16.53%), number of pods per plant (13.58%) and number of primary branches per plant (11.99%). [7, 6] reported number of pods per plant, [9] reported seed yield per plant, [5] reported seed yield per ha contributed maximum towards genetic divergence. However, days to 50% flowering (3.16%) and days to maturity (2.64%) have least contribution in divergence. Present finding are in confirmation with [15, 11].

Table-3 The mean values of 11 characters in 5 cluster in 30 genotypes of Pigeonpea.

Cluster	Days to 50% flowering	No of primary branch	Pod bearing length (cm)	No of pod per plant	Length of pod (cm)	No of seed per pod	Plant height (cm)	Days to maturity	100 seed weight	Seed yield per plant (g)	Seed yield per ha (kg)
I	110.25	13.60#	114.02	285.36#	5.74	3.94	141.50#	232.00	8.72	84.04#	701.50#
II	91.50#	18.00	122.30	470.20+	5.89	4.15	153.20	185.98#	8.12#	158.39	1300.30
III	113.83+	18.36+	121.20	423.03	5.45#	3.82#	148.00	232.37	8.49	142.70	1157.19
IV	112.42	17.97	138.35+	442.70	5.92	3.89	169.15+	236.58	9.52	165.57	1317.40
V	107.50	14.20	113.45#	376.15	7.23+	5.28+	149.60	256.50+	10.24+	166.42+	1325.72+

#, + indicates lowest and highest values, respectively

Table-4 Contribution of individual character towards divergence

Character	Days to 50% flower	No of primary branch	Pod bearing length	No of pod per plant	Length of pod	No of seed per pod	Plant height	Days to maturity	100 seed weight	Seed yield per plant	Seed yield per ha
Contribution in per cent (%)	3.16	11.99	6.78	13.58	6.85	7.71	6.71	2.64	7.38	16.65	16.53

Conclusion

From the present investigation, it was concluded that cluster II and cluster V were more divergent clusters seed yield per plant has maximum contribution in genetic divergence followed by seed yield per ha, number of pod per plant and number of

primary branches per plant. The genotypes of cluster V (K.L.S. and Asha) showed highest cluster mean values for most of the yield contributing characters, and the genotype of cluster II (UPAS120) showed superior performance as early flowering and early maturity. Therefore, genotypes from cluster II and cluster V can be

utilized as potential parents in crossing programme for improving more than one economic character such as high yield and early maturity.

Acknowledgement

Authors are very much thankful to the Department of Plant Breeding and Genetics for providing all the essential facilities and moral support to conduct the whole research programme and to obtain its significant findings. Authors are also greatly privileged to the Department of Agricultural Statistics, College of Agriculture, RVSKVV, Gwalior, (M.P.), for providing all the necessary and required information technology, moral support and co-operation.

Abbreviations

cm	=	centimeter
g	=	gram
ha	=	hectare
kg	=	kilogram
viz.	=	that is to say
%	=	per cent

Conflict of Interest: None declared

References

- [1] Darwin C. (1859) *The Origin of Species by Means of Natural Selection or the Preservation of Favored Races in the Struggle for Life. Philosophical Library, New York.*
- [2] Gohil R.H. (2006) *Research on Crops*, 7 (3), 748-750.
- [3] Katiyar P.K., Dua R.P., Singh I.P., Singh B.B. and Singh F. (2004) *Legume Research*, 27 (3), 164-170.
- [4] Mahalanobis P.C. (1936) *Proc. Natn. Acad. Sci. India*, 2, 49-55.
- [5] Niranjana Kumara B., Dharmaraj P.S. and Vijaya B Wali (2014) *International journal of advances in pharmacy, biology and chemistry*, 3(2), 404-409.
- [6] Panday P., Kumar R., Panday V. R. and Tripathi M. (2013) *American Journal of Plant Sciences*, (4), 2126-2130.
- [7] Rekha R., Prasanti L., Reddi Sekhar M., Latha P. and Sudhakar S. (2011) *Legume Res.*, 34(2), 139-142.
- [8] Rao C.R. (1952) *Advance Statistical Methods in Biometric Research. John Wiley and Sons, Inc, New York.*
- [9] Rao P. J. M., Upender M. and Bhaskar A. Vijay (2013) *International Journal of Applied Biology and Pharmaceutical Technology*, 4 (4), 48-51.
- [10] Rao U. Vasantha, Rao B. Govinda, Rao C. Panduranga and Rao V. Srinivasa (2010) *The Andhra Agricultural Journal*, 57(2), 156-163.
- [11] Reddy V., Guruvendra, Jayalakshmi V. and Sreenivas T. (2015) *Electronic Journal of Plant Breeding*, 6(2), 515-518.
- [12] Singh J., Kumar A. and Fiyaz R.A. (2015) *Legume Research*, 38(2), 169-173.
- [13] Singh M.N., Awasthi S.K. and Singh R.S. (2010) *Journal of Food Legumes*, 23(1), 82-83.
- [14] Singh R.K. and Choudhary B.D. (1977) *Biometrical methods in quantitative genetic analysis, Kalyani Publishers, New Delhi.*
- [15] Sreelakshmi Ch., Kumar, C.V.S. and Shivani D. (2011) *Electronic Journal of Plant Breeding*. 2(3), 413-416.
- [16] Thomber B.B., Aher R.P. and Dahat D.V. (2000) *Indian Journal of Agricultural Research*, 34 (2), 126-129.
- [17] Viramgama A.V. and Goyal S.N. (1994) *Gujarat Agriculture University Research Journal*, 19 (2), 65-71.