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Research Note

Genetic divergence studies in Pigeonpea inbreds

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Abstract

Quantitative assessment of genetic divergence in 47 pigeonpea genotypes (22 B-lines and 25 R-lines) with respect to seed yield and yield components clustered them into 10 different groups. Among the ten clusters, cluster I was the largest comprising of 35 genotypes, representing collections from Andhra Pradesh, Karnataka and Bihar, while the clusters IV, V, VI, VII, VIII and X comprised of one genotype each. The distribution pattern of genotypes into different clusters revealed no parallelism between genetic and geographic diversity. An analysis of inter-cluster D^2 values revealed higher divergence between cluster VIII and cluster IX, followed by cluster IX and X indicated that hybridization between parents selected from these clusters may result in maximum heterosis. Further, the results on cluster means revealed that there was no cluster with at least one genotype with all the desirable traits, indicating the need for judicious combination of all the targeted traits required hybridization between the selected genotypes from divergent clusters. In addition, number of seeds per pod, 100 seed weight, plant height, days to maturity and seed yield per plant together contributed for about 81.31 per cent of the total divergence and hence these traits to be emphasized during selection.

Keywords
Pigeonpea, parental lines, genetic divergence, heterosis.

Annually pigeonpea is grown in an area of 5.83 M ha in the world producing 4.40 M t with a productivity of 754.9 kg ha^{-1} (FAO, 2011). In India, pigeonpea is cultivated in 4.37 M ha with production of 2.86 M t . The leading states in pigeonpea production are Maharashtra (1.30 M ha), Karnataka (0.89 M ha), Madhya Pradesh (0.49 M ha), Uttar Pradesh (0.34 M ha), Gujarat (0.28 M ha) and Andhra Pradesh (0.64 M ha). These six states account for over 70% of the total pigeonpea area and production in India. Due to low productivity of pigeonpea in India (around 600 kg/ha), Indian Government annually imports about 0.5 to 0.6 M t of pigeonpea mainly from Myanmar and southern and eastern Africa (Saxena and Nadarajan, 2010).

Breeding and selection of high yielding genotypes and hybrids was therefore proposed as the best long term solution for minimizing the constraints underlying stagnant productivity in the crop. In this context, large and diverse germplasm collection of parental strains for hybridization and subsequent development of improved varieties is an invaluable source. With the development of commercial hybrid pigeonpea programme at ICRISAT in collaboration with ICAR (Indian Council of Agricultural Research), several genetically diverse CMS lines and their fertility restorers were developed which can be exploited for developing widely adaptable hybrids to different agro-ecological areas and cropping systems. The present study with 47 genotypes is an attempt in this direction to ascertain the nature and magnitude of genetic diversity in B and R lines in addition to identification of parents with wide genetic base for realizing maximum heterosis in the pigeonpea hybrids.

The present study was conducted during *kharif*, 2013 at College Farm of Agricultural College, Mahanandi 15° 51' N latitude and 78° 61' E longitude, at an altitude of 233.48 m above mean sea level, which falls under the Scarce Rainfall Agro-Climatic Zone of Andhra Pradesh. The experimental material for present investigation comprised of 22 B-lines and 25 R-lines obtained from International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru was evaluated in a randomized complete block design with two replications. The experimental materials was sown on August 8, 2013 in single-row plots with 3 m length with inter and intra-row spacing of 120cm and 30 cm, respectively. Border rows were planted around the entries to increase the precision of study and reduce border effect. All recommended agronomic practices were followed for parents and hybrids to keep the crop in good condition. Necessary and need based plant protection measures were also taken up to obtain a healthy crop. Observations were recorded on five randomly selected plants for nine characters such as days to 50% flowering, days to maturity, plant height, number of primary branches for plant, number of secondary branches for plant, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant. Using Mahalanobis D^2 statistic (1936) and Tocher's method, the genotypes were grouped into different clusters as described by Rao (1952).

The analysis of variance for 47 genotypes studied in the present investigation for yield and yield components revealed significant differences among the genotypes for all the characters studied indicating the presence of sufficient variation among the genotypes. Quantitative assessment of genetic divergence in 47 genotypes was made by adopting Mahalanobis D^2 statistic for yield and yield contributing characters. Wilk's criterion test was used based on the pooled effects of all the characters (Tables 1, 2). The 47 genotypes were grouped into ten clusters based on the relative magnitude of D^2 values. Further, among the ten clusters, cluster I was the largest comprising of 35 genotypes, representing collections from Andhra Pradesh, Karnataka and Bihar, while clusters II, III and IX consisted of two genotypes each from Andhra Pradesh. The clusters IV, V, VI, VII and VIII comprised of one genotype each from Andhra Pradesh. However, cluster X consisted of one genotype from Uttar Pradesh. The distribution pattern of genotypes into different clusters revealed no parallelism between genetic and geographic diversity as genotypes chosen from same eco-geographical region were found in different clusters as well as in the same cluster. Magar (2003) and Katiyar (2004) reported that the distribution of genotypes from different eco geographical regions into clusters was random indicating geographical distribution does not necessarily exhibit genetic divergence.

An analysis of the inter-cluster D^2 values of ten clusters obtained in the present study (Table 2) revealed highest divergence between cluster VIII and cluster IX (842.70), followed by cluster IX and X (786.19) indicating that genotypes from these clusters were highly divergent and hence selection of parents for hybridization from these clusters is suggested for realization of maximum heterosis. Sreelakshmi and Sameer kumar (2011) also reported greater diversity between genotypes from different clusters based on their inter-cluster distance. Minimum inter-cluster distance was observed between cluster V and VIII (73.46), indicating their close relationship and similarity with regards to the characters studied for most of the genotypes in the two clusters. Further, intra-cluster distance was observed to be zero for clusters IV, V, VI, VII,VIII and X, since these clusters comprised of only one genotype, each. In contrast, maximum intra-cluster distance was noticed for cluster lX (90.03). The genotypes included in cluster IX are therefore inferred to be more divergent than those in other clusters.

The cluster means for each of the nine characters are presented in Table 3. A perusal of these results revealed highest cluster mean for days to 50 per cent flowering (139.00), days to maturity (209.00), plant height (309.50), number of primary branches per plant (30.50), number of secondary branches per plant (120.50) in cluster X. However, highest cluster mean for number of pods per plant (315.50) was recorded in cluster VII; for number of seeds per pod (5.70) and 100 seed weight (19.88) in cluster IX; and for seed yield per plant (243.45) in cluster VI, indicating the importance of selection of genotypes from the corresponding clusters in hybridization programmes for affecting improvement in the respective traits. Further, minimum value for days to 50 per cent flowering (114.50) and number of seeds per pod (2.65) was recorded in cluster VIII; days to maturity (166.50) in cluster VII; plant height (97.00), number of secondary branches per plant (20.75), number of pods per plant (68.75) and seed yield per plant (57.75) in cluster III; and number of primary branches per plant (10.75) in cluster IX. An analysis of these results also revealed that there was no cluster with at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, judicious combination of all the targeted traits requires hybridization between the selected genotypes from divergent clusters.

Information on the relative contribution of various plant characters towards divergence was reported to aid the breeder in choice of parents for hybridization and effective selections (Visakho Shunyu Chaturvedi *et al.*, 2013). The number of times that each of the nine characters studied in the present investigation appeared first and their respective per cent contribution towards diversity is presented in Table 4. Number of seeds per pod contributed maximum (18.13 %) followed by 100 seed weight (17.76 %), plant height (17.67 %), days to maturity (16.65%) and seed yield per plant (11.10%) towards the total divergence. Contribution of the remaining characters to the total divergence was however, relatively low. Therefore, number of seeds per pod, 100 seed weight, plant height, days to maturity and seed yield per plant contributing to 81.31 per cent of the total divergence need to be stressed in selection of parents for hybridization.

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Table 1. Distribution of 47 genotypes of pigeonpea into different clusters

Cluster Number	Number of genotypes	Genotype(s)	Source
I	35	ICPB 2048, ICPL 20128, ICPB 2047, ICPL 87119, ICPL 20136, BRG1, ICPL 20098, ICPL 20117, ICPL 20116, ICPL 20093, ICPB 2151, ICPL 20111, ICPB 2188, ICPL 20137, ICPL 20108, ICPB 2170, ICPL 20120, ICPL 20123, ICPB 2195, ICPL 20204, ICPL 20186, ICPB 2198, ICPB 2098, ICPB 2197, ICPL 20129, ICPB 2199, ICPB 2189, ICPL 20103, ICPL 20126, ICPL 20106, ICP 8094, ICPL 20125, ICPL 20096, ICPL 20117, ICPL 20107.	Andhra Pradesh, Bihar, Karnataka
II	2	ICPB 2193 , ICPB 2196	Andhra Pradesh
III	2	ICPB 2078, ICPB 2101	Andhra Pradesh
IV	1	ICPL 99046	Andhra Pradesh
V	1	ICPB 2092	Andhra Pradesh
VI	1	ICPB 2194	Andhra Pradesh
VII	1	ICPB 2043	Andhra Pradesh
VIII	1	ICPB 2042	Andhra Pradesh
IX	2	ICPB 2166, ICPB 2209	Andhra Pradesh
X	1	ICPL 11811	Uttar Pradesh

Table 2. Average inter and intra cluster distances for 47 pigeonpea genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	64.06	124.94	265.96	105.84	109.22	116.27	119.89	168.52	509.31	204.60
II		18.93	166.42	202.66	152.00	203.99	161.78	203.99	580.02	357.58
III			28.37	254.99	332.76	331.19	286.74	423.15	426.18	678.30
IV				0.00	260.39	142.29	243.16	310.71	528.26	236.92
V					0.00	112.22	126.71	73.46	595.66	244.76
VI						0.00	218.33	224.61	391.91	216.95
VII							0.00	153.01	507.78	391.57
VIII								0.00	842.70	301.17
IX									90.03	786.19
X										0.00

Table 3.Cluster means for yield and yield components in 47 pigeonpea genotypes

Cluster Number	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of pods per plant	Number of seeds per pod	100-seed weight (g)	Seed yield per plant (g)
I	121.10	183.56	222.16	24.14	93.23	272.97	3.83	15.09	161.20
II	125.00	187.25	130.25	18.75	88.75	174.50	3.51	13.71	98.13
III	118.00	173.50	97.00	11.75	20.75	68.75	3.30	17.38	57.75
IV	118.50	190.50	216.50	22.50	99.00	303.00	3.55	19.00	181.25
V	121.50	173.00	225.00	22.50	97.50	200.50	3.56	13.41	148.75
VI	118.00	183.00	229.50	19.00	111.50	262.00	4.25	16.85	243.45
VII	119.00	166.50	195.00	17.50	68.00	315.50	3.75	13.60	164.00
VIII	114.50	177.50	222.00	15.00	58.00	233.00	2.65	11.27	106.25
IX	122.50	174.00	204.25	10.75	29.50	116.00	5.70	19.88	84.83
X	139.00	209.00	309.50	30.50	120.50	299.50	3.75	16.40	157.50

Table 4. Relative contribution of characters studied towards genetic divergence in pigeonpea

Character	Times Ranked 1st	Contribution (%)
Days to 50 per cent flowering	19	1.76
Days to maturity	180	16.65
Plant height (cm)	191	17.67
Number of primary branches per plant	93	8.60
Number of secondary branches per plant	55	5.09
Number of pods per plant	35	3.24
Number of seeds per pod	196	18.13
100-seed weight (g)	192	17.76
Seed yield per plant (g)	120	11.10