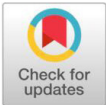


Research Article

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D² analysis in Lathyrus (*Lathyrus sativus* L.) germplasm lines**Sakshi Vilas Ingle^{1*}, Prema Manapure², Vandana Madke², Sudhir Patil² and Vandana Kalamkar³**¹Section of Genetics and Plant Breeding, College of Agriculture, Nagpur, India²College of Agriculture, Nagpur, India³SRA, Section of Agricultural Botany, College of Agriculture, Nagpur, India
(Dr.Panjabrao Deshmukh Krishi Vidyapeeth, Akola, MH-444104, India)**ABSTRACT**

Fifty-five genotypes were evaluated for a genetic divergence to identify potential parents for the lathyrus breeding program aimed at yield improvement. Mahalanobis D^2 statistics for eight characters viz. days to 50% flowering (on plot basis), days to maturity (on plot basis), plant height (cm), number of primary branches plant⁻¹, number of seeds pod⁻¹, number of pods plant⁻¹, 100 seed weight (g) and yield plant⁻¹ were used in this study for computing genetic divergence. The analysis of dispersion for eight characters using Wilk's criterion revealed a highly significant difference between genotypes for all eight characters. The fifty-five genotypes were grouped into seven clusters by Tocher's method. The maximum inter-cluster distance was recorded between cluster III and cluster VII ($D^2=15.40$) and in between cluster V and cluster VII ($D^2 = 14.75$) whereas the minimum inter-cluster distance was found between cluster IV and cluster VI ($D^2=3.56$). The canonical analysis indicated that yield plant⁻¹, 100 seed weight, number of pods plant⁻¹, number of seeds pod⁻¹, number of primary branches plant⁻¹ and days to 50% flowering were significant source of variation in vector I. Characters number of seeds pod⁻¹, number of pods plant⁻¹, days to 50% flowering and plant height were important source of variation in vector II. Number of seeds pod⁻¹, yield plant⁻¹ and days to 50% flowering were important characters in vector III. The canonical analysis and cluster mean studied together revealed the importance of number of pods plant⁻¹, yield plant⁻¹ and number of seeds pod⁻¹ as important contributors towards the total divergence. Hence, these traits form the criterion for the selection of parents for hybridization program. The 19 genotypes viz., EC-209071, NLK-39, IC-120491, NLK-37, NLK-56, NLK-6, NLK-40, NLK-49, NLK-38, NLK-54, NLK-73, EC-207071, NLK-42, NLK-74, BIOR-208, AKL-7, JRL-16, BIOR-231 and BIOR-222 were identified as potential and diverse parents for their use in crossing program.

Keywords: Germplasm lines, Lathyrus, D2, Clusters, Vector, Canonical analysis, Cluster mean, Divergence**I. INTRODUCTION**

Grass pea (*Lathyrus sativus* L.) is a food and fodder crop that belongs to the family Leguminosae and subfamily Papilionaceae, and has chromosome number $2n = 14$. The genus *Lathyrus* consists of 187 species and subspecies but only one species (*Lathyrus sativus* L.) is widely cultivated as a food crop [5]. Grass peas are used to be taken as roasted whole seeds, boiled whole seeds, traditional sauce, and local drinks [4]. The origin of *L. sativus* is unknown, however, its presumed center of origin is Southwest and Central Asia [17]. [15] reported that *L. sativus* contains 18-34% of the protein in seeds and 17% of the protein in mature leaves. [11] also reported the following values for *L. sativus*:- energy 362.3 kcal/kg; protein 31.6%; fat 2.7%; nitrogen-free extract 51.8%; crude fiber 1.1% and ash 2.2%. Grass pea is rich in lysine which is low in most cereals. However, it is deficient in methionine and cysteine sulfur-containing essential amino acids [9].

Despite the importance of *Lathyrus* for humans and animals, it has limited uses due to the presence of the neurotoxic compound (β -N-oxalyl- α , β -diaminopropionic acid (β - ODAP) contents. The neurotoxin compound causes irreversible paralysis of the lower limbs in human and the fore-limbs in animals and is known as Lathyrism. 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, W. Bengal, Madhya Pradesh, Chhattisgarh, and Maharashtra, but it is also grown in small pockets in other states contributing 4.5% total pulse production of the country.

The existence of genetic variability in the population is a prerequisite for planning any breeding program. This study helps in the estimation of the extent of variability in the population. The study of genetic divergence among the set of available genotypes will be useful in planning the hybridization program, because the success of the hybridization program depends upon the selection of suitable parents of diverse origins. Understanding genetic divergence can help plant breeders identify diverse genetic resources. This diversity can be used to develop new cultivars with improved traits, such as disease resistance, higher yields, or better adaptability to specific environmental conditions.

II. MATERIALS AND METHODS

The present investigation was undertaken during rabi 2022 at the research farm of Agricultural Botany Section, College of

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Agriculture, Nagpur to estimate the genetic divergence among 55 genotypes of lathyrus to identify the desirable and potential parents for hybridization. These 55 genotypes were grown in randomized block design. Data was recorded on five competitive plants for eight characters i.e., days to 50% flowering (on a plot basis), days to maturity (on a plot basis), 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). Mahalanobis D² statistics was used in this study for computing genetic divergence for the characters studied. Grouping of genotypes into different clusters and canonical analysis were done by using Tocher's method described by [14]. Selection of parents for hybridization from different clusters was done based on mean statistical distance as suggested by Bhatt.

III. RESULTS AND DISCUSSION

The mean squares for genotypes were highly significant for all eight characters which indicated significant variation among all the genotypes for eight characters it is presented in Table 1. The genotype Prateek (56.00 days) and RLK-1093 (57.67 days) was the earliest to attain 50% flowering the genotypes which attained 50% flowering late was NLK-3 (67.33 days) and JRL-115 (67 days). The genotype IC-120491 (115.33 days) matured earliest followed by NLK-39 (116 days), PUSA-90-2 (116 days), and the genotype NLK-6 (129 days) attained late maturity followed by BIOR-231 (128 days). The maximum plant height was shown by the genotype RLK-602 (95.33 cm) followed by BIOR-208 (89.93 cm) and the genotype Prateek (57.67 cm) showed minimum plant height followed by Mahateora (64.67cm). The genotype IC-120491 (4.90) followed by BIOR-222 (4.87) recorded maximum number of primary branches plant⁻¹, while minimum number of primary branches plant⁻¹ was shown by the genotype NLK-62 (3.50) followed by PUSA-56 (3.57) and NLK-68 (3.57). The maximum number of pods plant⁻¹ was produced by the genotype NLK-56 (109.34) followed by NLK-37 (106.73) and the minimum number of pods plant⁻¹ was produced by the genotype LSD-3 (32.33) followed by NLK-39 (32.76). The genotype BIOR-208 (3.83) had a maximum number of seeds pod⁻¹ followed by NLK-54 (3.37). The genotype EC-209071 (1.93) exhibited a minimum number of seeds pod⁻¹ followed by NLK-6 (2) and RLK-1093 (2.03) The genotype LSD-3 (11.93 g) had maximum seed weight followed by EC-209026 (11.77 g) and the genotype Ratan (6.27 g) had minimum followed by NLK-40 (6.30 g) The genotype NLK-49 (24 g) had maximum yield followed by NLK-38 (22.73 g), NLK-56 (22.60 g) and the genotype Prateek (8.27 g) had minimum yield followed by NLK-39 (8.83g) based on per se performance studied for yield and yield contributing characters among fifty-five genotypes, the genotypes NLK-49, NLK-38, NLK-56, NLK-54, NLK-37, NLK-42, NLK-73, and EC-207071 were found to be significantly superior 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, but their long-term potentiality is not known. Hence, the selection of superior parents which has the potential to produce superior genotype combinations, and identifying the genotype combinations based on genetic divergence will give the required information as compared to the information obtained from per se performance of genotypes. Therefore, the information on genetic divergence for assessment of the relative breeding potential of parental material along with the type of genetic component involved in

yield and yield contributing traits in lathyrus can be of immense help to lathyrus breeders.

The analysis of dispersion for the test of significance of difference in the mean values based on the Wilk's criterion revealed highly significant difference among genotypes for eight characters ($\chi^2 = 1790.02$ at 432 d.f.) Therefore, the data was further evaluated for D² and cluster analysis. Similar results were obtained by [1,6]. The contribution of each character towards genetic divergence is presented in Table 2. Contribution of yield plant⁻¹ (g) was maximum (46.33%) followed by number of seeds pod⁻¹ (20.27%), number of pods plant⁻¹ (19.93%), days to maturity (4.58%), 100 seed weight (g) (3.30%). This indicates that characteristics like yield plant⁻¹, number of seeds pod⁻¹, number of pods plant⁻¹, and days to maturity were important traits contributing towards genetic divergence and this study could be used in selecting desired genotypes for further selection and choice of parent for hybridization and creation of more variability. These observations confirmed with those reported by [6, 10]

The grouping of 55 genotypes into different clusters was done by Tocher's method and presented in Table 3 and Fig. 1. The entire genotypes (55) were grouped based on D² statistics into seven clusters. Cluster I was the largest comprising 29 genotypes, followed by Cluster II comprising 15 genotypes, cluster III and cluster IV comprised of single genotype in each cluster. Cluster V comprised 5 genotypes, cluster VI comprised of single genotype and cluster VII comprising of 3 genotype. The promising check Ratan was grouped into cluster V and Prateek, and Mahateora were grouped into cluster VII and cluster II respectively. There were many genotypes distributed in other cluster which were highly deviating from the promising check and hence offers good scope for improvement. From the data it can be seen that cluster I and cluster II had maximum number of genotypes. Those clusters that did not have any of the check varieties were genetically diverse from the checks and hence there is scope for the selection of potential genotypes for genetic improvement of yield and yield contributing characters. Similar findings were obtained by [8] in Lathyrus.

The values of the first three canonical vectors and canonical roots are presented in Table 4 and Table 5. The first three canonical roots accounted for 87.48 percent of the observed variability in the material studied ($\lambda_1 = 67.15\%$, $\lambda_2 = 11.69\%$, $\lambda_3 = 8.64\%$). The overall contribution of the three canonical roots to the total variability among 55 genotypes was 87.48 percent suggesting the major portion of differentiation in the first three phases. This indicates that differentiation for eight characters among 55 genotypes were completed in three phases.

The further coefficient in the first three canonical vectors shows that out of eight characters yield plant⁻¹, 100 seed weight, number of pods plant⁻¹, number of seeds pod⁻¹, number of primary branches plant⁻¹, and days to 50% flowering, contributed in vector I accounting for 67.15% of total variation. Characters number of seeds pod⁻¹, number of pods plant⁻¹, days to 50% flowering, and plant height were important characters in vector II which accounted for 11.69% of the total variation. Number of seeds pod⁻¹, yield plant⁻¹ and days to 50% flowering were important characters in vector III which accounted for 8.64% of total variation. From the data, it can be observed that the parents selected on the basis of characters like number of seeds pod⁻¹, days to 50% flowering, yield plant⁻¹, number of pods plant⁻¹ and 100 seed weight is expected to be genetically diverse. Similar findings were obtained by [12, 7] in Lathyrus.

Average intra and inter cluster distance among eight characters were worked out by Tocher's method and are presented in Table 6. Data shows that inter-cluster distance in most of the cases was higher than the intra-cluster distance. The intra cluster distance range from 0.00 to 5.66. Cluster V possessed highest intra cluster distance ($D^2 = 5.66$) followed by cluster VII ($D^2 = 5.41$) and cluster II ($D^2 = 5.09$). The average inter-cluster distance was maximum between cluster III and VII ($D^2 = 15.40$), followed by cluster V and cluster VII ($D^2 = 14.75$), cluster I and cluster VII ($D^2 = 13.08$), cluster III and cluster VI ($D^2 = 10.77$), cluster II and cluster V ($D^2 = 9.84$) and cluster II and cluster III ($D^2 = 9.83$) suggesting more variability in genetic makeup of genotypes included in these clusters. The inter-cluster distance was found minimum between cluster IV and cluster VI ($D^2 = 3.56$). From the data it can be observed that the average intra-cluster distance was maximum in cluster V, cluster VII, and cluster II and the average inter-cluster distance was maximum between cluster III and cluster VII and also in between cluster V and cluster VII. Widely diverged clusters remain distinct in different environments. Therefore, the genotypes belonging to the distant clusters may be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. Similar findings were obtained by [2, 13]

The cluster means for all eight characters are presented in Table 7 and discussed below. The comparison of cluster means for eight characters understudy marked considerable genetic differences between groups. The highest cluster mean for days to 50% flowering was recorded by cluster III (63.33) and cluster V (63) while cluster IV (59) followed by cluster VI (60.33) represented the lowest mean for days to 50% flowering. Highest cluster means for days to maturity was recorded by cluster VI (127) followed by cluster V (123.33) while cluster III (117) followed cluster VII (117.56) represented the lowest mean for days to maturity. The highest cluster mean for plant height was recorded by cluster VI (89.83) followed by cluster IV (86.10) while cluster VII (72.18) followed by cluster II (76.87) represented the lowest mean for plant height. For the number of primary branches plant⁻¹ highest cluster means were estimated by cluster IV (4.87) followed by cluster VI (4.57) and minimum cluster mean were estimated by cluster I (4.19) followed by cluster II (4.21). For number of pods plant⁻¹ highest cluster means was estimated by cluster V (101.18) followed by cluster III (99.25) and minimum cluster mean was estimated by cluster VII (37.38) followed by cluster VI (45.34). For the number of seeds pod⁻¹ highest cluster mean were estimated by cluster VI (3.83) followed by cluster IV (3.13) and minimum cluster mean was estimated by cluster III (1.93) followed by cluster II (2.59). For 100 seed weight highest cluster mean was estimated by cluster III (10.73) followed by cluster II (9.49) and the minimum cluster mean estimated by cluster V (7.59) followed by cluster VII (8.36). For yield plant⁻¹ highest cluster mean was estimated by cluster III (20.33) followed by cluster V (20.21) and minimum cluster mean was estimated by cluster VII (8.83) followed by cluster II (13.41). Over all study for cluster means considering all the characters indicated that cluster III possessed the highest

cluster mean for days to 50% flowering, number of pods plant⁻¹, 100 seed weight and yield plant⁻¹. Cluster VI showed the maximum mean for days to maturity, number of primary branches plant⁻¹, plant height and number of seeds pod⁻¹. Cluster VII possessed lowest mean for all the characters under study.

The variance for cluster means for all the characters indicated that maximum variation was accounted for number of pods plant⁻¹ (618.35) followed by plant height (36.24), yield plant⁻¹ (18.01), days to maturity (12.34), days to 50% flowering (2.82), 100 seed weight (0.99), number of seeds pod⁻¹ (0.33) and number of primary branches plant⁻¹ (0.06) [2] also reported the importance of above three characters for genetic divergence in lathyrus.

This observation slightly deviates from results obtained based on canonical method. However, the three characters number of pods plant⁻¹, yield plant⁻¹ and number of seeds pod⁻¹ were important source of variation as observed from both the method studied. Hence it is suggested that the selection of parents for hybridization and subsequent genetic improvement may be made based on 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 hybridization on the basis of these three characters namely number of pods plant⁻¹, yield plant⁻¹ and number of seeds pod⁻¹.

In the present study all possible combinations beyond the mean statistical distance $\bar{D} = 3.21$ formed from different clusters have been arranged in descending order of magnitude of genetic distance and promising ten cluster combinations have been presented in Table 8. Other practical consideration like the number of pods plant⁻¹, yield plant⁻¹, number of seeds pod⁻¹, number of primary branches plant⁻¹ and plant height etc. should be taken into account while choosing the genotypes as parents. On this basis, nineteen genotypes viz., EC-209071, NLK-39, IC-120491, NLK-37, NLK-56, NLK-6, NLK-40, NLK-49, NLK-38, NLK-54, NLK-73, EC-207071, NLK-42, NLK-74, BIOR-208, AKL-7, JRL-16, BIOR-231, and BIOR-222 were identified as potential and diverse parents for their use in crossing program. These findings are in close agreement with those reported by [7, 16, 3].

IV. CONCLUSION

Significant differences were observed for 55 genotypes. The characters like days to 50% flowering, number of seeds pod⁻¹, number of pods plant⁻¹, and yield plant⁻¹ were identified to contribute maximum towards genetic divergence from canonical analysis studied, cluster means to estimate, and contribution of individual characters to divergence. Fifty five genotypes were grouped into seven clusters. Ten inter-cluster combinations were identified for selecting promising diverse genotypes to be included in the crossing program to get potential transgrates. Nineteen genotypes viz., EC-209071, NLK-39, IC-120491, NLK-37, NLK-56, NLK-6, NLK-40, NLK-49, NLK-38, NLK-54, NLK-73, EC-207071, NLK-42, NLK-74, BIOR-208, AKL-7, JRL-16, BIOR-231, and BIOR-222 were identified as potential and diverse parents for their use in crossing program.

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	BIOR-208	60.33	127.00	89.93	4.57	45.34	3.83	9.00	15.27
2	BIOR-231	59.67	128.00	76.40	4.30	73.57	2.77	8.10	15.37
3	BIOR-222	59.00	120.00	86.10	4.87	67.15	3.13	8.57	16.77
4	NLK-48	61.33	125.00	85.97	4.53	61.02	2.33	8.70	11.07
5	NLK-102	63.00	121.67	79.27	3.63	86.99	2.67	9.10	20.00
6	NLK-6	64.33	129.00	88.40	4.10	101.07	2.00	9.83	19.80
7	NLK-42	60.00	118.00	84.43	4.80	84.45	2.90	9.03	22.03
8	NLK-37	59.33	124.67	83.97	4.40	106.73	2.87	7.27	22.07
9	NLK-44	60.67	121.67	78.13	3.77	61.29	2.70	9.67	15.93
10	NLK-68	63.67	118.67	86.93	3.57	75.15	2.67	9.07	17.33
11	NLK-36	59.33	119.00	81.93	4.10	67.17	3.30	9.23	20.20
12	NLK-39	62.67	116.00	76.93	3.67	32.76	3.07	8.97	8.83
13	NLK-56	63.33	119.67	81.80	4.47	109.34	2.50	8.30	22.60
14	NLK-62	66.00	119.33	81.43	3.50	52.65	2.83	9.20	13.60
15	NLK-50	66.33	119.00	82.60	4.40	64.22	2.87	9.03	16.38
16	NLK-3	67.33	123.33	71.47	3.90	51.22	3.03	9.37	14.48
17	NLK-94	61.67	120.00	83.40	3.97	88.65	2.27	8.57	17.00
18	NLK-47	59.00	117.33	85.63	4.20	84.03	2.73	8.23	18.73
19	NLK-63	66.33	119.00	67.10	4.43	82.31	2.80	9.07	20.83
20	NLK-5	64.33	121.67	79.13	4.27	65.83	3.07	8.73	17.63
21	NLK-49	61.33	119.67	80.57	4.10	89.08	2.93	9.27	24.00
22	NLK-74	62.00	120.33	84.63	4.20	86.28	2.83	8.80	21.20
23	NLK-67	62.67	122.00	87.13	4.40	86.71	2.90	8.47	21.13
24	NLK-38	62.00	121.33	78.87	3.90	92.33	2.90	8.53	22.73
25	NLK-55	63.00	120.33	76.30	4.00	89.11	2.37	8.73	18.30
26	NLK-70	63.33	119.33	83.70	4.30	73.94	2.80	9.23	18.93
27	NLK-53	63.00	118.67	83.80	4.73	73.30	2.77	9.07	18.05
28	NLK-51	64.67	117.67	70.27	4.43	58.56	3.20	8.27	15.36
29	NLK-73	61.67	120.33	85.00	4.47	68.78	3.13	9.97	21.39
30	NLK-54	62.00	119.00	80.67	4.17	66.33	3.37	10.13	22.50
31	IC-120491	62.67	115.33	81.93	4.90	33.49	3.03	9.33	9.40
32	EC-209081	61.67	121.00	69.30	4.07	73.10	3.00	9.80	20.97
33	EC-209072	66.33	119.33	76.17	4.53	63.68	2.73	10.53	18.30
34	EC-209071	63.33	117.00	77.20	4.37	99.25	1.93	10.73	20.33
35	EC-209026	62.67	124.33	74.20	4.03	49.55	2.63	11.77	15.23
36	EC-207071	59.33	119.00	79.73	4.70	67.25	3.03	10.57	21.23
37	LSD-3	65.33	121.00	78.10	4.17	32.33	2.87	11.93	10.90
38	JRL-115	67.00	117.33	84.83	4.17	61.82	2.97	11.33	20.50
39	JRL-16	62.67	121.33	67.90	4.20	62.89	2.43	10.33	15.60
40	RLK-1093	57.67	122.33	87.60	4.40	61.32	2.03	9.77	11.80
41	RLK-602	59.67	123.00	95.33	3.97	69.95	2.40	8.13	13.56
42	RLK-1045	62.33	117.67	75.37	3.90	97.44	2.10	9.67	19.70
43	RLK-579	60.33	118.67	71.13	4.30	77.89	2.50	10.17	19.70
44	NIC-18773	61.33	121.00	78.43	3.83	42.33	2.70	10.43	11.86
45	AKL-12	65.33	121.67	76.20	4.27	57.42	2.07	10.93	12.80
46	AKL-19	61.33	120.33	68.87	4.07	78.16	2.40	10.03	18.68
47	AKL-7	62.67	122.33	67.57	4.10	87.00	2.30	7.83	15.50
48	PUSA-24	64.67	122.67	70.97	4.37	85.19	2.37	8.97	17.47
49	PUSA-90-2	63.67	116.00	73.87	4.57	87.01	2.70	8.53	19.93
50	PUSA-56	65.00	117.33	75.13	3.57	71.95	2.53	10.47	18.73
51	KH-1	60.33	119.00	77.50	4.63	45.14	2.73	10.37	12.73

53	NLK-40	65.33	122.33	75.37	4.00	102.61	2.80	6.30	17.97
52	Ratan (Check)	62.67	121.00	80.00	4.10	86.14	3.50	6.27	18.63
54	Prateek (Check)	56.00	121.33	57.67	4.70	45.89	2.73	6.77	8.27
55	Mahateora (Check)	63.67	125.00	64.67	4.90	62.99	2.50	7.23	11.32
	Grand Mean	62.52	120.57	79.52	4.23	72.09	2.73	9.35	17.61
	S.E.(m) ±	1.47	2.17	4.55	0.20	4.99	0.18	0.49	1.22
	C V%	4.06	3.12	9.92	8.01	12.00	11.30	9.08	12.03
	C D%	4.11	6.08	12.77	0.55	14.00	0.50	1.38	3.43

Table 2. Contribution of individual characters towards divergence

Sr.No.	Characters	Timeranked 1 st	Percent Contribution
1	Days to 50% flowering	44	2.96%
2	Days to maturity	68	4.58%
3	Plant height (cm)	11	0.74%
4	Number of primary branches plant ⁻¹	28	1.89%
5	Number of pods plant ⁻¹	296	19.93%
6	Number of seeds pod ⁻¹	301	20.27%
7	100 seed weight (g)	49	3.30%
8	Yield plant ⁻¹ (g)	688	46.33%
	Total	1485	
	Tocherscut-offvalue	29.48	

Table 3. Grouping of 55 genotypes of lathyrus into different clusters

Cluster	Number of genotypes	Name of the genotypes
I	29	NLK-74, NLK-67, NLK-42, NLK-73, EC-207071, NLK-36, EC-209081, NLK-54, NLK-38, NLK-49, NLK-63, PUSA-90-2, NLK-70, NLK-102, RLK-579, NLK-47, JRL-115, AKL-19, NLK-53, NLK-55, NLK-5, EC-209072, PUSA-56, NLK-68, PUSA-24, RLK-1045, NLK-94, NLK-50, NLK-44
II	15	EC-209026, JRL-16, AKL-12, NLK-3, NIC-18773, KH-1, NLK-62, LSD-3, NLK-51, NLK-48, RLK-1093, RLK-602, BIOR-231, AKL-7, Mahateora
III	1	EC-209071
IV	1	BIOR-222
V	5	NLK-37, NLK-56, NLK-6, NLK-40, Ratan
VI	1	BIOR-208
VII	3	NLK-39, IC-120491, Prateek

Table 4. Three canonical roots and their contribution expressed as per cent of the total variation

Root	Eigen value	Per cent contribution
λ_1	1002.19	67.15
λ_2	174.47	11.69
λ_3	129.07	8.64
Total	1305.73	87.48
Sum of all canonical roots		100
Residual		12.52

Table 5. Values of first three vectors

Sr.No.	Characters	Vector I	Vector II	Vector III
1	Days to 50% flowering	0.01622	0.17852	0.20380
2	Days to maturity	-0.02463	-0.19912	-0.12831
3	Plant height (cm)	-0.02093	0.04172	-0.17552
4	Number of primary branches plant ⁻¹	0.04838	-0.02543	-0.01781
5	Number of pods plant ⁻¹	0.40986	0.25543	-0.82900
6	Number of seed pod ⁻¹	0.35375	0.80039	0.34131
7	100 seed weight (g)	0.46133	-0.26174	-0.03868
8	Yield plant ⁻¹ (g)	0.70028	-0.38952	0.32502

Table 6. Average intra and inter cluster distance D2 values in lathyrus

Cluster	I	II	III	IV	V	VI	VII
I	4.48	8.19	6.14	5.52	5.91	7.22	13.08
II		5.09	9.83	6.17	9.84	6.46	7.82
III			0.00	8.34	6.44	10.77	15.40
IV				0.00	6.89	3.56	9.74
V					5.66	8.70	14.75
VI						0.00	9.15
VII							5.41

\bar{D} = 3.21 *Bold figures are average intra-cluster distance*

Table 7. Cluster means for eight characters

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches plant ⁻¹	Number of pods plant ⁻¹	Number of seeds pods ⁻¹	100 seed weight (g)	Yield plant ⁻¹ (g)
I	62.66	119.53	79.12	4.19	77.57	2.77	9.38	19.64
II	62.69	122.29	76.87	4.21	57.86	2.59	9.49	13.41
III	63.33	117.00	77.20	4.37	99.25	1.93	10.73	20.33
IV	59.00	120.00	86.10	4.87	67.15	3.13	8.57	16.77
V	63.00	123.33	81.91	4.21	101.18	2.73	7.59	20.21
VI	60.33	127.00	89.93	4.57	45.34	3.83	9.00	15.27
VII	60.44	117.56	72.18	4.42	37.38	2.94	8.36	8.83
SD	1.68	3.51	6.02	0.24	24.86	0.57	0.99	4.24
Variance	2.82	12.34	36.24	0.06	618.35	0.33	0.99	18.01

Table 8. Selection of genotypes based on inter-cluster distances and cluster mean

Sr.No.	Cluster combination	Average inter-cluster distance	Cross combination	Traits
1	III x VII	15.40	EC-209071 x NLK-39 } IC-120491 }	Number of seeds pod ⁻¹ , Number of pods plant ⁻¹ , Yield plant ⁻¹
2	V x VII	14.75	NLK-37 } x NLK-39 } NLK-56 } IC-120491 } NLK-6 } NLK-40 }	Number of seeds pod ⁻¹ , Yield plant ⁻¹
3	I x VII	13.08	NLK-49 } x NLK-39 } NLK-38 } IC-120491 } NLK-54 } NLK-73 } EC-207071 } NLK-42 } NLK-74 }	Early maturity
4	III x VI	10.77	EC-209071 x BIOR-208	Number of seeds pod ⁻¹ , Number of pods plant ⁻¹ , Yield plant ⁻¹
5	II x V	9.84	AKL-7 } x NLK-37 } JRL-16 } NLK-56 } BIOR-231 } NLK-6 }	Number of pods plant ⁻¹ , Yield plant ⁻¹
6	II x III	9.83	AKL-7 } x EC-209071 } JRL-16 } BIOR-231 }	Number of seeds pod ⁻¹ , Number of pods plant ⁻¹ , Yield plant ⁻¹
7	IV x VII	9.74	BIOR-222 x NLK-39 } IC-120491 }	Seed weight, Number of primary branches plant ⁻¹
8	VI x VII	9.15	BIOR-208 x NLK-39 } IC-120491 }	Seed weight, Number of primary branches plant ⁻¹
9	V x VI	8.70	NLK-37 } x BIOR-208 } NLK-56 } NLK-6 }	Number of pods plant ⁻¹ , Yield plant ⁻¹
10	III x IV	8.34	EC-209071 x BIOR-222	Number of seeds pod ⁻¹ , Yield plant ⁻¹

 $\bar{D} = 3.21$

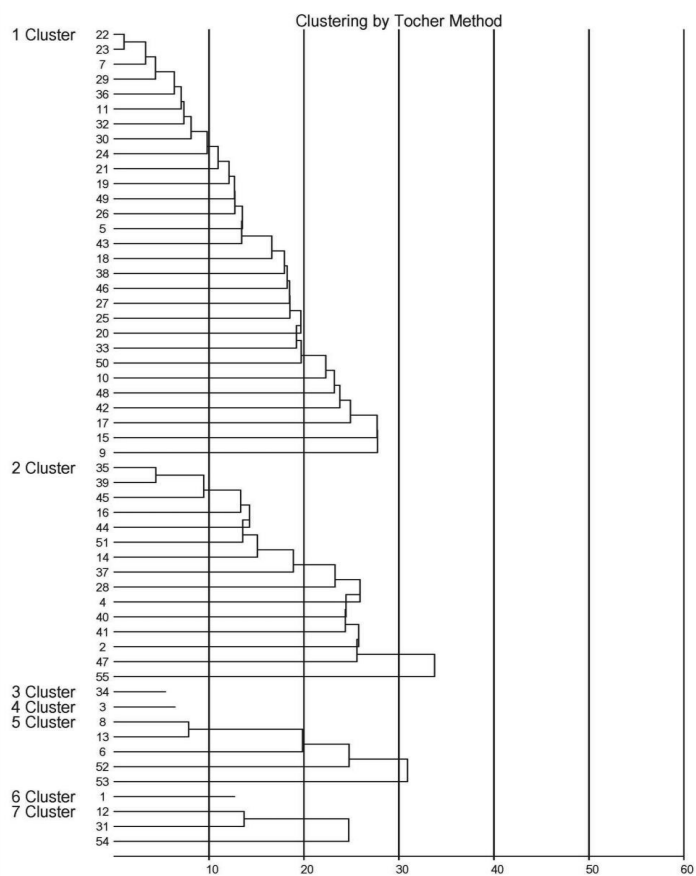


Fig.1. Dendrogram showing clustering by Tocher's method

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