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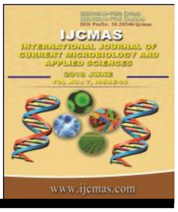

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Genetic Divergence among Pigeonpea Genotypes Using Mahalonobis D^2 Statistics

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ABSTRACT

Keywords

Mahalanobis D^2 statistic, Pigeonpea, Cluster analysis, Cluter mean, % contribution

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The present study was conducted to evaluate the genetic divergence among twenty five pigeonpea germplasm using Mahalonobis D^2 statistics for seven different traits during kharif 2015. Analysis of variance depicted the significant differences among the traits which indicated the presence of variability in the germplasm. D^2 clustering grouped the genotypes into ten clusters. Based on the intercluster distance (1844.86) cluster VIII and X were the most diversified clusters and genotypes from these clusters can be used in the hybridization programme for further improvement. The selection and choice of genotypes as parents mainly depends upon contribution of characters towards divergence. The maximum contribution to genetic divergence was contributed by days to fifty percent flowering and single plant yield followed by number of seeds per pod, plant height and hundred seed weight. Hence selection for these traits would be rewarding in selection of genotypes for hybridization programme.

Introduction

Pigeonpea [*Cajanus cajan* L. Millsp.] is an important food legume crop all over 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. If consumed in combination with cereals, it makes well-balanced human diet. 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. 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 D^2 statistics has been found useful in selecting genetically divergent parents for hybridization Mahalanobis. (1936). Therefore in this study D^2 statistics is used to identify the extent of genetic diversity.

Materials and Methods

Experiment detail

A total of two hundred pigeon pea genotypes of diverse origin obtained from International Crop Research Institute for Semi-Arid Tropics, Hyderabad were used in this experimental study. Out of two hundred genotypes, 26 genotypes such as TO 201, TO202, TO 203, TO206, TO 215, TO266, TO270, TO233, TO235, TO236, TO 240, TO237, TO244, TO265, TO268, TO230, TO247, TO234, TO263, TO272, TO275, TO276, TO287, TO226, TO243 were used for genetic variability studies. The experiment was laid out in a Randomized Block Design with two replication under irrigated conditions at the Research block of Department of Plant Breeding and Genetics, Agricultural and Research institute, Madurai, during *kharif* 2015. Each genotype was raised in two rows of three metre length with a spacing of 60×30 cm.

Data collection

The observations were recorded on five randomly selected plants in each replication and average was worked out and used for statistical analysis. The randomly selected plants in all genotypes were labelled for recording the observations.

The following quantitative characters were studied *i.e.*, days to fifty percent flowering (DFF), plant height (PH) (cm), number of primary branches per plant (PB), number of pods per plant (NP), number of seeds per pod (SP), hundred seed weight (HSW) (g), single plant yield (SPY) (g).

Statistical analysis

The mean values for the seven biometrical traits were utilized for the analysis of variance test to test the significance variability in the traits. Then the data were analysed for diversity using Mahalanobis D^2 statistic (Mahalanobis, 1936).

Results and Discussion

In the present study, twenty six genotypes were grouped totally into ten clusters which represent the presence of maximum diversity and it could be used for further crop improvement programme.

Cluster I had maximum number of genotypes (8) where all the other nine clusters had two genotypes per cluster (Table 1). The pattern of distribution of pigeonpea genotypes in various clusters revealed existence of considerable diversity present in the material (Nag and Sharma, 2012). The genotypes included within the cluster had narrow variability whereas, genotypes between clusters exhibit wider variability. Thus, it depicted that twenty six genotypes of different 10 clusters are of heterogenous origin. These results are in conformity with Pandey *et al.*, (2013).

The average intra and inter cluster distances of seven quantitative traits of pigeonpea genotypes were presented in the Table 2. The maximum intra cluster distance was recorded for the cluster X (1168.27) followed by cluster I (775.70). It indicated the presence of genetic divergence in the genotypes within these clusters. The minimum intra cluster distance were observed for cluster II (23.25) followed by cluster III (26.24). It revealed that the genotypes within these clusters are genetically similar with narrow variability. These results were similar with the earlier findings of Murthy and Dorairaj (1990) and Thombre *et al.*, (2000).

Table.1 D^2 cluster by 26 genotypes for seven quantitative traits of pigeon pea

CLUSTER	Number of Genotypes	Name of the genotypes
I	8	APK1, TO201, TO202, TO203, TO206, TO215, TO266, TO270
II	2	TO233, TO235
III	2	TO236, TO 240
IV	2	TO237. TO244
V	2	TO265, TO268
VI	2	TO230, TO247
VII	2	TO234, TO263
VIII	2	TO272, TO275
IX	2	TO276, TO287
X	2	TO226, TO243

Table.2 Average of intra (bold) and inter cluster distances of seven quantitative traits

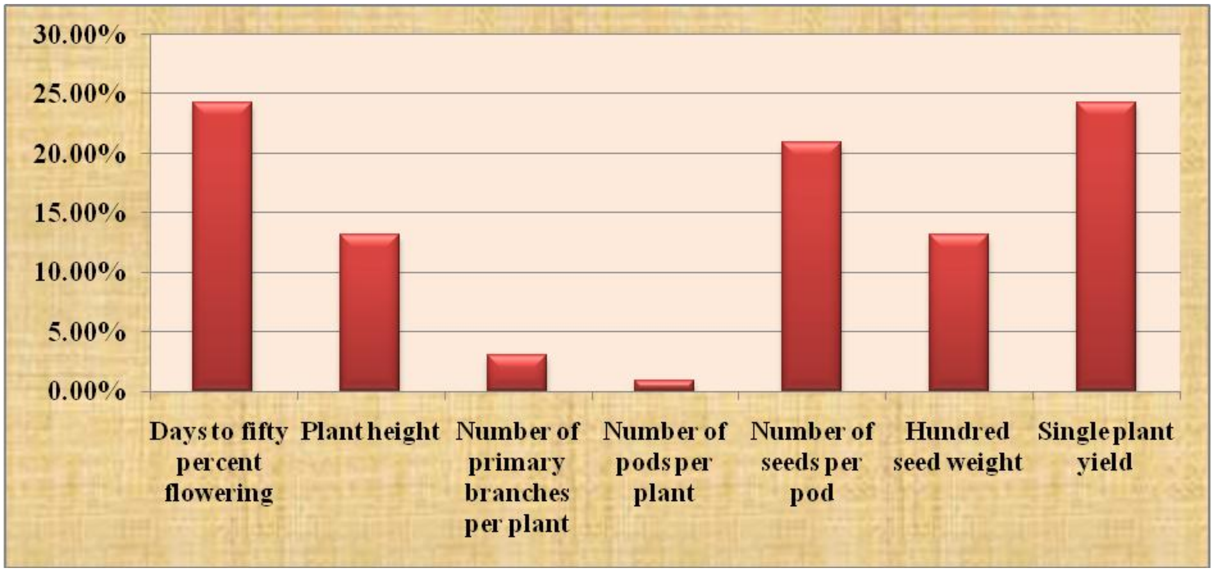
CLUSTER	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**775.70**	590.40	594.37	589.75	592.38	594.81	598.28	599.23	595.52	1646.74
II	590.40	**23.25**	74.67	37.90	42.49	105.56	81.10	101.60	90.49	1835.65
III	594.37	74.67	**26.24**	80.93	80.07	156.17	134.90	47.38	153.41	1841.54
IV	589.75	37.90	80.93	**30.98**	62.16	91.11	98.60	105.92	84.55	1835.51
V	592.38	42.49	80.07	62.16	**42.85**	133.19	67.28	103.01	108.91	1835.09
VI	594.81	105.56	156.17	91.11	133.19	**44.84**	148.26	181.02	73.95	1834.44
VII	598.28	81.10	134.90	98.60	67.28	148.26	**54.34**	153.71	105.42	1833.37
VIII	599.23	101.60	47.38	105.92	103.01	181.02	153.71	**71.14**	176.21	1844.86
IX	595.52	90.49	153.41	84.55	108.91	73.95	105.42	176.21	**75.77**	1832.95
X	1646.74	1835.65	1841.54	1835.51	1835.09	1834.44	1833.37	1844.86	1832.95	**1168.27**

Table.3 Cluster mean values for seven quantitative traits of pigeon pea for 26 genotypes

CLUSTER	DFF	PH	PB	NP	SP	HSW	SPY
I	97.44	213.38	8.56	86.81	4.25	9.38	6.81
II	94.75	261.50	9.25	78.00	4.00	8.38	10.77
III	77.75	239.50	7.50	48.50	4.00	9.23	6.95
IV	99.50	231.75	9.50	190.75	4.00	7.70	6.50
V	84.25	300.75	15.75	95.25	4.00	9.03	5.31
VI	126.75	186.00	7.75	84.50	4.00	7.20	5.27
VII	87.50	343.75	13.50	136.00	4.00	7.55	6.35
VIII	72.75	236.25	11.75	90.25	4.00	6.53	6.28
IX	116.25	243.25	6.75	147.25	4.00	4.78	4.52
X	98.75	214.50	10.75	111.50	5.50	7.23	6.34

Table.4 Relative contribution of seven quantitative traits of pigeon pea towards divergence

Character	No. of first rank	% contribution
Days to fifty percent flowering	79	24.31
Plant height	43	13.23
Number of primary branches per plant	10	3.08
Number of pods per plant	3	0.92
Number of seeds per pod	68	20.92
Hundred seed weight	43	13.23
Single plant yield	79	24.31
Total	325	100.00



Maximum inter cluster distance (1844.86) between the cluster X and cluster VIII followed by cluster X and III with the distance 1841.54. Selection of genotypes between these clusters will exhibit more vigorous heterotic recombinants with wider variations in the segregating populations. Similarly Manyasa (2009) and Gupta *et al.*, (2008) suggested that the genotypes belonging to these clusters may further be used as parents for hybridization programme to develop desirable types because crosses between genetically divergent parents will generate transgressive segregants.

Cluster mean values were furnished in the Table 3. Cluster VI recorded the highest mean value (126.75) for days to fifty percent flowering while the least value (72.75) in cluster VIII. Plant height recorded the highest mean value (343.75) in the cluster VII whereas the least value (186.00) in the cluster VI. Cluster V had the highest mean value (15.75) for number of primary branches per plant whereas the least value (6.75) in the cluster IX. Cluster IV had the highest mean value (190.75) for number of pods per plant and the least value (48.50) for number of pods per plant in the cluster III. Cluster X recorded the highest mean value (5.50) of number of seeds per pod. Cluster I had the highest mean value (9.38) for hundred seed weight whereas the hundred seed weight and the single plant yield with the lowest mean value (4.78) and (4.52) respectively were recorded in cluster IX. The highest single plant yield (10.77) recorded in the cluster II. Critical assessment of clusters showed that clusters were heterogeneous within themselves and between each other based on major character relation (Satapathy and Panigrahi, 2015) (Table 4). The experimental findings of cluster analysis are in general agreement with the findings of Sarma and Roy (1994), Nandan *et al.*, (1996), Basawarajaiah *et al.*, (2000) and Gohil (2006).

In this context, the highest contribution in the manifestation of genetic divergence contributed by days to fifty percent flowering and single plant yield which is in accordance with (Navneet *et al.*, 2017) followed by seeds per pod followed by plant height and hundred seed weight. The genotypes TO272, TO275 in the cluster VIII have highest mean value 236.25 for plant height whereas the genotypes TO226, TO243 of the cluster X recorded more number of seeds per pod. Thus selection of genotypes for hybridization between these clusters will yield more variable segregants.

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