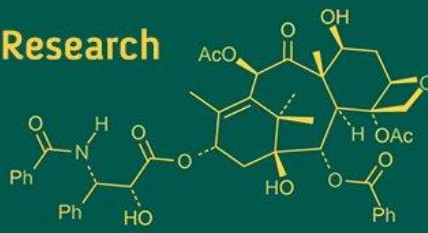
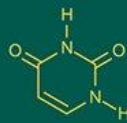


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Multivariate analysis of genetic divergence in *Lathyrus* (*Lathyrus sativus* L.) germplasm

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Abstract

The present investigation entitled was carried out during the *Rabi* season of 2024-25 at the Research Farm of the Agricultural Botany Section, College of Agriculture, Nagpur. Sixty one genotype with three check were evaluated for genetic divergence to identify potential parents for lathyrus breeding programme aimed at yield improvement. Mahalanobis D^2 statistics for ten 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 seed yield plant⁻¹, harvest index (%), ODAP content (%) were used in this study for computing genetic divergence. The analysis of dispersion for ten characters using Wilk's criterion, revealed highly significant difference between genotypes for all ten characters. The sixty four genotypes were grouped into fourteen clusters by Tocher's method. Cluster I was largest comprising of 41 genotypes. Cluster XIII possessed highest intra cluster distance ($D^2 = 28.61$). The characters like days to number of seeds pod⁻¹, number of pods plant⁻¹, and yield plant⁻¹, number of primary branches plant⁻¹, number of seeds pod⁻¹ were identified to contribute maximum towards genetic divergence from canonical analysis studied, cluster mean estimate and contribution of individual characters to divergence. Ten inter cluster combination were identified for selecting promising diverse genotypes to be included in crossing programme to get potential variety. Twenty seven genotypes viz. AKL-19, NLK-94, NLK-67, NLK-62, NLK-51, EC-209081, NLK-39, NLK-54, NLK-74, NLK-48, EC-2609071, NLK-6, AKL-7, JRL-16, BIOR-231, NLK-49, IC-120472, NLK-37, IC-120491, NLK-40, KH-1, NLK-102, NLK-5, PUSA-24, AKL-12, NLK-44, BIOR-222 were identified as potential parents and can be attempted to use these genotypes in crossing programme.

Keywords: Genetic diversity, Cluster, Lathyrus, ODAP content, Tocher's method

Introduction

Lathyrus (*Lathyrus sativus* L.) is a member of the Leguminosae family, it is a significant crop rich in protein (28%), next to soybeans (43%). Papilionaceae is a subfamily of lathyrus with chromosomal number $2n=14$. *Lathyrus* has extensive tolerance of drought, water logging soil. Analysis of genetic diversity in relation to geographical distribution may contribute to the identification of centers of genetic diversity and elucidate the origins and domestication history of cultivated crop species. The edible *Lathyrus* (*Lathyrus sativus* L.) originated in the Mediterranean region of West Central Asia. It was domesticated in North India, where remains dating back 3600 years have been found. The predominant cultivation practice for *Lathyrus* (*Lathyrus sativus* L.) in India is the relay cropping system, commonly referred to as the "utera" system. The crop is well adapted to diverse environmental conditions, exhibiting considerable tolerance to drought as well as resilience under conditions of excessive rainfall. *Lathyrus* (*Lathyrus sativus* L.) is relatively resistant to many diseases and insect pests. The effectiveness of a crop improvement programme is largely determined by the extent of genetic variability available within the breeding material. Genetic diversity serves as the foundation for plant breeding by providing opportunities to select diverse parents with desirable traits for hybridization. Systematic evaluation of germplasm enables the identification of genetic differences among accessions for important agronomic characters, thereby supporting the development of improved cultivars. Furthermore, characterization of germplasm contributes to the efficient conservation and utilization of valuable genetic resources in future breeding programmes.

Multivariate statistical methods, particularly Mahalanobis D^2 analysis, are widely employed to assess genetic divergence among crop genotypes. This approach groups genotypes into different clusters by considering variation across several quantitative traits simultaneously, thereby providing a comprehensive measure of genetic diversity. The clustering pattern helps breeders to identify genetically diverse parents for hybridization. Crosses involving genotypes from distantly related clusters are expected to produce greater genetic variation and increase the probability of obtaining superior recombinants in subsequent generations. Estimation of genetic diversity not only supports the selection of superior genotypes but also contributes to the development of high-yielding, climate-resilient, and low-ODAP cultivars with improved adaptability. Therefore, systematic evaluation of available germplasm for genetic divergence is an important step toward the effective genetic improvement of *Lathyrus*

Materials and Methods

The present research work was undertaken during Rabi 2024-25 at Research farm of Agricultural Botany Section, College of Agriculture, Nagpur to estimate the genetic diversity among 64 germplasm of *Lathyrus*. These 64 germplasm were grown in RBD (Randomized Block Design) for ten characters and data was recorded on five competitive plants. These characters are days to 50% flowering (plot wise), days to maturity (plot wise), plant height (cm), number of primary branches plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, 100 seed weight (g), seed yield plant⁻¹(g), harvest index (%), ODAP content (%). The recorded observations were statistically analyzed using analysis of variance (ANOVA) to evaluate the existence of significant variation among the genotypes for the studied traits. Genetic divergence was assessed through Mahalanobis D^2 analysis, and the genotypes were classified into distinct clusters using Tocher's clustering technique. Mean intra-cluster and inter-cluster distances were computed to measure the degree of genetic diversity within and among clusters. The percentage contribution of each trait to the overall genetic divergence was also determined, while canonical vector analysis was employed to identify the characters responsible for the observed variability. The findings of these analyses were utilized to identify genetically diverse and agronomically promising genotypes that can serve as potential parents in future hybridization and crop improvement programmes.

Result and Discussion

The mean squares for genotypes were highly significant for all ten characters which indicated significant variation among all the genotypes for the characters under study. Among 64 genotypes, the genotype Mahateora (57.66 days) attained earliest flowering followed by IC-120472 (58.33), NLK-49 (58.66 days) and NLK-63 (58.66 days). The genotype which attained 50% flowering late were NLK-74 (65.66 days) followed by AKL-12 (65.00 days), NLK-73 (65.00 days) and EC-209026 (65.00 days). The genotype BIOR- 231 (115.66 days) matured earliest followed by NLK-36 (116 days), NLK-102 (116 days), NLK-53 (116 days) and the genotype NLK-63 (127.33 days) attained late maturity followed by NLK-94 (124.33 days). The genotype NLK-3 (90.29 cm) was tallest followed by NLK-55 (89.56 cm) and the genotype RLK-1045 (67.17 cm) was shortest

followed by IC-120491 (68.57 cm) and IC-120472 (68.77 cm). The genotype NLK-55 (5.20) and NLK-70 (5.20) recorded maximum number of primary branches plant⁻¹ while minimum number of primary branches plant⁻¹ was recorded by the genotype NLK-63 (3.60) followed by NLK-94 (3.70). The genotype AKL-19 (91.51) produced maximum number of pods plant⁻¹ followed by AKL-12 (90.47) and NLK-37 (88.80). The minimum number of pods plant⁻¹ was produced by the genotype NLK-54 (45.69) followed by NLK-3 (55.47) and BIOR-222 (57.58). The genotype NLK-37 (3.82) followed by NLK-3 (3.71), NLK-48 (3.70) and NLK-6 (3.70) had maximum number of seed pod⁻¹. The genotype IC-120469 (1.99) exhibited minimum number of seeds pod⁻¹. The genotype Mahateora (11.48 g) had maximum seed weight followed by RLK-1045 (11.47g) and the genotype NLK-63 (5.66 g) had minimum seed weight followed by PUSA-90-2 (6.23 g). The genotype NLK-49 (59.56 g) had maximum yield and the genotype JRL-115 (10.81g) had minimum yield followed by KH-1 (11.64 g) and IC-120491 (11.79 g). The genotype IC-120491 (51.63%) had maximum harvest index followed by PUSA-56 (51.61%) and the genotype NLK-47 (22.42%) had minimum harvest index. The genotype Ratan (0.236 %) contain less ODAP followed by NLK-73 (0.250 %), Prateek (0.279 %) and Mahateora (0.276 %). Although per se performance provides a preliminary indication of the breeding value of a genotype, it does not adequately reveal its potential for producing desirable progenies over successive generations. Based on the evaluation of yield and its associated traits among sixty-four genotypes of *Lathyrus*, NLK-49, JRL-115, IC-120472, NLK-63, BIOR- 231 NLK-36, NLK-102, NLK-53, NLK-55, NLK-70, RLK-1045, NLK-37, NLK-3, NLK-6, NLK-48, AKL-12, AKL-19, NLK-37 exhibited superior performance compared with the check variety Ratan. These genotypes recorded higher values for important yield-attributing characters such as number of pods per plant, number of seeds per pod and 100-seed weight. The grouping of 64 genotype into different clusters was done by Tocher's method. The entire genotypes (64) were grouped on the basis of D^2 statistics into 14 clusters. Cluster I was largest comprising of 41 genotypes, followed by cluster II comprising of 5 genotypes, cluster III, IV, V, VI, VII, and VIII, comprising of single genotype and cluster IX comprising of 4 genotypes again cluster X, XI, XII comprising of single genotype and cluster XIII comprising of 4 genotypes at last cluster XIV comprising of single genotype. Studied by Yadav *et al.* (2026) and Das *et al.* (2026) The promising check Ratan, Prateek and Mahateora grouped into cluster IX. The coefficients of the first three canonical vectors revealed the relative contribution of different traits to genetic divergence among the genotypes. In vector I, which explained 19.87% of the total variation, major contributions were observed from days to 50% flowering, ODAP content (%), number of pods plant⁻¹. Vector II accounted for 16.23% of the total variation, where number of seed pod⁻¹, number of primary branches plant⁻¹, number of pods plant⁻¹, days to 50% flowering, 100 seed weight, plant height. In vector III, contributing 14.63% of the total variation, 100 seed weight, harvest index, number of primary branches plant⁻¹, days to 50% flowering were the key characters influencing divergence. The results indicate that genotypes selected based on traits such as number of seeds pod⁻¹, days to 50% flowering, seed yield plant⁻¹, number of pods plant⁻¹, and

100 seed weight are likely to exhibit substantial genetic diversity and may serve as promising parents for hybridization programs. Başaran and Saritaş (2026) The intra cluster distance range from 0.00 to 28.61. Cluster XIII possessed highest intra cluster distance ($D^2 = 28.61$) followed by cluster II ($D^2 = 16.92$) and cluster I ($D^2 = 13.70$) and cluster IX ($D^2 = 12.66$). The average inter cluster distance was maximum between XI and cluster XIV ($D^2 = 224.69$), followed by cluster V and cluster XIV ($D^2 = 204.77$), cluster X and cluster XIV ($D^2 = 211.95$). The inter cluster distance was found to be minimum between cluster VIII and cluster XII ($D^2 = 9.66$). From the data it can be observed that the average intra cluster distance was maximum in cluster XIII, cluster II, cluster I and cluster IX and the average inter cluster distance was maximum in cluster XI and XIV and also in between cluster X and cluster XIV. Widely diverged clusters remain distinct in different environment Therefore, genotypes originating from widely separated clusters can be utilized in hybridization programs to generate a broader range of variability among the segregating progenies. The comparison of cluster means for ten characters under study marked considerable genetic difference between groups. Highest cluster mean for days to 50% flowering was recorded by cluster X (64.33) followed by cluster XII (64.00) and cluster VI (63.67) while cluster XIV (58.67) followed by cluster V (59.00) and cluster IX (60.67) represented the lowest mean for days to 50% flowering. Highest cluster means for days to maturity was recorded by cluster XIV (126.00) followed by cluster XIII (122.67) and cluster IX (121.42) while cluster II (118.13) followed by cluster X (118.33) and cluster I (119.60) represented the lowest mean for days to maturity. Highest cluster mean for plant height was recorded by cluster IV (89.56) followed by cluster XIII (84.76) and cluster XII (82.75) while cluster II (74.85) followed by cluster XI (68.57) and cluster V (68.73) represented the lowest mean for plant height. Highest cluster mean for number of primary branches plant⁻¹ was recorded by cluster IV (5.21) followed by cluster V (4.60) and cluster IX (4.55) while cluster III and cluster VII (3.80) represented the lowest mean for number of primary branches plant⁻¹. Highest cluster mean

for number of pods plant⁻¹ was recorded by cluster X (88.59) followed by cluster VI (79.26) and cluster IX (78.72) while cluster VII (60.92) and cluster III (61.96) represented the lowest mean for number of pods plant⁻¹. Highest cluster mean for number of seeds per pod was recorded by cluster VI (3.70) followed by cluster VIII (3.31) and cluster IV (3.30) while cluster III (2.00) followed by cluster XIV (2.10) and cluster V (2.10) represented the lowest mean for number of seeds per pod. Highest cluster mean for 100 seed weight, cluster IX (10.77) followed by cluster II (10.75) while cluster XIII (7.10) and cluster IV and cluster XII (7.25) represented the lowest mean for 100 seed weight. Highest cluster mean for Seed yield plant⁻¹ was recorded by cluster XIV (59.56) while cluster V (10.82) followed by cluster XI (11.80) and cluster III (14.99) represented the lowest mean for Seed yield plant⁻¹. Highest cluster mean for harvest index was recorded by cluster XI (51.64) followed by IX (45.50) and cluster (45.36) while cluster X (31.46) followed by XIII (32.52) represented the lowest mean for harvest index. Highest cluster mean for ODAP was recorded by cluster XI (0.61) followed by cluster X (0.58) and cluster II (0.55) while cluster IX (0.26) followed by cluster VIII and cluster XII (0.44). The 64 genotypes exhibited significant differences for the traits under study. The characters like days to number of seeds pod⁻¹, number of pods plant⁻¹, and Seed yield plant⁻¹, Number of primary branches plant⁻¹, number of seeds pod⁻¹ were identified to contribute maximum towards genetic divergence from canonical analysis studied, cluster mean estimate and contribution of individual characters to divergence. Sixty four genotypes were grouped into fourteen clusters. Ten inter cluster combination were identified for selecting promising diverse genotypes to be included in crossing programme to get potential variety. Twenty seven genotypes viz. AKL-19, NLK-94, NLK-67, NLK-62, NLK-51, EC-209081, NLK-39, NLK-54, NLK-74, NLK-48, EC-2609071, NLK-6, AKL-7, JRL-16, BIOR-231, NLK-49, IC-120472, NLK-37, IC-120491, NLK-40, KH-1, NLK-102, NLK-5, PUSA-24, AKL-12, NLK-44, BIOR-222 were identified as potential parents and we can use these genotype in crossing programme.

Table 1. ANOVA

Source of variation	d.f.	Mean sum of squares									
Replications	2	2.72	27.13	0.71	0.007	7.71	0.006	0.158	3.48	0.05	0.0002
Genotypes	63	10.71**	22.10**	79.81**	0.35**	271.52**	0.516**	3.61**	110.80**	108.8**	0.019**
Errors	126	1.46	14.24	44.72	0.06	37.25	0.060	0.21	4.22	5.30	0.0004

Table 2: Range, Grand mean and S.E for various characters in Lathyrus

Sr. No	Characters	Range		Grand mean	S.E. difference
		Min	Max		
1	Days to 50% flowering	57.66	65.66	61.86	0.70
2	Days to maturity	115.66	127.33	119.85	2.17
3	Plant height (cm)	67.17	90.29	78.77	3.86
4	No. of primary branches plant ⁻¹	3.60	5.20	4.23	0.15
5	No. of pods plant ⁻¹	45.69	91.51	76.10	3.52
6	No. of seeds pod ⁻¹	1.99	3.82	2.81	0.14
7	100 seed weight (g)	5.66	11.48	8.95	0.26
8	Seed Yield plant ⁻¹ (g)	10.81	59.56	19.36	1.18
9	Harvest index (%)	22.42	51.63	40.99	1.33
10	ODAP content (%)	0.236	0.630	0.51	0.01

Table 3: Contributions of individual characters towards divergence

Sr No.	Characters	Time ranked 1 st	Percent contribution
1	Days to 50% flowering	79	3.92%
2	Days to maturity	1	0.05%
3	Plant height (cm)	8	0.4%
4	Number of primary branches plant ⁻¹	86	4.27%
5	Number of pods plant ⁻¹	144	7.14%
6	Number of seeds pod ⁻¹	141	6.99%
7	100 seed weight (g)	312	15.48%
8	Yield plant ⁻¹ (g)	182	9.03%
9	Harvest index (%)	526	26.09%
10	ODAP content (%)	537	26.64%
	Total	2016	39.20%

Table 4: Grouping of 64 genotypes of lathyrus into different clusters

Cluster	Number of genotypes	Name of the genotypes
I	41	IC-120472, EC-209081, LSD3, IC-18773, EC-209071, EC-209081, EC-207071, NLK-38, NLK-50, EC-209026, EC-209072, NLK-68, EC-209026, NLK-102, BIOR-208, NLK-102, NIC-118773, NLK-42, NLK-70, NLK-56, RLK-579, NLK-36, NLK-39, IC-120491, NLK-74, RLK-602, AKL-19, NLK-94, NLK-67, NLK-62, NLK-51, BIOR-231, IC-120472, NLK-37, NLK-40, KH-1, NLK-5, PUSA-24, AKL-12, NLK-44, BIOR-222
II	5	JRL-16, RLK-1045, RLK-1093, PUSA-56, NLK-54
III	1	IC-120469
IV	1	NLK-55
V	1	JRL-115
VI	1	NLK-48
VII	1	AKL-7
VIII	1	IC-120469
IX	4	NLK-73, Prateek, Ratan, Mahateora
X	1	NLK-6
XI	1	IC-120491
XII	1	NLK-53
XIII	4	NLK-63, PUSA-90-2, NLK-47, NLK-3
XIV	1	NLK-49

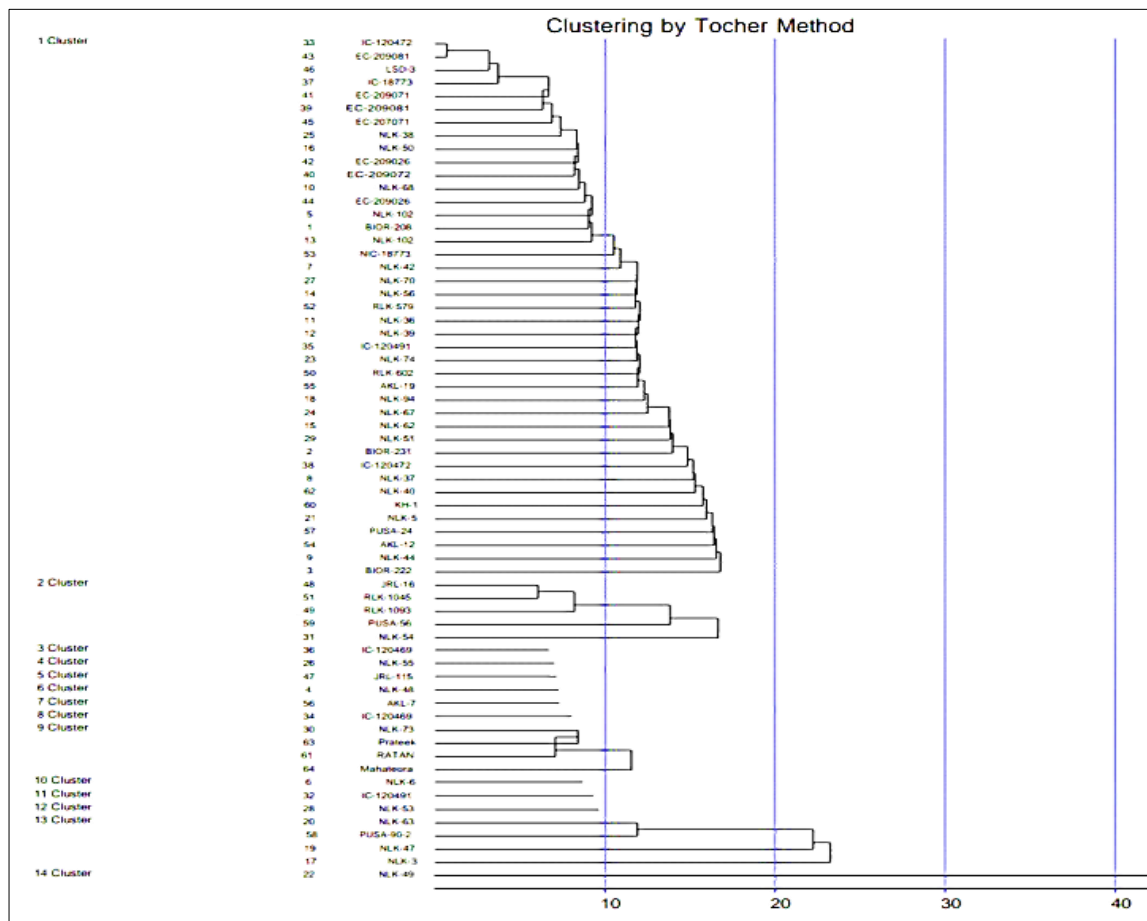
**Fig 1:** Dendrogram showing clustering by tocher's method

Table 5: Three canonical roots

Root	Eigen value	Per cent contribution
λ_1	1.98788	19.87
λ_2	1.62382	16.23
λ_3	1.46376	14.63
Total	5.07546	50.73
Sum of all canonical roots		100

Table 6: Values of first three vectors

Sr. No.	Characters	Vector I	Vector II	Vector III
1	Days to 50% flowering	0.47242	0.25168	0.03622
2	Days to maturity	-0.36783	-0.35975	-0.28172
3	Plant height (cm)	-0.36550	0.13151	-0.48839
4	Number of primary branches plant ⁻¹	-0.19986	0.47365	0.13373
5	Number of pods plant ⁻¹	0.08838	0.41838	-0.06121
6	Number of seed pod ⁻¹	-0.01600	0.48053	-0.36064
7	100 seed weight (g)	-0.23035	0.18934	0.58451
8	Yield plant ⁻¹ (g)	-0.42618	-0.02897	0.00043
9	Harvest index (%)	-0.24474	-0.11771	0.42412
10	ODAP content (%)	0.40840	-0.33031	-0.08699

Table 7: Average intra and inter cluster distance

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	13.70	21.49	18.66	21.30	23.76	20.89	26.19	21.01	86.53	25.12	23.96	22.66	31.19	159.49
II		16.92	23.40	43.89	23.41	33.87	23.56	35.05	86.29	38.12	24.99	43.58	52.65	165.66
III			0.00	31.01	21.82	40.36	23.45	23.13	77.01	50.25	16.37	14.42	33.62	176.03
IV				0.00	31.54	14.90	36.01	12.62	77.60	26.89	51.10	13.61	23.03	155.57
V					0.00	33.44	23.26	25.00	103.57	28.57	31.63	31.04	37.94	204.77
VI						0.00	19.22	10.24	73.20	10.41	54.36	25.62	25.96	147.87
VII							0.00	20.46	65.14	33.56	49.79	28.14	35.20	147.35
VIII								0.00	53.45	21.90	44.82	9.66	23.92	185.78
IX									12.66	117.64	128.61	70.32	105.35	181.82
X										0.00	46.80	36.38	32.26	211.95
XI											0.00	41.25	53.99	224.69
XII												0.00	22.30	186.97
XIII													28.61	176.93
XIV														0.00

Bold figures are average intra cluster distance $\bar{D} = 54.34$

Table 8. Cluster means for ten 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 pod ⁻¹	100 seed weight (g)	Yield plant ⁻¹ (g)	Harvest index (%)	ODAP content (%)
I	62.10	119.60	78.92	4.24	77.68	2.82	8.77	19.05	41.89	0.54
II	60.93	118.13	74.85	4.08	70.22	2.53	10.75	18.09	44.24	0.55
III	61.00	119.67	76.47	3.80	61.96	2.00	8.33	14.99	45.36	0.49
IV	61.67	120.00	89.56	5.21	75.41	3.30	7.25	20.21	34.61	0.49
V	59.00	119.33	68.73	4.60	73.10	2.10	9.67	10.82	32.57	0.54
VI	63.67	120.00	76.53	4.40	79.26	3.70	9.35	22.51	32.57	0.51
VII	63.33	119.67	81.44	3.80	60.92	2.30	10.69	20.37	33.64	0.47
VIII	62.33	119.67	69.65	4.41	76.65	3.31	8.70	15.41	35.36	0.44
IX	60.67	121.42	80.32	4.55	78.72	3.09	10.77	22.44	45.50	0.26
X	64.33	118.33	78.61	4.30	88.59	3.70	9.36	15.31	31.46	0.58
XI	62.00	121.33	68.57	3.80	63.28	2.61	8.71	11.80	51.64	0.61
XII	64.00	116.00	82.75	4.30	75.60	2.51	7.25	15.90	37.80	0.44
XIII	61.58	122.67	84.76	3.85	73.99	2.98	7.10	17.75	32.52	0.51
XIV	58.67	126.00	78.86	4.51	69.28	2.10	8.90	59.56	37.85	0.49
SD	1.70	2.31	6.07	0.39	7.58	0.57	1.24	11.83	6.31	0.08
Variance	2.91	5.37	36.90	0.15	57.46	0.33	1.55	140.17	39.85	0.006

Table 9: Selection of genotypes based on inter cluster distances and cluster mean

Sr. No.	Cluster combination	Average inter-cluster distance	Cross combination	Traits
1	XI x XIV	224.69	IC-120491 x NLK-49	Seed weight, Number of primary branches plant ⁻¹
2	X x XIV	211.95	JRL-115 x NLK-49	Early maturity
3	V x XIV	204.77	NLK-6 x NLK-49	Early maturity, Yield plant ⁻¹
4	XII x XIV	186.97	NLK-53 x NLK-49	Early maturity
5	VIII x XIV	185.78	IC-120469 x NLK-49	Early maturity, Seed weight
6	IX x XIV	181.82	NLK-73, Prateek, Ratan, Mahateora } x NLK-49	Number of seeds pod ⁻¹ , Number of pods plant ⁻¹ , Yield plant ⁻¹ , ODAP
7	XIII x XIV	176.93	NLK-63 } x NLK-49 PUSA-90-2, NLK-47, NLK-3	Seed weight, Number of primary branches plant ⁻¹
8	III x XIV	176.03	NLK-54, IC-120469 } x NLK-49	Seed weight, Number of primary branches plant ⁻¹
9	II x XIV	165.66	BIOR-222, JRL-16, x RLK-1045, RLK-1093, PUSA-56 } NLK-49	Number of pods plant ⁻¹ , Yield plant ⁻¹
10	I x XIV	159.49	IC-120472, EC-209081, LSD3, IC-18773, EC-209071, EC-209081, EC-207071, NLK-38, NLK-50, EC-209026, x NLK-49 EC-209072, NLK-68, EC-209026, NLK-102, BIOR-208, NLK-102, NIC-118773, NLK-42, NLK-70, NLK-56, RLK-579, NLK-36, NLK-39, IC-120491, NLK-74, RLK-602, AKL-19, NLK-94, NLK-67, NLK-62, NLK-51, BIOR-231, IC-120472, NLK-37, NLK-40, KH-1, NLK-5, PUSA-24, AKL-12, NLK-44	Number of seeds pod ⁻¹ , Number of pods plant ⁻¹ , Yield plant ⁻¹ , Early maturity

 $\bar{D} = 54.34$ **Conclusion**

Significant differences were observed for sixty-four germplasm. Data were recorded on five competitive plants for 10 quantitative 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 pods plant⁻¹, number of seeds pods⁻¹, 100 seed weight (g), yield plant⁻¹ (g), harvest index (%) and ODAP content (%). Mahalanobis generalized distance (Mahalanobis 1928 and Rao 1952) was used in this investigation for computing genetic divergence for quantitative characters. The sixty-four germplasm exhibited significant differences for the traits under study. The characters like days to number of seeds pod⁻¹, number of pods plant⁻¹, and yield plant⁻¹, Number of primary branches plant⁻¹, number of seeds pod⁻¹ were identified to contribute maximum towards genetic divergence from canonical analysis studied, cluster mean estimate and contribution of individual characters to divergence. Sixty four genotypes were grouped into fourteen clusters. Ten inter cluster combination were identified for selecting promising diverse germplasm to be included in

crossing programme to get potential variety. Twenty seven genotypes viz. AKL-19, NLK-94, NLK-67, NLK-62, NLK-51, EC-209081, NLK-39, NLK-54, NLK-74, NLK-48, EC-2609071, NLK-6, AKL-7, JRL-16, BIOR-231, NLK-49, IC-120472, NLK-37, IC-120491, NLK-40, KH-1, NLK-102, NLK-5, PUSA-24, AKL-12, NLK-44, BIOR-222 were identified as potential parents and we can use these germplasm in crossing programme.

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