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The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(11): 2422-2426

www.thepharmajournal.com
Received: 17-09-2023
Accepted: 20-10-2023

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Studies on genetic divergence in pigeonpea germplasm

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Abstract
The nature and extent of genetic diversity were assessed among 75 elite genotypes of pigeonpea using Mahalanobis D^2 statistics. Based on the genetic distance, all the 75 genotypes were grouped into 10 different clusters. Cluster I was the largest with 45 genotypes followed by cluster II with 19 genotypes and cluster VI with 4 genotypes. The maximum inter cluster distance was recorded between clusters IX and X followed by clusters VII and IX and clusters V and IX. The minimum inter cluster distance was noticed between clusters IV and V. The maximum intra-cluster distance was recorded by cluster I followed by cluster VI and cluster II. The crossing between entries belonging to cluster pairs having large inter-cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in pigeonpea. The characters *viz*., days to maturity, seed yield plant^{-1}, number of pods plant^{-1}, days to 50% flowering and 100-seed weight. Hence, these characters could be given due importance for selection of genotypes for further improvement.

Keywords: Genetic diversity, pigeonpea, cluster analysis, transgressive segregants, yield

1. Introduction
Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the second most important pulse crop of India after chickpea, commonly known as Arhar, Red gram and Tur. 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 foods. In fact, this crop has diversified uses such as food, feed, fodder and fuel (Magadum *et al*., 2013) [1]. Compared to other food legumes, breeding in pigeonpea has been more challenging due to various crop specific traits and highly sensitive nature to biotic and abiotic stresses. The final target of any plant breeding programme is to develop improved genotypes which are better than the existing ones in producing the economic yield. This requires genetic amelioration through maximum utilization of allelic resources to develop ideal genotype (Pandey *et al*., 2013) [2].
In any crop, germplasm serves as a valuable source of base population and providing scope for wide variability. The more diverse the parents, the greater are the chances of obtaining higher amount of heterotic expression in F_1's and broad spectrum of variability in segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding program (Gangapur *et al*., 2014) [3]. The information about the nature and magnitude of genetic diversity existing in the available germplasm of a particular crop is crucial for selection of diverse parents, which upon hybridization may provide a wide spectrum of gene recombinations for quantitatively inherited traits. Earlier workers considered distances in place of origin as index of genetic diversity and used it for selection of parents for hybridization programme. However, the genetic diversity of the selected parents has not been always found to be based on factors such as geographic diversity/place of release or ploidy level (Murty and Arunachalam, 1966 and Bhatt, 1970) [4, 5]. Hence, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedures, such as D^2 cluster analysis. Keeping in view, an experiment was taken up to study genetic diversity for selecting the diverse parents for hybridization programme aimed at isolating desirable segregants for seed yield and other important characters in pigeonpea.

2. Materials and Methods

2.1. Experimental detail

The experimental material comprised of 75 elite pigeonpea genotypes including three wild relatives *viz*., *Cajanus scarabaeoides*, *Cajanus platycarpus* and *Rhyncosia minima* were evaluated in a randomized complete block design with three replications at Norman E. Borlaug Crop Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand during kharif season. The experimental site falls in the humid subtropical zone and located between 79° 30' E longitude and 29° 03' N latitude with an altitude of 243.83 meters above the mean sea level. Each genotype was raised in single row plots of 4 m length with intra-row and inter-row spacing of 20 cm and 60 cm, respectively. The recommended package of practices relevant to the crop was followed throughout the experimental period.

2.2. Data collection

The observations were recorded on five randomly selected competitive plants of a genotype in each replication for eleven characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number pods plant^{-1}, number of clusters plant^{-1}, pod length (cm), number of seeds pod^{-1}, 100-seed weight (g) and seed yield plant^{-1} (g).

2.3. Statistical analysis

The mean data of 75 genotypes for eleven quantitative traits were subjected to the analysis of variance to test the significance for each character as suggested by Panse and Sukhatme (1967)[6]. Genetic divergence among all the genotypes was estimated using the D^2 statistic of Mahalanobis (1936) [7] and the grouping of the genotypes into different clusters were done by using the procedure of Rao (1952) [8].

3. Results and Discussion

The analysis of variance revealed significant differences among 75 genotypes for all the characters under study, indicating considerable variation among the genotypes. The Mahalanobis D^2 cluster analysis grouped all the 75 genotypes into ten distinct non-overlapping clusters (Table 1 and Figure 1). Among 10 clusters, cluster I was the largest with 45 genotypes followed by cluster II with 19 genotypes and cluster VI with 4 genotypes. Clusters III, IV, V, VII, VIII, IX and X were solitary with single genotype in each cluster. The discrimination of genotypes into discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Earlier workers have also reported substantial genetic divergence in the pigeonpea materials (Sreelakshmi *et al*., 2010; Rekha *et al*., 2011; Nag and Sharma, 2012; Pandey *et al*., 2013; Prasad *et al*., 2013; Muniswamy *et al*., 2014 and Singh *et al*., 2014) [9, 10, 11, 2, 12, 13, 14]. Presence of substantial genetic diversity among the parental material screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable segregants for seed yield and other important characters. The distribution of genotypes indicated that the geographical diversity and genetic diversity were not related and there are forces other than geographical separation which are responsible for diversity such as natural and artificial selection, exchange of breeding material, genetic drift and environmental variation. Similar results were reported by Gupta *et al*. (2008) [15], Sreelakshmi *et al*. (2010) [9], Nag and Sharma (2012) [11], Pandey *et al*. (2013) [2] and Singh *et al*. (2014) [14].

Clusters III, IV, V, VII, VIII, IX and X were solitary with single genotype in each cluster which revealed the presence of wide genetic divergence for various characters. The presence of solitary clusters indicated extreme phenotypic performance in positive or negative directions for one or the other characters. Sreelakshmi *et al*. (2010) [9], Rekha *et al*. (2011) [10], Shunyu *et al*. (2013) [16] and Singh *et al*. (2014) [14] also observed solitary clusters in their study.

The estimates of average intra- and inter-cluster distances were presented in Table 2. In the present study, maximum intra-cluster distance was shown by cluster I (13.68) followed by cluster VI (13.43) and cluster II (11.14). Diversity among the clusters varied with inter cluster distance from 5.88 (cluster IV and V) to 124.83 (cluster IX and X). The maximum inter cluster distance of 124.83 was observed between cluster IX and X followed by cluster VII and IX (98.96), cluster V and IX (92.37) and cluster IV and IX (91.95). The lowest inter cluster distance was noticed between cluster IV and V (5.88). The smallest inter cluster distance indicates less diversity between the genotypes contained in these clusters. It indicates close relationship and similarity of the genotypes for most of the characters. However, these genotypes can be undertaken for hybridization in order to exploit variation for the specific characters for which the genotypes of the two clusters shown marked difference. In order to increase the possibility of isolating good segregants in the segregating generations it would be ideal to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances. Similar results were reported by Sreelakshmi *et al*. (2010) [9], Rekha *et al*. (2011) [10], Nag and Sharma (2012) [11], Pandey *et al*. (2013) [2], Prasad *et al*. (2013) [12], Shunyu *et al*. (2013) [16], Muniswamy *et al*. (2014) [13] and Singh *et al*. (2014) [14].

Considering the mean performance of clusters for different traits (Table 3), clusters III, IV, V, VII, VIII, IX and X each with one genotype *viz*., MATH 1-3, TAT 144, GAUT 210, GAUT 98023, *C. scarabaeoides*, *C. platycarpus* and *Rhynchosia minima* had high mean values for most of the desirable traits. The cluster VI with overall score of 46 across the eleven characters secured first rank, followed by cluster VII (48) and cluster III (48). Hence, the genotypes of these clusters can be used in hybridization programme to produce higher yielding progenies. Joshi and Dhawan (1966)[17] reported that inclusion of more diverse parents (within a limit) is believed to increase the changes for obtaining stronger heterosis and broad spectrum of variability in segregating generations. The cluster VI recorded the highest mean value for number of seeds pod^{-1}, 100-seed weight and seed yield plant^{-1}, while cluster VII recorded highest mean value for number of pods plant^{-1} and number of clusters plant^{-1}. Cluster IX had lowest mean values for days to 50% flowering and days to maturity. None of the clusters contained genotypes with all the desirable characters that could be directly selected and utilized. However, for improvement of a particular character, identified accessions from different clusters could be used (Mahajan *et al*., 2010) [18]. Recombination breeding between genotypes of different clusters can be done to combine the desirable characters of different accessions.

Further, the efficacy of D^2 statistics is improved by its applicability to estimate the relative contribution of the various characters towards genetic divergence (Table 4). In

the present study, days to maturity contributed maximum of 38.23% towards divergence followed by seed yield plant^{-1} (22.92%), number of pods plant^{-1} (12.43%), days to 50% flowering (10.70%) and 100-seed weight (9.95%). Hence, these characters could be given due importance for selection of genotypes for further improvement. The contribution of remaining characters *viz*., pod length (2.95%), number of seeds pod^{-1} (1.23%), plant height (0.83%), number of primary branches plant^{-1} (0.61%) and number of clusters plant^{-1} (0.14%) were very low and number of secondary branches plant^{-1} contributed nothing towards total divergence. The low contribution to genetic divergence by these characters might be due to the fact that selection towards uniformity in these characters could have caused an eroding effect on genetic diversity. Das and Borthakur (1973)[19] reported that genetic variability was reduced in the course of selection. There is a possibility of operation of similar phenomenon in characters showing less contribution towards the genetic divergence in the present investigation also.

Table 1: Composition of 10 clusters in pigeonpea

Cluster number	Number of accessions	Constituent genotypes
I	45	PA 235, TAT 103, PA 300, PA 409, PA 429, PA 406, PA 415, PA 392, PA 374, PA 421, PUSA 2001-3, AL 1455, PA 419, AL 1401, PA 414, ICPL 9815, IC 4-1, CORG 99-4, ICPL 88099, UPAS 120, ICPL 1, PA 411, PA 291, AL 345, ICPL 90025, AL 201, RTS 1, ICPL 87115, PUSA 2002-1, P 80-14, PA 288, CORG-1, PUSA 2003-1, ICA 4, ICPL 93081, PA 273, ICPL 86029, PA 116, ICPL 91031, ICPL 870-2775, PA 134, IPA 94-4, PA 351, PA 325, PA 426
II	19	ICPL 98004, PUSA 941, ICPL 86020, PUSA 2001-1, PUSA 2001-2, ICPL 85010, PUSA 951, ICPL 94001, ICPL 98024, ICPL 91011, ICPL 288, ICPL 98009, ICPL 87728, ICPL 86005, ICPL 93021, ICPL 88023, PA 111, ICPL 83024, ICPL 84023
III	1	MATH 1-3
IV	1	TAT 144
V	1	GAUT 210
VI	4	H 82-1, PA 402, PUSA 992, PA 337
VII	1	GAUT 98023
VIII	1	*C. scarabaeoides*
IX	1	*C. platycarpus*
X	1	*Rhynchosia minima*

Table 2: Average inter and intra cluster (diagonal) D^2 values of 10 clusters in pigeonpea

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	13.68	23.08	17.82	18.96	19.15	19.93	26.10	45.01	77.80	73.92
II		11.14	31.58	36.18	36.10	35.13	42.41	34.46	58.87	83.71
III			0.00	12.41	13.75	21.81	13.24	46.82	87.11	62.13
IV				0.00	5.88	15.72	13.98	52.91	91.95	63.46
V					0.00	15.30	14.77	54.33	92.37	64.83
VI						13.43	22.79	57.86	90.46	74.44
VII							0.00	58.01	98.96	60.12
VIII								0.00	53.25	72.56
IX									0.00	124.83
X										0.00

Table 3: Cluster means for eleven characters in pigeonpea

Clusters	DFF	DM	PH	NPB	NSB	NP	NC	PL	NSP	HSW	SYP	Total score
I	88.83 (4)	148.28 (4)	188.01 (5)	11.44 (7)	6.54 (6)	272.48 (4)	166.51 (4)	5.87 (5)	4.41 (6)	8.94 (2)	53.25 (4)	51 (V)
II	70.28 (2)	129.32 (3)	175.42 (7)	9.84 (9)	5.60 (8)	216.51 (7)	139.63 (7)	6.02 (2)	4.42 (5)	8.12 (6)	46.09 (5)	58 (VII)
III	94.67 (5)	159.67 (6)	203.67 (1)	14.67 (2)	9.33 (1)	308.33 (2)	185.33 (2)	5.73 (6)	4.00 (9)	7.75 (7)	38.33 (7)	48 (III)
IV	106.33 (9)	164.33 (8)	185.67 (6)	12.67 (4)	7.67 (2)	275.67 (3)	174.67 (3)	5.37 (7)	4.47 (4)	8.84 (3)	53.33 (3)	52 (VI)
V	104.67 (8)	163.67 (7)	189.33 (4)	13.33 (3)	7.67 (3)	245.33 (6)	145.67 (5)	6.43 (1)	4.13 (8)	8.83 (4)	61.33 (2)	51 (IV)
VI	96.33 (6)	157.83 (5)	201.17 (2)	12.17 (6)	7.50 (4)	250.75 (5)	142.67 (6)	5.93 (3)	4.23 (7)	10.60 (1)	66.50 (1)	46 (I)
VII	98.67 (7)	170.67 (9)	198.00 (3)	12.33 (5)	6.67 (5)	324.33 (1)	205.67 (1)	5.93 (4)	4.53 (2)	8.36 (5)	43.67 (6)	48 (II)
VIII	72.67 (3)	125.67 (2)	61.33 (9)	10.00 (8)	5.67 (7)	115.00 (8)	83.33 (8)	2.63 (9)	4.47 (3)	3.65 (9)	16.67 (8)	74 (VIII)
IX	35.67 (1)	75.67 (1)	85.67 (8)	5.33 (10)	1.67 (10)	54.33 (9)	38.00 (9)	4.20 (8)	4.93 (1)	5.82 (8)	13.67 (9)	74 (IX)
X	126.67 (10)	192.67 (10)	49.00 (10)	23.00 (1)	4.33 (9)	47.67 (10)	35.00 (10)	1.40 (10)	2.00 (10)	1.36 (10)	6.00 (10)	100 (X)

Values in the parentheses are the score given based on the mean performance of each cluster for a particular trait

Table 4: Contribution of 11 characters towards genetic divergence in pigeonpea

Characters	Number of times ranked first	Contribution (%)
Days to 50% flowering	297	10.70
Days to maturity	1061	38.23
Plant height (cm)	23	0.83
Number of primary branches plant^{-1}	17	0.61
Number of secondary branches plant^{-1}	0	0.00
Number of pods plant^{-1}	345	12.43
Number of clusters plant^{-1}	4	0.14
Pod length (cm)	82	2.95
Number of seeds pod^{-1}	34	1.23
Hundred seed weight (g)	276	9.95
Seed yield plant^{-1} (g)	636	22.92

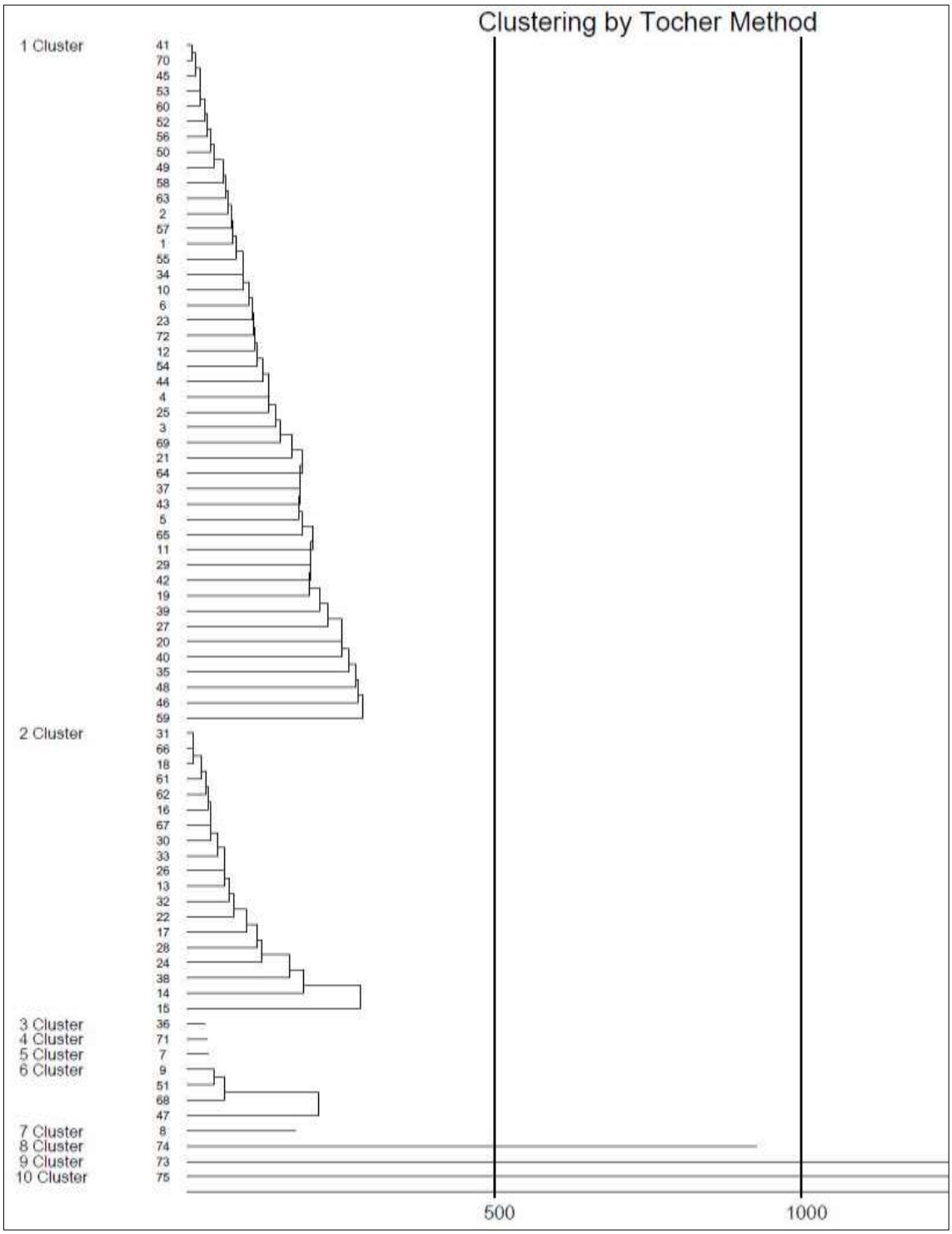

Fig 1: Cluster diagram comprising 75 pigeonpea genotypes grouped into ten clusters

4. Conclusion

The crossing between the entries belonging to cluster pairs having large inter-cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in pigeonpea. Considering the mean performance for different characters of genotypes belonging to diverse clusters, the promising genotypes for exploitation as parents in hybridization programme were H 82-1, Pusa 992, PA 337, PA 402, MATH 1-3, TAT 144, GAUT 210, GAUT 98023, *C. scarabaeoides*, *C. platycarpus* and *Rhynchosia minima*. These genotypes may be recommended for crossing with the genotypes of the clusters showing high inter cluster distances mentioned above for isolating transgressive segregants.

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