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GENETIC DIVERGENCE FOR SELECTION OF PARENTS FOR HYBRIDIZATION IN *LATHYRUS*

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ABSTRACT

Fifty-seven genotypes were evaluated for genetic divergence to identify the likely desirable and potential parents for *lathyrus* breeding programme aimed at yield and earliness improvement. These genotypes were grown in randomized completed block design replicated thrice and observations were recorded for days to 50 % flowering, days to maturity, plant height (cm), number of primary branches plant^{-1} , number of pods plant^{-1}, number of seeds pod^{-1}, 100 seed weight (g) and yield plant^{-1}(g). Mahalanobi's generalized distance for eight characters was used in this study for computing genetic divergence.

The analysis of dispersion for eight corrected variables using Wilk's criterion, revealed highly significant difference between genotypes for aggregate of the eight characters. The 57 genotypes were grouped into eight clusters by Tocher's method. The maximum inter cluster distance was recorded between cluster IV and cluster VIII (110.67). The canonical analysis indicated that the plant height at maturity, number of pods plant^{-1}, yieldplant$^{-1,}$ days to 50 % flowering, number of seeds pod$^{-1,}$, number of primary branches plant^{-1} and days to maturity were significant and important sources of variation in the vector I and in vector II. In vector III, days to 50 % flowering, days to maturity, number of seeds pod^{-1} and 100 seed weight were important sources of variation. The genotypes belonging to distant cluster exhibiting high performance in the desirable direction for plant height, yield plant^{-1}, days to 50 % flowering and number of pods plant^{-1} were identified as the potential parents for hybridization programme. The 20 genotypes *viz*., L-3, L-31, L-33, L-25, L-32, JRL-16, RLK-279, L-37, RLK-1045, L-44, L-14, L-07, L-08, RLK-240, L-39, L-05, RLK-602, L-16 and BioR-208 were identified as potential and diverse parents for their use in crossing programme.

(Key words : *Lathyrus*, genetic divergence, hybridization, D^{2}statistics)

INTRODUCTION

Lathyrus is an important pulse crop and considered as a model crop for sustainable agriculture. The cultivation of lathyrus is predominant in India, Bangladesh, Ethiopia and Nepal. In India, its cultivation is mainly confined to states of U. P., Bihar, West Bengal, Madhya Pradesh, Chhattisgarh, Maharashtra and also in small pockets of other states. It is a very sturdy crop with a deep penetrating root system and can be grown on a wide range of soil types. The importantance of this crop as a pulse is due to its high seed protein content (28%) as reported by Mehra (1991).Sharma and Padmanabham (1969) analysed and reported that the protein quality of lathyrus seed is better than any other pulse crop. When other crops fail, lathyrus often becomes the principal food source for the poor. Indeed, it may be the only source of food available during drought and famine. However, eating large amount of lathyrus can cause "neurolathyrism" an irreversible paralysis of the lowest limbs. *Lathyrus* varieties generally have low yield potential, poor plant type and high neurotoxin content which is unstable over environment (Ramanujam *et al.,* 1980). First step in direction of *lathyrus* improvement is to create gene pool of superior line with desirable agronomical traits, from which the genetically diverse cultivars could be identified, evaluated and utilized in plant breeding programme, hence to know the performance of constantly emerging new accessories and genetic distance among themselves, genetic divergence need to be accessed for choice of parent for crop improvement programme. Therefore, the present study was conducted to study the genetic divergence in *lathyrus*.

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MATERIALS AND MEKTHODS

Fifty-seven genotypes of diverse eco-geographical background including fifty-four genotypes and three checks Ratan, Pratik and Mahateora of *lathyrus* were grown in randomized complete block design with three replications during *rabi* 2011 in the farm of Agril. Botany Section, College of Agriculture, Nagpur. Each genotype was grown in single row plot with inter and intra row spacing of 45 cm and 15 cm. The recommended cultural practices were followed to raise good crop. The data were recorded on five randomly selected plants in each replication on eight characters like plant height (cm). number of primary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, 100 seed weight (g) and yield plant^{-1} (g) except days to 50% flowering and days to maturity for which all the plants in the row were considered. The data were subjected to the statistical and biometrical analysis. In order to assess the genetic diversity among distinct genotypes, the D^2 statistics developed by Mahalanobis (1928) were utilized, grouping of genotypes into different clusters and canonical analysis were done by using Tocher's method described by Rao (1952). Selection of parents for hybridization from different clusters was done on the basis of mean statistical distance as suggested by Bhatt (1970).

RESULTS AND DISCUSSION

The mean squares for genotypes were highly significant for all eight characters *i.e.*days to 50% flowering, days to maturity, plant height at maturity, number of primary branches plant^{-1}, number of pods plant$^{-1.}$,100 seed weight and yield plant^{-1}. This indicates significant variation among all the genotypes for the eight characters. The wide variability for yield plant^{-1}, and yield contributing characters were also observed by Shanmugasundaram and Rangasamy (1994) in blackgram and Bhalekar (2008) in *lathyrus*. The genotype RLK-279 (65.67days) took maximum number of days to 50 % flowering whereas, the genotype L-03 (50.67 days) and L-32 (50.67 days) was earliest as observed from table 1. The genotype BioR-231 (126.33 days) took maximum number of days to maturity whereas the maximum height was recorded by genotype RLK-602 (76.93 cm) and minimum by genotype L-03 (38.40 cm). The maximum number of primary branches were recorded by genotype BioR-222 (6.07) and minimum was recorded by genotype L-34 (3.47). The maximum seeds pod^{-1} was recorded by genotype Bio R-208 (3.47) and minimum was recorded by genotype L-41(2.0). The maximum pods plant^{-1}was recorded by genotype JRL-16 (93.27) and minimum was recorded by the genotype L-03 (42.4). The genotype BioR-208 (8.07) recorded maximum 100 seed weight while, the genotype L-36 (6.33 g) recorded minimum 100 seed weight. The maximum grain yield plant^{-1} was recorded by genotype BioR-208 (23.19 g) whereas, minimum in genotype L-40 (6.45 g). On the basis of *per se* performance studied for yield and yield contributing characters among fifty-seven genotypes, the genotypes L-14, L-44, BioR-208, BioR-222, JRL-16 and RLK-1045 were found to be either significantly superior or at par with Ratan for yield and important yield components like number of pods plant^{-1}, number of seeds pod^{-1} and 100-seed weight (g). The *per se* performance of genotypes gives only some indication of their usefulness in selecting a potential genotype combination and identifying the genotype combinations on the basis of genetic divergence will give the required information from *per se* performance of genotypes.

The analysis of dispersion for test of significance of differences in the mean values based on Wilk's criterion revealed highly significant difference between the genotypes for aggregate of eight characters (X^2=1.4660 E+03 at 448 d.f.). Therefore, the data were further evaluated for D^2 and cluster analysis. The per cent contribution of individual character toward genetic divergence is taken as the measure for relative importance of the characters towards genetic divergence. In present study, data regarding the per cent contribution of individual characters towards genetic divergence are given in table 2. The plant height at maturity exhibited maximum contribution towards genetic divergence (36.59%) followed by seed yield plant^{-1} (30.95%) and number of seeds pod^{-1}(14.79%). These observations were in conformity with those reported by Nambdoori (1997) and Palkar *et al.*(2019) that plant height, 100 seed weight and days to maturity exhibited maximum contribution towards genetic divergence.

The data regarding grouping of 57 genotypes are given in table 3 and fig 1. The entire genotypes on the basis of D^2 statistics were grouped into eight clusters. Cluster II was the largest comprising of 20 genotypes. The next largest cluster was cluster V which included 16 genotypes, cluster I and cluster VI included 12 and 5 genotypes each. Cluster III, cluster IV, cluster VII and cluster VIII included only one genotype each. The promising check Ratan and Mahateora were grouped in cluster V, fourteen other genotypes were also included in the same cluster. Similarly, in cluster II, 19 genotypes along with promising check Prateek were included. The results on distribution of genotypes are not varying from check variety. But there were many genotypes distributed in other cluster which were deviating from promising check and hence offers scope for improvement.

The values of first three canonical vectors and canonical roots are given in table 4 and table 5. The first two canonical roots accounted for 60.576% of the observed variability in material ($\bullet_1$=38.464% and $\bullet_2$=22.112%). The overall contribution of the three canonical roots to total variability among 57 genotypes was 70.729 % suggesting the completion of major portion of differentiation in first three phases. This indicated that differentiation for eight characters among 57 genotypes was nearly completed upto 70.729 % in three phases and still 29.27% differentiation is yet to complete. Further the coefficient in the first three canonical vectors indicates that out of eight quantitative characters the plant height at maturity, pods plant^{-1}, days to 50 % flowering, seeds pod^{-1}, number of primary branches and days to maturity were significant and important sources of variation in the vector I, which was major axis of differentiation accounting for 38.464 per cent of total variation. Primary branches, days to maturity, days to 50%

Table 1. Mean performance of genotypes for different characters

Sr. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height at maturity (cm)	No. of primary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Yield plant^{-1} (g)
1	L-01	52.33	118.67	42.13	4.13	51.13	2.33	6.97	6.46
2	L-02	52.33	120.33	47.07	4.33	56.87	2.47	7.03	11.28
3	L-03	50.67	118.00	38.40	3.93	42.40	2.13	6.70	6.72
4	L-04	58.33	124.67	55.87	4.27	71.60	2.60	7.13	15.08
5	L-05	52.00	119.00	45.80	4.07	63.13	2.47	7.20	7.82
6	L-06	56.33	122.67	54.07	4.13	68.60	2.67	7.00	9.79
7	L-07	51.33	121.33	58.27	4.00	66.27	2.33	6.83	9.78
8	L-08	56.33	122.33	57.80	3.93	62.33	2.80	7.10	11.78
9	L-09	58.00	121.00	53.47	3.67	59.47	3.07	7.37	15.34
10	L-10	55.33	124.67	61.80	4.13	68.00	3.13	6.90	14.46
11	L-11	57.67	124.00	59.80	4.67	70.87	2.27	7.10	9.71
12	L-12	52.67	117.67	44.33	3.93	48.93	2.67	6.53	7.24
13	L-13	57.33	123.67	54.20	3.73	64.93	2.67	7.03	14.36
14	L-14	56.33	123.00	57.33	4.20	85.73	3.00	7.33	20.64
15	L-15	56.33	124.33	64.13	5.13	81.80	2.60	7.30	17.52
16	L-16	54.67	119.67	45.80	3.80	55.67	2.80	7.00	9.97
17	L-17	58.33	124.00	53.13	4.13	69.73	2.27	6.60	7.94
18	L-18	56.33	123.67	56.53	4.40	71.93	2.47	7.37	12.56
19	L-19	59.33	124.33	63.80	5.20	79.13	3.33	7.47	15.74
20	L-20	54.67	120.33	47.13	3.80	54.53	2.33	6.43	7.43
21	L-21	54.33	121.33	52.20	4.20	50.27	2.67	7.40	10.65
22	L-22	57.67	122.33	54.73	4.60	68.40	2.40	7.27	9.77
23	L-23	56.00	124.67	50.53	3.67	48.73	2.20	7.53	6.80
24	L-24	54.67	122.33	56.60	4.33	63.47	2.73	6.63	10.18
25	L-25	54.67	121.00	50.93	4.20	56.87	2.40	6.70	7.41
26	L-26	58.33	123.67	57.40	5.20	70.67	2.93	7.10	11.42
27	L-27	61.67	124.33	55.07	4.20	54.33	2.80	7.03	13.54
28	L-28	60.33	124.67	53.20	4.60	69.87	2.53	6.90	13.79

(Contd.)

29	L-29	52.33	118.00	42.93	3.67	48.13	2.33	6.93	7.16
30	L-30	55.67	122.33	49.00	3.67	61.27	2.73	6.97	14.15
31	L-31	55.33	123.33	53.47	4.20	57.27	2.60	6.73	7.81
32	L-32	50.67	119.33	48.53	4.00	64.20	2.27	7.23	13.08
33	L-33	55.33	122.67	53.13	4.27	56.20	2.47	7.20	7.52
34	L-34	58.33	122.67	48.07	3.47	53.53	2.47	6.87	11.10
35	L-35	60.67	125.33	60.60	5.27	72.00	2.47	7.33	14.50
36	L-36	59.33	126.00	58.73	5.13	81.27	2.93	6.33	19.28
37	L-37	51.00	119.33	44.87	3.53	51.33	2.67	7.13	13.24
38	L-38	56.67	118.67	54.13	3.73	56.07	2.87	6.77	7.82
39	L-39	54.67	120.33	47.67	4.40	66.47	2.20	6.93	8.00
40	L-40	56.33	120.67	46.60	4.13	47.73	2.27	6.83	6.45
41	L-41	51.33	119.00	48.67	4.80	64.13	2.00	6.47	9.72
42	L-42	58.33	126.00	63.93	5.33	83.93	2.20	6.80	17.56
43	L-43	55.67	124.33	62.53	4.86	62.80	2.20	6.60	9.47
44	L-44	52.33	119.67	66.33	5.60	87.00	2.93	7.27	20.87
45	BioR-208	61.67	125.67	76.40	4.13	85.93	3.47	8.07	23.19
46	BioR-231	60.33	126.33	67.20	4.73	80.13	2.60	7.60	18.92
47	Bio-222	59.33	117.67	76.60	6.07	87.47	2.87	6.93	20.26
48	JRL-16	64.67	119.67	54.93	4.20	93.27	2.47	7.93	23.11
49	JRL-115	63.67	118.67	69.87	4.53	87.27	2.80	8.00	15.85
50	RLK-1093	56.67	120.67	74.60	4.40	74.40	2.67	7.00	17.96
51	RLK-602	60.00	122.33	76.93	4.93	78.27	2.53	7.33	10.53
52	RLK-1045	62.67	119.33	65.60	4.00	86.00	3.20	7.17	22.78
53	RLK-279	65.67	118.00	51.80	3.87	54.93	2.40	6.83	8.58
54	RLK-240	63.33	120.67	55.60	4.40	62.20	2.40	6.53	8.05
55	Ratan	62.67	122.33	60.73	4.60	67.67	2.53	6.87	14.27
56	Prateek	56.67	120.67	56.60	4.47	57.40	2.07	6.73	7.42
57	Mohateora	63.00	125.33	63.60	4.80	65.53	2.80	7.13	11.46
	Grand Mean	56.99	121.88	55.99	4.35	66.13	2.59	7.04	12.32
	SE(m)±	1.1107	1.6688	1.7021	0.3025	4.2653	0.1020	0.2579	0.8716
	CD 5%	3.1122	4.6762	4.7693	0.8478	11.9517	0.2858	0.7227	2.4424
	CV%	3.3756	2.3718	5.2657	12.0216	11.1714	6.8273	6.3422	12.2588

Table 2. Contribution of individual character to divergence

Sr. No.	Source	Time ranked I	Contribution %
1	Days to 50 % flowering	203	12.72
2	Days to maturity	2	0.13
3	Plant height at Maturity (cm)	584	36.59
4	Number of primary branches plant^{-1}	14	0.88
5	Number of pods plant^{-1}	46	2.88
6	Number of seeds pod^{-1}	236	14.79
7	100 seed weight (g)	17	1.07
8	Yield plant^{-1} (g)	494	30.95
	Total	1596	100

Table 3 Grouping of 57 genotypes of lathyrus in different clusters

Cluster	Total no. of genotypes	Genotypes
I	12	L-01,L-05,L-12,L-16,L-20,L-25,L-29,L-31,L-33,L-34,L-39,L-40
II	20	L-02,L-04,L-06,L-07,L-08,L-09,L-11,L-13,L-17,L-18,LL-21,L-22,L-23, L-24,L-26,L-27,L-28,L-30,L-38, Prateek
III	1	L-32
IV	1	L-3
V	16	L-10,L-14,L-15,L-19,L-35,L-36,L-42,L-43,L-44,BioR-231,BioR-222, JRL-115,RLK-1093,RLK-1042,Ratan, Mahateora
VI	5	L-37, L-41,JRL-16,RLK-279,RLK-240
VII	1	RLK-602
VIII	1	BioR-208

Table 4. The value of first three canonical vectors and canonical roots

Vector	Days to 50% flowering	Days to maturity	Plant height at maturity	No. of primary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Yield plant^{-1} (g)
I	0.343	30.304	0.502	0.308	0.414	0.319	-0.067	0.406
II	0.068	0.229	0.156	0.489	-0.261	-0.373	-0.601	-0.332
III	0.772	0.276	-0.038	-0.411	-0.318	0.066	0.066	-0.217

Table 5. Value of three canonical root and their contribution expressed as per cent of the total variation

Root	Value	Contribution in %
• 1	3.077	38.464
• 2	1.769	22.112
• 3	0.812	10.153
Total	5.658	70.729
Sum of canonical root	7.999	-
Residual	2.3415	29.271

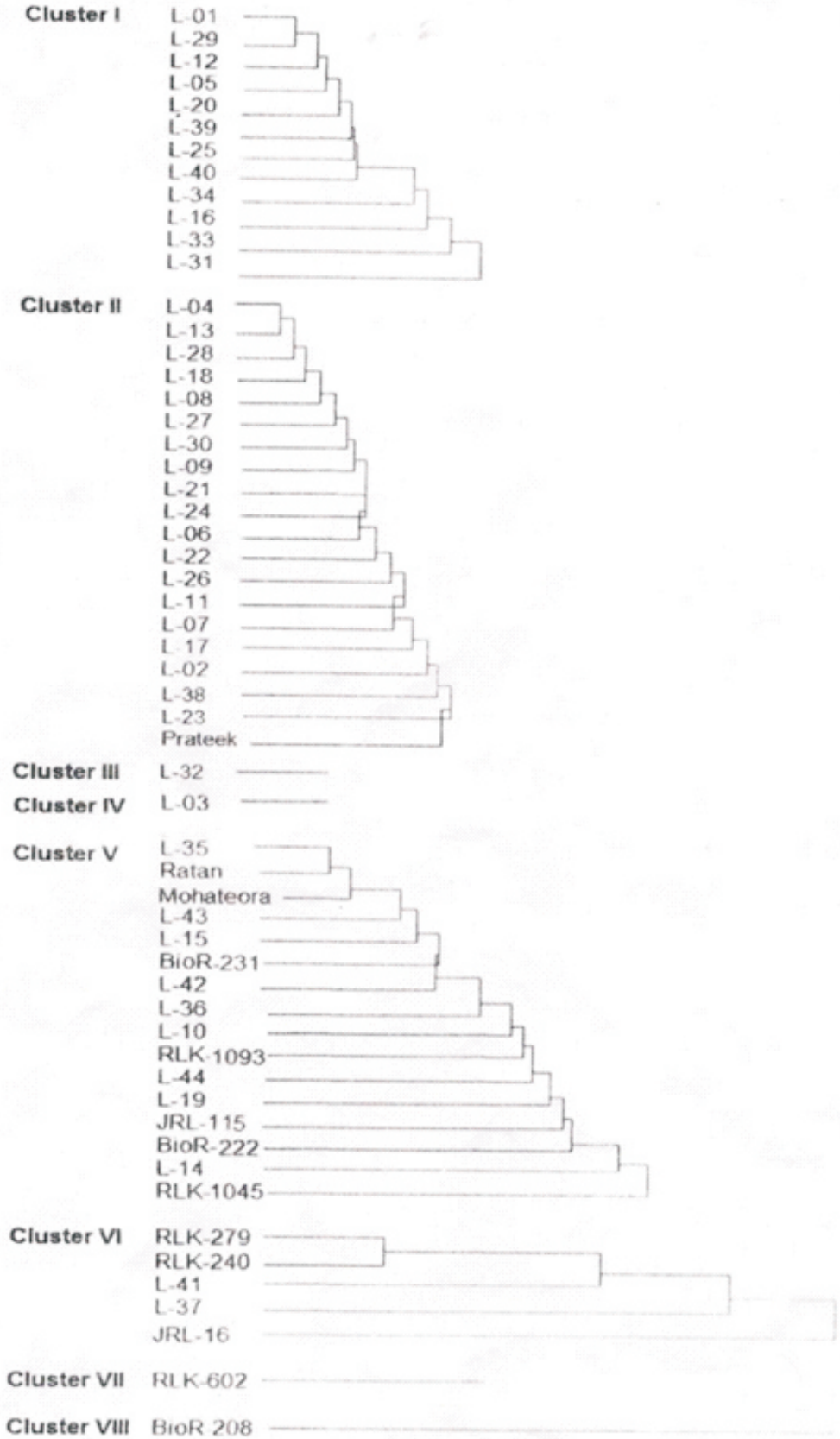

Fig. 1 Dendrogram showing clustering by Tocher's method

flowering were secondary axis of differentiation which accounted for 22.11% of variation. Important characters in vector III were days to 50 % flowering, days to maturity, number of seeds pod^{-1} and 100 seed weight accounting to 10.153% of variation. This result suggested that parents selected on the basis of characters like days to 50 % flowering, days to maturity, plant height, number of seeds pod^{-1}, number of primary branches and yield plant $^{-1}$ may be expected to be genetically diverse.

Average intra and inter cluster statistical distance among eight characters are given in table 6. The intra cluster variation ranged from 0 to 27.39. Cluster VI possessed highest intra cluster distance (D=27.639) followed by cluster V (D=13.25) and cluster II (D=7.24). Cluster III, IV and VII and VIII had zero intra cluster distance as these cluster groups consisted single genotype. The average inter-cluster distance was maximum between cluster IV and cluster VIII (D=110.67) followed by cluster I and cluster VIII (D=74.99). The inter-cluster distance was found to be minimum between cluster I and cluster IV (D=8.56). The cluster which are highly diverge would be more stable. Therefore, the genotypes belonging to the distant clusters may be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. These findings are in conformity with the findings of Bhalekar (2008) and Rahman *et al*. (2010) in *lathyrus* whose results revealed that diverse clusters exhibited different mean values for wide spectrum of variation and more stable for almost all the characters.

Overall study for cluster means considering all the characters indicated that cluster VIII possessed the highest cluster mean for number of pods plant^{-1}, number of seeds pod^{-1}, 100 seed weight and grain yield plant^{-1}. Cluster VII showed the maximum mean for plant height and number of primary branches. Cluster IV possessed lowest mean for days to 50% flowering and days to maturity. The variance of cluster means for all the characters indicated that the maximum variation was accounted by plant height (197.99), number of pods plant^{-1} (197.62), yield plant^{-1} (28.22) and days to 50% flowering (17.69). The variance was lowest for number of primary branches (0.15), number of seeds pod^{-1} (0.16) and 100 seed weight (0.17).

This observation is slightly deviating from results obtained on the basis of canonical method. However, three characters plant height, yield plant^{-1} and days to 50 % flowering were important sources of variation as observed from both the methods studied. Hence, it is suggested that the selection of parent for hybridization and subsequent genetic improvement may be made on the basis of the characters, exhibiting maximum variation and expected to be genetically diverse. Thus, from this study it can be reported that the parent may be selected for height, yield plant^{-1}and days to 50 % flowering. This indicated that these characters are less governed by additive gene effect, even if they were under polygenic control and therefore, selection of these characters would be more effective for yield improvement. In accordance to this result, Uikey *et al.* (2018)also reported high heritability along with high genetic advance for number of pods plant^{-1}, number of immature pods plant^{-1}, dry pod yield plant^{-1}, 100 pod weight, shelling per cent, oil content and hundred kernal weight in groundnut.

Bhatt (1973) suggested that the application of multivariate analysis method was more efficient than eco-geographical diversity method for selecting the parents and attempting crosses among them. In present study, all possible combinations beyond the mean statistical distance ÉDÉ formed from different clusters have been arranged in descending order of magnitude of genetic distance and promising thirteen cluster combinations are presented in table 8. The practical consideration like earliness,seed yield plant^{-1}and number of pods plant^{-1} were also taken into account while choosing the genotypes from selected cluster combination. The present study projected the importance of 20 genetically diverse parents viz., L-3, L-31, L-25, L-32, JRL-16, RLK-279, L-37, RLK-1045, L-44, L-14, L-11, L-07, L-08, RLK-240, L-39, L-05, RLK-602, L-16 and BioR-208 which are recommended to be crossed to identify potential transgrates for high yield and adaptation.

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