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Original Research Article

Studies on Genetic Divergence among Explored Germplasm from Eastern Vidarbha and Selected Varieties in Lathyrus (*Lathyrus sativus* L.)

Avinash V. Khillari*, Amol E. Patil, Megha R. Puttawar and V.S. Jayde

Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani-431402, Maharashtra, India
**Corresponding author*

A B S T R A C T

Fourty four germplasms were explored and collected from Bhandara, Gondia, Gadchiroli and Chandrapur districts of eastern Vidarbha of Maharashtra. Their genetic divergence was compared with thirteen selected varieties. Collectively fifty seven genotypes were evaluated for genetic divergence to study genetic resemblance and to identify potential parents for lathyrus breeding programme aimed at yield and earliness improvement. These genotypes were grown in randomized block design replicated thrice and observations were recorded for eight characters i.e. days to 50% flowering, days to maturity, plant height (cm), number of primary branches, seeds pod^{-1}, pods plant^{-1}, 100 seed weight (g) and grain yield^{-1}. Mahalanobis generalized distance for eight characters was used in this study for computing genetic divergence. The analysis of dispersion for eight correlated 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, pods plant^{-1}, yield 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, in vector II primary branches, days to maturity, days to 50% flowering were important source of variation. In vector III days to 50% flowering, days to maturity, number of seeds pod^{-1} and 100 seed weight were important source of variation. The genotypes belonging to distant cluster and exhibiting high performance in the desirable direction for plant height, yield plant^{-1}, days to 50% flowering and 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-11, L-07, L-08, RLK-240, L-39, L-05, RLK-602, L-16, BioR-208 were identified as potential and diverse parents for their use in future crop improvement and breeding programme.

Keywords

Lathyrus, Exploration, Genetic divergence, Cluster analysis, Genetic resemblance

Introduction

Lathyrus (*Lathyrus sativus* L.), (2n =14) is herbaceous winter pulse crop belonging to family leguminosae and sub family Fabaceae. It is an important pulse crop and considered as a model crop for sustainable agriculture. The most probable origin of Lathyrus is Europe and Western Asia including India. In India, the remains of *Lathyrus sativus* were dated as old as 2000 B.C. (Pandey *et al.,* 1995). The cultivation of Lathyrus is predominant in India, Bangladesh, Ethiopia and Nepal. The crop is sturdy with a deep penetrating root system and grown on residual moisture hence

considered as a model crop for sustainable agriculture. It can be grown on wide range of soil types including very light soils and heavy clays. Lathyrus serves better alternative to the traditional pulse crop like chickpea and pigeon-pea especially in the area under dry land conditions (Thakur and Rai 1985, Lal *et al.*, 1986). The importance of this crop as a pulse is due to its high seed protein content i.e. 28% (Mehra, 1991). Sharma and Padmanabhan (1969) analyzed and reported that the protein quality of lathyrus seed is better than any other pulse crop. There are about 150 species in the genus Lathyrus that comprise of 15 sections among which grass pea is one (Smartt, 1994). When other crops fail, lathyrus often becomes the principle food source for the poor. Indeed, it may be the only source of food available in the time of drought and famine. Thus, the important breeding aspects in lathyrus breeding programme are to develop varieties with higher yield, high protein, low ODAP content and wider adaptability. Lathyrus varieties generally have low yield potential, poor plant type and high neurotoxin content which is unstable over environment (Ramanujam *et al.*, 1980). The cause of relatively poor success in grain legume in achieving substantial progress is the lack in genetic diversity. The success of a systemic breeding programme depends mainly on judicious selection of promising parents from gene pool. The importance of genetic diversity in crop improvement has long been appreciated by breeder but basic difficulty was recognizing and estimating such diversity. The genetic diversity which is basis of plant breeding is produced due to inheritant genetic differences in plant species and is the major interest of plant breeder. The more divergence the parents within overall limits of fitness, the greater are chances of heterotic F_1's and broad spectrum of variability in segregating generations (Arunachalam, 1981 and Falconer, 1981). Therefore, the first step is to initiate a hybridization programme is to asses genetic diversity and thereby identify genetically diverse parent. In this paper we reported the extent and pattern of polymorphism among collected lathyrus germplasm and selected varieties. We further reported the genetic distance present between the germplasm studied and selected the best diverse germplasm to use as parents in further hybridization programme for exploitation of the heterosis and to select promising parent material for future crop improvement programme.

Materials and Methods

The present study was conducted during *rabi* 2011-2012 at research farm of Agricultural Botany Section, College of Agriculture, Nagpur. The experimental material comprised of 57 genotypes. Out of 57 genotypes, L-1 to L-44 genotypes were explored from different regions of Bhandara, Gondia, Gadchiroli and Chandrapur districts of eastern Vidarbha of Maharashtra state of India (Fig. 2) and remaining 13 genotypes were varieties accessed from different sources. These 57 genotypes showed in Table 1 were grown in *rabi* 2011-2012 in three replications. In *rabi* 2011-12, the 57 germplasm were grown in RBD design in three replications with the spacing of 45 cm × 15 cm accommodating 15 plants in each row. The data were recorded on five randomly selected plants from each genotypes on days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g) and yield per plant (g) except days to 50% flowering and days to maturity which was recorded on plot basis. The analysis of variance was performed to test the significance difference among the genotypes for characters studied as per

Panse and Sukhatme (1954). Partitioning the variance and covariance into genotypic, phenotypic and environmental components was done as suggested by Fisher and Yates (1958). The data was subjected to Mahalanobis D^2 statistics to measure the genetic divergence as suggested by Rao (1952).

Results and Discussion

The analysis of variance for various characters is presented in table 2. The mean squares for 57 genotypes were highly significant for all eight characters. This indicates significant genetic variation among all the genotypes for the eight characters. The relative contribution of individual character for divergence is presented in table 3. The plant height at maturity (ranked first 584 times out of 1596 total number of combinations) has contributed maximum (36.59%) to genetic divergence. This was followed by yield plant^{-1} (ranked first 494 times out of 1596 total number of combinations) which contributed to 30.95% and seed pod^{-1} (14.79 %). The distance values obtained for all the 1596 pairs obtained by following Mahalanobis D^2 statistics were used to group the 57 genotypes into diverse clusters. Fifty seven genotypes were used to construct dendrogram based on D^2 and the results are presented in Figure 1.

These genotypes were grouped into eight clusters. Cluster second was the largest consisting of 20 genotypes followed by cluster V with 16 genotypes, cluster I, VI with 12 and 5 genotypes each and cluster III, IV, VII and VIII were solitary clusters with a single genotype each. This indicated the presence of appreciable amount of diversity among the genotypes studied. The appearance of solitary clusters may be the outcome of intensive selection or the complete stoppage of gene flow within the species. But in the plant breeding point of view this will prove the worthy breeding material. The promising check Ratan and Mahateora were grouped in cluster V whereas check Prateek was grouped into cluster II. This indicates that are not varying much from check varieties. There were many genotypes distributed in other cluster which were different from promising check and hence offers scope for improvement. Similar results were also obtained by Pandey et.al. (2000).The average intra and inter cluster distance by Tocher's method given in table 4. The intra cluster variation ranged from 0 to 27.39. Cluster VI possessed highest intra cluster distance (D=27.39) followed by cluster V (13.25) and cluster II (7.24). Cluster III, IV, VII and VIII had zero intra cluster distance as these groups are solitary. The average inter cluster distance was maximum between cluster IV and cluster VIII (110.67) followed by cluster I and cluster VIII (74.99). It could be observed that there were large variations in the mean performance of genotypes included in diverse clusters given in table 5.

Genotypes of cluster VIII possessed the highest cluster mean for days to maturity, number of pods plant^{-1}, number of seeds pod^{-1}, hundred seed weight and grain yield plant^{-1}. Cluster VII showed the maximum mean for plant height, number of primary branches. The variance of cluster means for all the characters indicated that the maximum variation was accounted by plant height (197.99), number of pod plant^{-1},(197.62), yield palnt^{-1} (28.22) and days to 50 % flowering (17.59). Thus it can be inferred that these characters of parent namely plant height, yield plant-1, days to 50 % flowering can be selected for hybridization. Bhalekar (2009), and Rahman (2010) also observed similar results in lathyrus.

Table.1 Genotypes of lathyrus used for present study

Sr. No.	Genotypes	Site of Collection of Sr. No. 1 to 44	Sr. No.	Genotypes	Site of Collection
1	L-01	Bhandara	31	L-31	Gadchiroli
2	L-02	Bhandara	32	L-32	Gadchiroli
3	L-03	Bhandara	33	L-33	Gadchiroli
4	L-04	Bhandara	34	L-34	Gadchiroli
5	L-05	Bhandara	35	L-35	Gadchiroli
6	L-06	Bhandara	36	L-36	Gadchiroli
7	L-07	Bhandara	37	L-37	Gadchiroli
8	L-08	Bhandara	38	L-38	Chandrapur
9	L-09	Bhandara	39	L-39	Chandrapur
10	L-10	Bhandara	40	L-40	Chandrapur
11	L-11	Bhandara	41	L-41	Chandrapur
12	L-12	Bhandara	42	L-42	Chandrapur
13	L-13	Gondia	43	L-43	Chandrapur
14	L-14	Gondia	44	L-44	Chandrapur
15	L-15	Gondia		**Other accessions.**	
16	L-16	Gondia	45	BioR-208	IARI
17	L-17	Gondia	46	BioR-231	IARI
18	L-18	Gondia	47	BioR-222	IARI
19	L-19	Gondia	48	JRL-16	Raipur
20-	L-20	Gondia	49	JRL-115	Raipur
21	L-21	Gondia	50	RLK-1093	Raipur
22	L-22	Gondia	51	RLK-602	Raipur
23	L-23	Gondia	52	RLK-1045	Raipur
24	L-24	Bhandara	53	RLK-279	Raipur
25	L-25	Bhandara	54	RLK-240	Raipur
26	L-26	Gondia		**Checks**	
27	L-27	Gondia	55	Ratan	
28	L-28	Bhandara	56	Prateek	
29	L-29	Gondia	57	Mohateora	
30	L-30	Bhandara			

Table.2 Analysis of variance for various characters

Source of variance	DF	Mean sum of squares							
		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)
Replication	2	4.43	22.11	20.90	0.10	146.92	0.03	0.02	4.14
Genotype	56	41.40**	18.73**	233.66**	0.88**	463.41**	0.30**	0.40**	68.81**
Error	112	3.70	8.35	8.69	0.27	54.58	0.03	0.20	2.28

** Significant at 1% level.

Table.3 Relative contribution of individual character to divergence

Sr. No.	Source	Time ranked 1st	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	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.4 Average intra and inter cluster distance by Tocher's method

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**3.905**	9.595	9.848	8.561	33.389	18.928	41.929	74.995
II		**7.240**	11.674	21.710	18.601	17.135	27.450	46.878
III			**0.00**	9.808	27.726	18.560	51.718	63.668
IV				**0.00**	54.520	27.265	74.329	110.676
V					**13.258**	29.675	23.264	22.816
VI						**27.397**	45.537	61.608
VII							**0.00**	36.355
VIII								**0.000**

(D =27.728)

Figures in bold indicates intra cluster distance.

Table.5 Cluster means for eight characters in lathyrus

Sr. No.	Cluster	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 pods^{-1}	100 seed weight (g)	Yield plant^{-1} (g)
1	I	54.472	120.333	47.333	4.006	54.97	2.444	6.861	7.586
2	II	56.717	122.633	54.483	4.230	63.15	2.577	7.045	11.158
3	III	50.667	119.333	48.533	4.000	64.2	2.267	7.233	13.080
4	IV	50.667	118.000	38.400	3.933	42.4	2.133	6.700	6.717
5	V	58.833	123.000	64.837	4.875	78.13	2.767	7.127	16.973
6	VI	59.200	119.333	51.173	4.160	65.17	2.387	6.980	12.541
7	VII	60.000	122.333	76.933	4.933	78.27	2.533	7.333	10.530
8	VIII	61.667	125.667	76.400	4.133	85.93	3.467	8.067	23.193
	SD	4.2068	2.5174	14.0709	0.3950	14.0577	0.4100	0.4149	5.3125
	Variance	17.6974	6.3373	197.9923	0.1561	197.6201	0.1681	0.1721	28.2233

Table.6 Selection of cluster combinations, potential parents and cross combination on the basis of genetic diversity

Sr. No.	Cluster combination	Average inter-cluster distance	Cross combination	Traits
1	IV × VIII	110.677	L-3 x BioR-208	Early maturity
2	I × VIII	74.995	L-16, L-12, L-31 } x BioR-208	Plant height
3	IV × VII	74.329	L-3 x RLK-602	Early maturity
4	III × VIII	63.668	L-32 x BioR-208	Yield
5	VI × VIII	61.608	JRL-16, RLK279, BioR208, L-37 } x	Number of pods plant^{-1}, Yield
6	IV × V	54.520	RLK-1045, L-44, L-14 } x L-3	Yield
7	III × VII	51.718	L-32 x RLK-602	Number of pods plant^{-1}
8	II × VIII	46.878	L-11, L-07, L-08 } x BioR-208	Plant height
9	VI x VII	45.537	JRL-16, RLK-240, RLK-279 } x RLK-602	Number of pods plant^{-1}
10	I x VII	41.929	L-39, L-05, L-31 } x RLK-602	Number of pods plant^{-1}
11	VII x VIII	36.355	RLK-602 x BioR-208	Plant height, Number of pods plant^{-1}
12	I x V	33.389	L-16, L-39, L-05 } x RLK-45, L-44, L-14	Yield
13	V x VI	29.675	RLK-45, L-44, L-14 } x JRL-16, L-37, RLK-279	Yield

(D =27.728)

Table.7 Cross combination identified for implementing crossing programme

cross combination
L-03 L-31 L-33 L-25 L-32 JRL-16 RLK-279 L-37 L-11 L-07 L-08 RLK-602 X BioR-208
L-32 JRL-16 RLK-240 RLK-279 L-39 L-05 L-31 X RLK-602
RLK-602 RLK-1045 L-44 L-14 X L-03
L-16 L-39 L-05 RLK-1045 X L-14
RLK-1045 L-44 L-14 JRL-16 X L-37 RLK-279

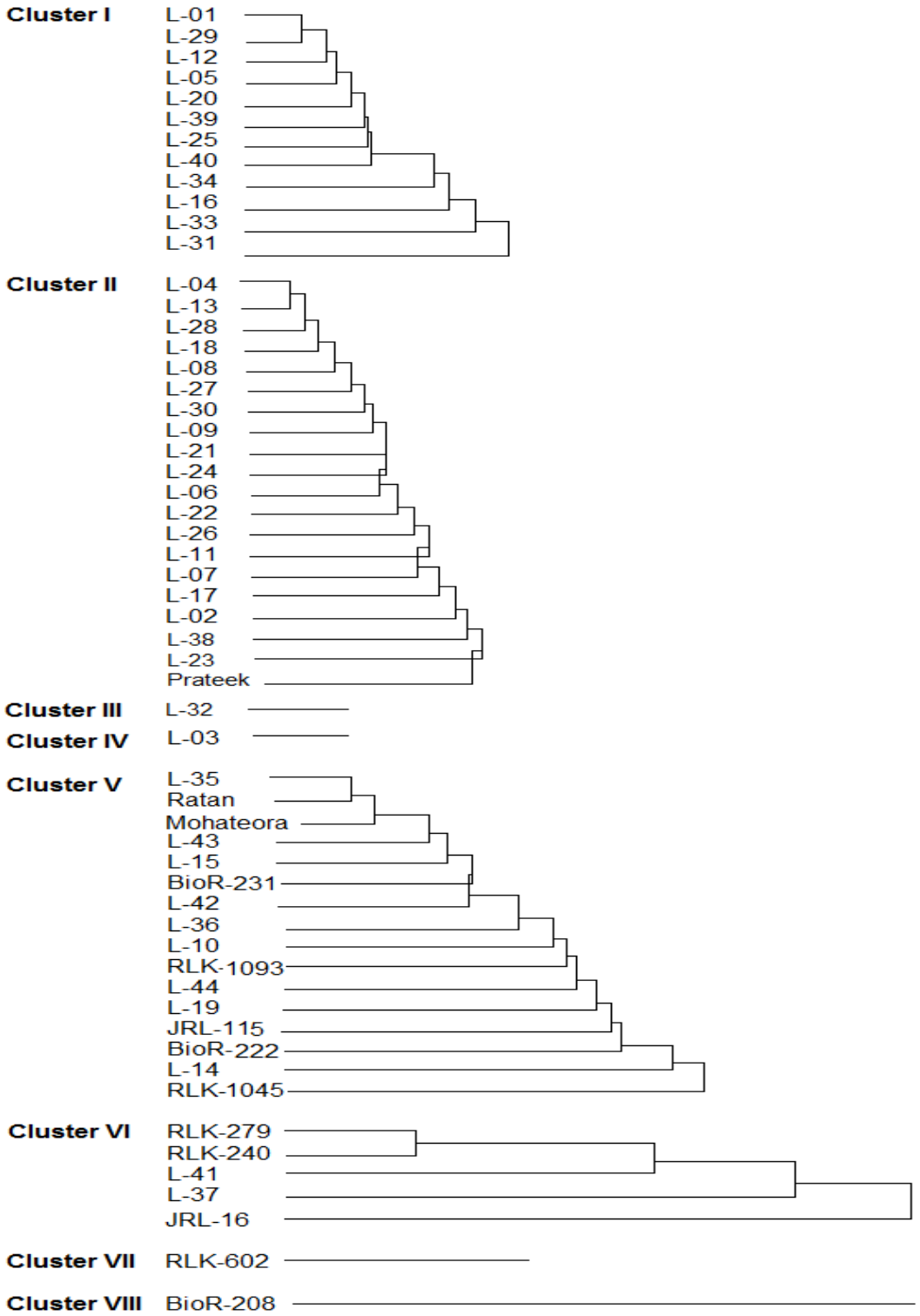

Fig. 1 Dendrogram showing clustering by Tocher's method

Fig.2 Map showing the sites of germplasm exploration and collection

The genotypes belonging to distant cluster and exhibiting high performance in the desirable direction for plant height, yield plant^{-1}, days to 50% flowering and pods plant^{-1} were identified as the potential parents for hybridization programme. On this basis twenty 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-11, L-07, L-08, RLK-240, L-39, L-05, RLK-602, L-16, BioR-208 were identified as potential and diverse parents for their use in development of parent material for crop improvement programme and crossing programme which are recommended to be crossed in following combination, table 6 and 7, to identify

potential transgrates for high yield and adaptation. Therefore it can be concluded that for yield, cluster III X VIII, cluster IV X V, cluster I X V and cluster V X VI will prove promising combinations whereas for earliness, cluster IV X VIII, Cluster IV X VII will be the best combinations for achieving earliness.

References

Arunachalam V. 1981. Genetic distance in plant. Indian Journal of Genetics and Plant Breeding.41: 226-236.

Bhalekar AP, Gawande VL, Ghorpade PB. 2009. Genetic divergence studies and selection of parents for hybridization in lathyrus. Journal of Food Legume. 22(4): 299-301.

Falconer DS. 1981. Introduction to Quantitative Genetics, Ed. 2.Longmans Green, London/New York.

Fisher RA and Yates F.1958. Statistical tables for biological, agricultural and medical research 5th Halner Pub. Co., New York.

Lal MS, Agrawal and Chitale NW.1986. Genetic improvement of chicking vetch (*Lathyrus sativs* L.) in Madhy Pradesh. India lathyrus and Lathyrism. Proceeding of International conference. Third world medical foundation, New York. Pp 279-305.

Mehra RB. 1991. Genetic improvement of lathyrus problem and potentialities. Genetic improvement of Pulse crop. 2: 205-213.

Pandey RL, Chitale MW, Sharma RN, Kashyap OP, Agrawal SK, Geda AK, Chandrakar H K and Agrawal K K.1995. Catalouge on Grasspea (*Lathyrus Sativus* L.) Germplasm, Dept. of Plant Breeding and Genetics, IGKV, Raipur, India.

Pandey RL, Rastogi NK, Geda AK. 2000. Genetic diversity in relation to grain yield and neurotoxin in grasspea (*Lathyrus* sp.) genetic resources. Indian Journal of Plant Genetic Resources. 2000. 3 (1):0971-8141

Panse vg and Sukhatme PV. 1954. Statistical Methods for Agricultural Workers. ICAR, New Delhi. Pp 54-57.

Rahman S, Molla MR, Nazim-ud-Dowla MAN. 2010. Assessment of Genetic Diversity in Grasspea (*Lathyrus sativus* L.) Genotypes Using Morphological Markers. Academic Journal of Plant Science. 3 (2):85-91

Ramanujam S, Sethi KL and Rao SLN. 1980. Stability of neurotoxin in khesari. Indian Journal of Genetics and Plant Breeding. 40:300-304.

Rao C. 1952. Advanced statistical methods in biometric research. John Wiley and sons, Znc. Newyork.

Sharma DS and Padmanabhan. 1969. Food Science and Tech. In: IE Liener (Ed), Academic Press, New York. Pp 209-233.

Smartt J. 1994. Grain Legumes, Evolution and genetic resources. Cambridge University Press, Cambridge, U.K. Pp.200.

Thakur H.C., and B. Rai.1985. Cultivation of khesari in paddy follows. Indian farming. 35: (9)10-45.