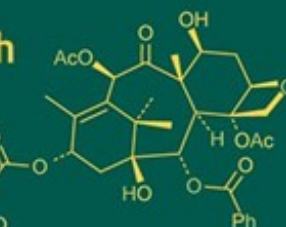
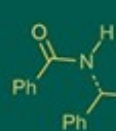


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Morphological characterization of germplasm of *Lathyrus* (*Lathyrus sativus* L.)

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ABSTRACT

The present investigation was undertaken to assess the morphological variability and characterize a diverse set of *Lathyrus* germplasm based on important qualitative traits. The study was conducted during the Rabi season of 2024–25 at the Research Farm of the Agricultural Botany Section, College of Agriculture, Nagpur. A total of 27 germplasm along with 3 checks, were evaluated under field conditions using suitable morphological descriptors. Considerable variation was observed among the germplasm for characters associated with flowering, maturity, plant architecture, branching, pod formation, seed characteristics and yield. The observed variability indicated the presence of substantial genetic differences within the evaluated germplasm. Characterization of the germplasm enabled the identification of distinct genotypes possessing desirable morphological and yield-related attributes. Such variability provides valuable opportunities for the selection of promising genotypes and parental materials for future breeding programmes. The information generated from this study can also contribute to the effective documentation, conservation and utilization of lathyrus genetic resources for the development of high-yielding and well-adapted cultivars. Morphological characterization of *Lathyrus* germplasm was carried out using qualitative descriptors. Variation was observed for plant growth habit, internode length, stem colour and wing width, and branch arrangement, while all genotypes were indeterminate. Leaf characters included colour, leaflet shape, tendril size and persistence, with pubescence restricted to the leaf margin. Flower traits varied for bud size, flower and vein colour, and calyx colour. Pod characters included shape, curvature, beak shape, colour, constriction and dehiscence. Seed variation was recorded for shape, coat colour, pattern colour and surface, while cotyledons were yellow.

Keywords: Characterization, *Lathyrus*, Germplasm, Descriptor

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.

The genetic resources available within a crop species provide the foundation for developing improved cultivars. Germplasm collections generally contain considerable variation for plant architecture, flowering behaviour, maturity, yield attributes, seed characteristics and adaptability. Proper characterization of this variation is essential for identifying genetically and phenotypically distinct accessions and for determining their potential value in crop improvement programmes. The foremost objective of this study was a phenotypic characterization of lathyrus germplasm based on DUS descriptors for various morphological characters, (Pandey, 2000) [1]. Systematic evaluation of germplasm also helps in detecting desirable traits that can be in

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incorporated into breeding populations. Morphological characterization is one of the simplest and most practical approaches for preliminary assessment of genetic variation in germplasm. It involves the systematic recording of qualitative traits that describe differences among genotypes. Characters such as plant height, branching pattern, flowering and maturity duration, pod characteristics, seed traits and yield-related attributes can provide useful information for distinguishing accessions and assessing their agronomic potential. The use of standardized morphological descriptors facilitates the identification, documentation and maintenance of germplasm and reduces duplication within collections. Identification of genotypes possessing desirable characteristics such as early flowering, suitable plant stature, greater pod production, improved seed size and higher seed yield can support the selection of promising materials for breeding. Moreover, information generated through morphological evaluation can serve as a basis for selecting diverse parents and planning subsequent breeding and genetic studies. Therefore, the present investigation was undertaken to characterize a diverse set of lathyrus germplasm using important morphological traits. The study aims to assess the extent of observable variation among the germplasm, identify promising accessions with desirable characteristics, and generate useful information for the effective conservation, utilization and genetic improvement of lathyrus.

Materials and Methods

In *Rabi* 2024-25, the 27 germplasm lines with 3 checks were grown in RBD (Randomized Block Design) in 3 replications. The germplasm represented diverse genetic material and was assessed under field conditions to determine the extent of variation in important qualitative morphological traits. **Table 1.** Include list of germplasm. The lathyrus germplasm were characterized based on a set of distinct morphological descriptors covering plant, leaf, flower, pod and seed characteristics. Observations were recorded at appropriate growth stages and at maturity by visually assessing representative plants, leaves, flowers, pods and seeds from each germplasm accession. The morphological descriptors were selected to capture the phenotypic variation present among the germplasm. Plant characteristics were recorded during the vegetative and reproductive stages. The observations included plant growth habit, plant type, internode length, stem colour, stem wing width and branch arrangement. Plant growth habit and plant type were assessed based on the overall architecture and appearance of the plant. Internode length and stem wing width were recorded from representative plants, while stem colour and branch arrangement were determined based on their observable phenotypic expression. Leaf characteristics were recorded from fully developed, representative

leaves of each germplasm accession. The descriptors included (L_T) leaf type, (L_C) leaf colour, (L_S) leaflet shape, (L_{PL}) leaf petiole length (cm), presence or absence of (L_{Tr}) leaf tendrils, (L_P) leaf persistence, (P_{OP}) presence of pubescence and (P_L) peduncle length. (L_C) Leaf colour and (L_S) leaflet shape were assessed visually, whereas (L_P) leaf petiole and peduncle length were measured in centimetres using a suitable measuring scale. The presence or absence of tendrils and pubescence and the persistence of leaves were also recorded for each accession. Flower characters were recorded during the flowering stage. The observations included (F_{BS}) flower bud shape, (F_{BSi}) flower bud size, (F_S) flower size, (F_C) flower colour, (F_{VC}) flower vein colour and (C_C) calyx colour. Flower bud and flower size were recorded from representative flowers, while flower colour, vein colour and calyx colour were assessed visually. The observations were taken when the flowers were sufficiently developed to allow clear identification of the respective characteristics. Pod characteristics were recorded at the appropriate pod-development and maturity stages. The descriptors included (P_S) pod shape, (P_C) pod curvature, (P_{BS}) pod beak shape, (I_{PC}) immature pod colour, (M_{PC}) mature pod colour, (C_{OP}) constriction of pod between seeds and (P_D) pod dehiscence. (I_{PC}) Immature pod colour was recorded during the developing pod stage, whereas mature pod colour and other pod characters were recorded at physiological maturity. Pod curvature, beak shape and constriction between seeds were assessed visually, while pod dehiscence was recorded based on the tendency of mature pods to split or release seeds. Seed characteristics were recorded after harvesting and proper drying of the seeds. The descriptors included (S_S) seed shape, (S_{Si}) seed size, (S_{CC}) seed coat colour, (S_{CS}) seed coat surface, (S_{CPC}) seed coat pattern colour and (C_{OC}) cotyledon colour. Seed shape, seed coat surface and seed coat colour were assessed visually using representative seeds from each germplasm accession. Seed size was assessed using appropriate measurements or descriptor categories, while seed coat pattern colour and cotyledon colour were recorded based on their observable expression after examining the seeds. For each germplasm accession, observations were recorded systematically for all the above-mentioned morphological descriptors. Qualitative characters were classified into their respective descriptor categories based on the observable phenotypic expression, whereas measurable characters such as internode length, stem wing width, leaf petiole length and peduncle length were recorded quantitatively. The recorded data were tabulated and compared among the germplasm accessions to identify the extent of morphological variation. The characterization data were subsequently used to distinguish the accessions and identify morphologically diverse and potentially useful germplasm for future breeding programmes.

Table 1. List of the germplasm

Sr. No.	Genotype	Source	Sr. No.	Genotype	Source
1	AKL-19	Akola	16	NLK-49	Sindewahi
2	NLK-94	Amgaon	17	IC-120472	NBPGR, Akola
3	NLK-67	Chamorshi	18	NLK-37	Chamorshi
4	NLK-62	Amgaon	19	IC-120491	NBPGR, Akola
5	NLK-51	Nawegaonbandh	20	NLK-40	Nagpur
6	EC-209081	Rome	21	KH-1	Raipur
7	NLK-39	Chamorshi	22	NLK-102	Sakoli
8	NLK-54	Amgaon	23	NLK-5	Amgaon
9	NLK-74	Nawegaonbandh	24	PUSA-24	IARI, New Delhi
10	NLK-48	Amgaon	25	AKL-12	Akola
11	EC-209071	Rome	26	NLK-44	Amgaon
12	NLK-6	Chamorshi	27	BIOR222	IARI, New Delhi
13	AKL-7	Akola	28	Ratan (Check)	IARI, New Delhi
14	JRL-16	Raipur	29	Prateek(Check)	Raipur

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Sr. No.	Genotype	Source	Sr. No.	Genotype	Source
15	BIOR-231	IARI, New Delhi	30	Mahateora(Check)	Raipur

Results and discussion

In the present study morphological characters of 27 lathyrus germplasm along with 3 checks were recorded as per the descriptor published by ICARDA Rome and presented in Table 2. Include, In Plant growth habit spreading type was in 11 genotype (36.66), prostrate type in 6 genotype (20.00), erect type in 5 genotype (16.66) and semi-erect type in 8 genotype (26.66). Plant type was observed same which is indeterminate in all genotype (100). Internode length was small in 10 genotype (33.33), medium in 14 genotype (46.66) and large in 6 genotype (20.00). Stem colour was observed green in 17 genotype (56.66), purple green in 10 genotype (33.33) and light green in 3 genotype (10.00). Stem wing width was observed narrow in 9 genotype (30.00), Medium in 10 genotype (33.33) and wide in 21 genotype (70.00). Branch arrangement was mainly on lower part of the plant in 18 genotype (60.00) and evenly distributed throughout whole plant in 12 genotype (40.00). Leaf type was simple in all 30 genotype (100). Leaf colour was green in 5 genotype (16.66), dark green in 13 genotype (43.33), purple green in 9 genotype (30.00) and light green in 3 genotype (10.00). Leaflet shape was linear in 10 genotype (33.33), Lanceolate in 20 genotype (66.66). Leaf tendrils was short in 7 genotype (23.33), Medium in 8 genotype (26.66) and large in 15 genotype (50.00). Leaf persistence was high in 5 genotype (16.66), low in 3 genotype (10.00) and moderate in 22 genotype (73.33). Pubescence was observed only on leaf margin in all 30 genotype (100). Flower bud shape was observed intermediate in all 30 genotype (100). Flower bud size was small in 13 genotype (43.33), medium in 14 genotype (46.66) and large in 3 genotype (10.00). Flower colour was blue in 18 genotype (60.00) and white in 12 genotype (40.00). Flower vein colour was green in 5 genotype (16.66), Blue in 9 genotype (30.00), violet in 15 genotype (50.00) and white in 1 genotype (3.33). Calyx colour was green purple in 12 genotype (40.00), Light green in 7 genotype (23.33) and green in 11 genotype (36.66). Pod shape was observed broad linear in all 30 genotype (100). Pod curvature was straight in 20 genotype (66.66) and slightly curve in 10 genotype (33.33). Pod beak shape was observed pointed in all 30 genotype (100). Immature pod colour was green in 8 genotype (26.66), Dark green in 12 genotype (40.00) and light green in 10 genotype (33.33). Mature pod colour was grey in 10 genotype (33.33), yellow green in 9 genotype (30.00) and light grey in 11 genotype (36.66). Constriction of pod was medium in 19 genotype (63.33) and slight in 11 genotype (36.66). Pod dehiscence was low shattering in 12 genotype (40.00), medium shattering in 8 genotype (26.66) and

high shattering in 10 genotype (33.33). Seed shape was square in 8 genotype (26.66), obtriangular in 6 genotype (20.00), and rhomboid in 9 genotype (30.00) and triangular in 7 genotype (23.33). Seed coat colour was grey in 9 genotype (30.00), grey mottled in 10 genotype (33.33) and grey white in 11 genotype (36.66). Seed coat surface was observed smooth in all 30 genotype (100). Seed coat pattern colour was green in 11 genotype (36.66), cream in 6 genotype (20.00), black in 8 genotype (26.66) and brown in 5 genotype (16.66) and brown in 5 genotype (16.66). Cotyledon colour was observed yellow in all 30 genotype (100). Ramya *et al.* (2024) [2] conducted morpho-molecular characterization of grass pea germplasm and identified considerable diversity among the accessions. Important variability was observed for traits such as plant height, petiole length, days to maturity, number of pods per plant and 100-seed weight. Plant height, petiole length and 100-seed weight exhibited high heritability coupled with high genetic advance. Indumathi *et al.* (2026) [3] evaluated 48 grass pea germplasm accessions, including checks, using 21 morphological characters based on DUS descriptors. Diversity was observed for 14 of the 21 characters.

P_{GH}: Plant growth habit (1= Prostrate, 2= Spreading, 3= Semi erect, 4= Erect); *P_T*: Plant type (1= Indeterminate); *I_L*: Internode length (3= Small, 5= Medium, 7= Large); *S_C*: Stem colour (1= Light green, 2= Green, 3= Purple green); *S_{WW}*: Stem wing width (3= Narrow, 5= Medium, 7= Wide); *B_A*: Branch arrangement (1= Evenly distributed throughout whole plant, 2= Mainly on lower part of the plant); *L_T*: Leaf type (3= Simple); *L_C*: Leaf colour (1= Light green, 2= Green, 3= Dark green, 9= purple green); *L_S*: Leaflet shape (1= Linear, 2= Lanceolate); *L_{Te}*: Leaf tendrils (1= Short, 2= Medium, 9= Large); *L_P*: Leaf persistence (3= Low, 5= Moderate, 7= High); *P_{OP}*: Presence of pubescence (4= Only on leaf margin); *F_{BS}*: Flower bud shape (2= Intermediate); *F_{BSi}*: Flower bud size (3= Small, 5= Medium, 7= Large); *F_C*: Flower colour (1= White, 3= Blue, 7= Pink); *F_{VC}*: Flower vein colour (1= Blue, 3= Violet, 9= Green, white); *C_C*: Calyx colour (1= Light green, 2= Green, 3= Green purple); *P_S*: Pod shape (5= Broad linear); *P_C*: Pod curvature (1= Straight, 2= Slightly curve); *P_{BS}*: Pod beak shape (1= Pointed); *I_{PC}*: Immature pod colour (2= Light green, 3= Green, 4= Dark green); *M_{PC}*: Mature pod colour (1= Yellow green, 3= Grey, 9= Light grey); *C_{OP}*: Constriction of pod (3= Slight, 5= Medium); *P_D*: Pod dehiscence (3= Low shattering, 5= Medium shattering, 7= High shattering); *S_S*: Seed shape (2= Triangular, 3= Rhomboid, 4= Square, 5= Obtriangular); *S_{CC}*: Seed coat colour (1= Grey white, 3= Grey, 9= Grey mottled); *S_{CS}*: Seed coat surface (1= Smooth); *S_{CPC}*: Seed coat pattern colour (1= Cream, 2= Green, 3= Brown, 5= Black); *C_{OC}*: Cotyledon colour (1= Yellow)

Table 2. Frequency distribution for different morphological characters of lathyrus

Sr No.	Morphological characters	Total No. of genotypes	Frequency (%)
1	Plant growth habit: i Spreading	11	36.66
	ii Prostrate	6	20.00
	iii Erect	5	16.66
	iv Semi erect	8	26.66
2	Plant type: Indeterminate	30	100
3	Internode length: i Small	10	33.33
	ii Medium	14	46.66
	iii Large	6	20.00
4	Stem colour: i Green	17	56.66
	ii Purple green	10	33.33
	iii Light green	3	10.00

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Sr No.	Morphological characters	Total No. of genotypes	Frequency (%)
5	Stem wing width: i Narrow	9	30.00
	ii Medium	10	33.33
	iii wide	11	70.00
6	Branch arrangement: i Mainly on lower part of the plant	18	60.00
	ii Evenly distributed throughout whole plant	12	40.00
7	Leaf type: i Simple	30	100
8	Leaf colour: i Green	5	16.66
	ii Dark green	13	43.33
	iii Purple green	9	30.00
	iv Light green	3	10.00
9	Leaflet shape: i Linear	10	33.33
	ii Laceolate	20	66.66
10	Leaf tendrils: i Short	7	23.33
	ii Medium	8	26.66
	iii Large	15	50.00
11	Leaf persistence: i High	5	16.66
	ii Low	3	10.00
	iii Moderate	22	73.33
12	Presence of pubescence : Only on leaf margin	30	100
13	Flower bud shape: Intermediate	30	100
14	Flower bud size: i Small	13	43.33
	ii Medium	14	46.66
	iii Large	3	10.00
15	Flower colour: i Blue	17	60.00
	ii White	12	40.00
	iii Pink	1	
16	Flower vein colour: i Green	5	16.66
	ii Blue	9	30.00
	iii Violet	15	50.00
	iv white	1	3.33
17	Calyx colour: i Green purple	12	40.00
	ii Light green	7	23.33
	iii Green	11	36.66
18	Pod shape: Broad linear	30	100
19	Pod curvature: i Straight	20	66.66
	ii Slightly curve	10	33.33
20	Pod beak shape: Pointed	30	100
21	Immature pod colour: i Green	8	26.66
	ii Dark green	12	40.00
	iii Light green	10	33.33
22	Mature pod colour: i Grey	10	33.33
	ii Yellow green	9	30.00
	iii Light grey	11	36.66
23	Constriction of pod: i Medium	19	63.33
	ii Slight	11	36.66
24	Pod dehiscence: i Low shattering	12	40.00
	ii Medium shattering	8	26.66
	iii High shattering	10	33.33
25	Seed shape: i Square	8	26.66
	ii Obtriangular	6	20.00
	iii Rhomboid	9	30.00
	iv Triangular	7	23.33
26	Seed coat colour: i Grey	9	30.00
	ii Grey mottled	10	33.33
	iii Grey white	11	36.66
27	Seed coat surface: Smooth	30	100

(continued on next page)

Sr No.	Morphological characters	Total No. of genotypes	Frequency (%)
28	Seed coat pattern colour: i Green	11	36.66
	ii Cream	6	20.00
	iii Black	8	26.66
	iv Brown	5	16.66
29	Cotyledon colour: Yellow	30	100

Table 3. Frequency of descriptor scores in 30 genotypes of *Lathyrus sativus* L. for different morphological characters.

Sr No.	Character	Descriptor score								
		1	2	3	4	5	6	7	8	9
1	P_{GH}	6	11	8	5					
2	P_T	30								
3	I_L		10		14		6			
4	S_C	3	17	10						
5	S_{WW}			9	10		21			
6	B_A	12	18							
7	L_T			30						
8	L_C	3	5	13						9
9	L_S	10	20							
10	L_{Te}	7	8							15
11	L_P			3		22		5		
12	P_{OP}				30					
13	F_{BS}		30							
14	F_{BSi}			13		14		3		
15	F_C	12		17				1		
16	F_{VC}	9		15						6
17	C_C	7	11	12						
18	P_S					30				
19	P_C	20	10							
20	P_{BS}	30								
21	I_{PC}		10	8	12					
22	M_{PC}	9		10						11
23	C_{OP}			11		19				
24	P_D			12		8		10		
25	S_S		7	9	8	6				
26	S_{CC}	11		9						10
27	S_{CS}	30								
28	S_{CPC}	6	11	5		8				
29	C_{OC}	30								

Table 4. Morphological characters for *Lathyrus sativus* L.

Sr No.	Genotypes	Characters													
		PGH	PT	IL	SC	SWW	BA	LT	LC	LS	LTe	LP	POP	FBS	FBSi
1	AKL-19	4	1	3	2	3	2	3	2	1	1	7	4	2	3
2	NLK-94	1	1	5	1	7	2	3	9	2	2	5	4	2	7
3	NLK-67	4	1	5	2	5	1	3	3	2	2	5	4	2	3
4	NLK-62	2	1	7	1	3	1	3	3	2	1	7	4	2	3
5	NLK-51	2	1	3	2	3	2	3	3	1	2	5	4	2	5
6	EC-209081	3	1	3	2	5	1	3	9	1	1	3	4	2	5
7	NLK-39	3	1	3	1	3	2	3	2	2	9	7	4	2	7
8	NLK-54	2	1	3	2	3	2	3	2	2	1	5	4	2	5
9	NLK-74	3	1	3	2	5	2	3	3	1	1	3	4	2	3
10	NLK-48	4	1	5	2	7	2	3	3	2	9	5	4	2	3
11	EC-209071	4	1	5	2	5	2	3	9	1	2	3	4	2	7
12	NLK-6	3	1	3	3	3	2	3	9	1	9	7	4	2	5
13	AKL-7	4	1	5	3	3	1	3	2	2	9	5	4	2	3

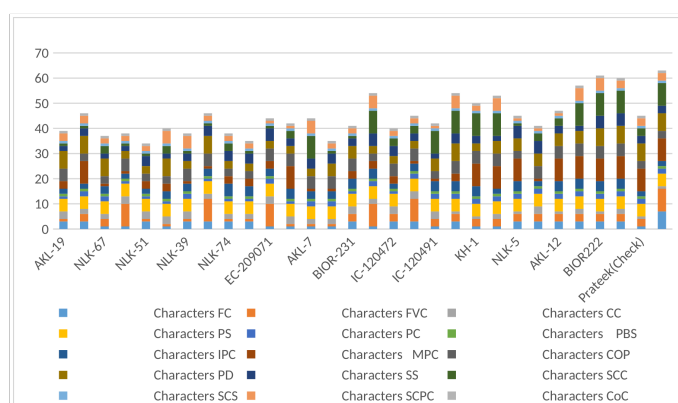
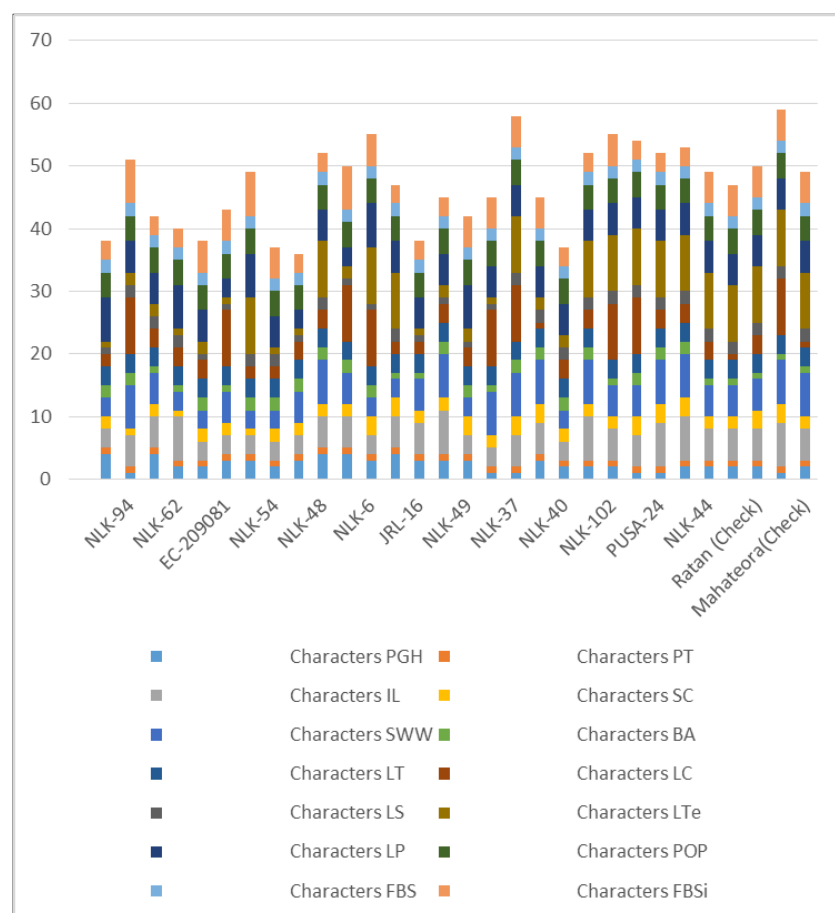
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Sr No.	Genotypes	Characters														
		PGH	PT	IL	SC	SWW	BA	LT	LC	LS	LT _e	LP	POP	FBS	FBSi	
14	JRL-16	3	1	5	2	5	1	3	2	1	1	5	4	2	3	
15	BIOR-231	3	1	7	2	7	2	3	3	1	2	5	4	2	3	
16	NLK-49	3	1	3	3	3	2	3	3	1	2	7	4	2	5	
17	IC-120472	1	1	3	2	7	1	3	9	1	1	5	4	2	5	
18	NLK-37	1	1	5	3	7	2	3	9	2	9	5	4	2	5	
19	IC-120491	3	1	5	3	7	2	3	1	2	2	5	4	2	5	
20	NLK-40	2	1	3	2	3	2	3	3	2	2	5	4	2	3	
21	KH-1	2	1	7	2	7	2	3	3	2	9	5	4	2	3	
22	NLK-102	2	1	5	2	5	1	3	9	2	9	5	4	2	5	
23	NLK-5	1	1	5	3	5	2	3	9	2	9	5	4	2	3	
24	PUSA-24	1	1	7	3	7	2	3	3	2	9	5	4	2	3	
25	AKL-12	2	1	7	3	7	2	3	3	2	9	5	4	2	3	
26	NLK-44	2	1	5	2	5	1	3	3	2	9	5	4	2	5	
27	BIOR222	2	1	5	2	5	1	3	1	2	9	5	4	2	5	
28	Ratan (Check)	2	1	5	3	5	1	3	3	2	9	5	4	2	5	
29	Prateek(Check)	1	1	7	3	7	1	3	9	2	9	5	4	2	5	
30	Mahateora(Check)	2	1	5	2	7	1	3	1	2	9	5	4	2	5	

Table 5. Morphological characters for *Lathyrus sativus* L.

Sr No.	Genotypes	Characters														
		FC	FVC	CC	PS	PC	PBS	IPC	MPC	COP	PD	SS	SCC	SCS	SCPC	CoC
1	AKL-19	3	1	3	5	1	1	2	3	5	7	2	1	1	3	1
2	NLK-94	3	3	2	5	2	1	2	9	3	7	3	1	1	3	1
3	NLK-67	1	3	2	5	2	1	3	1	3	7	2	3	1	2	1
4	NLK-62	1	9	3	5	1	1	2	1	5	3	2	1	1	2	1
5	NLK-51	3	1	3	5	1	1	2	3	3	3	4	1	1	2	1
6	EC-209081	1	1	3	5	1	1	3	3	3	7	2	3	1	5	1
7	NLK-39	3	1	3	5	2	1	3	1	5	3	3	1	1	5	1
8	NLK-54	3	9	2	5	1	1	3	1	5	7	4	1	1	2	1
9	NLK-74	3	1	2	5	1	1	5	3	3	3	4	3	1	2	1
10	NLK-48	3	1	2	5	1	1	4	3	3	3	4	1	1	2	1
11	EC-209071	1	9	3	5	2	1	3	3	5	3	5	1	1	1	1
12	NLK-6	1	1	3	5	1	1	4	9	5	3	3	3	1	1	1
13	AKL-7	1	1	2	5	2	1	3	1	5	3	4	9	1	5	1
14	JRL-16	1	1	2	5	2	1	3	1	5	5	4	1	1	2	1
15	BIOR-231	3	3	3	5	1	1	4	3	5	5	3	1	1	2	1
16	NLK-49	1	9	2	5	2	1	4	3	3	3	5	9	1	5	1
17	IC-120472	3	3	3	5	1	1	2	3	5	3	4	3	1	2	1
18	NLK-37	3	9	3	5	2	1	3	1	5	3	3	3	1	2	1
19	IC-120491	1	3	3	5	2	1	4	1	3	5	2	9	1	1	1
20	NLK-40	3	3	1	5	2	1	4	3	5	7	4	9	1	5	1
21	KH-1	1	3	1	5	2	1	4	9	5	3	3	9	1	2	1
22	NLK-102	1	3	2	5	2	1	2	9	5	5	2	9	1	5	1
23	NLK-5	3	3	1	5	2	1	4	9	3	5	5	1	1	1	1
24	PUSA-24	3	3	3	5	2	1	2	1	5	5	5	3	1	1	1
25	AKL-12	3	3	1	5	2	1	4	9	5	5	3	3	1	1	1
26	NLK-44	3	3	2	5	2	1	4	9	5	5	2	9	1	5	1
27	BIOR222	3	3	1	5	2	1	4	9	5	7	5	9	1	5	1
28	Ratan (Check)	3	3	2	5	2	1	4	9	5	7	5	9	1	3	1
29	Prateek(Check)	1	3	1	5	2	1	2	9	3	7	3	3	1	3	1
30	Mahateora(Check)	7	9	1	5	2	1	2	9	3	7	3	9	1	3	1

(continued on next page)



Conclusion

The morphological evaluation of 27 *Lathyrus* germplasm accessions along with three checks revealed substantial phenotypic diversity across several plant, leaf, flower, pod and seed descriptors. The greatest variation was observed for growth habit, internode length, stem and leaf colour, leaflet shape, tendril size, floral pigmentation, pod colour, pod curvature, pod dehiscence, seed shape and seed coat characteristics. Several traits, including plant type, leaf type, flower bud shape, pod shape, pod beak shape, seed coat surface and cotyledon colour, remained uniform and consequently had limited value for discrimination within the evaluated material. The diversity identified in the present study can be useful for germplasm identification, documentation, conservation and selection of contrasting parents in *Lathyrus* improvement programmes. In particular, variation in plant architecture and pod shattering deserves further attention because these characteristics may contribute to the development of desirable genotypes. The characterized germplasm can serve as valuable breeding material, and its further evaluation using quantitative traits, multi-

environment testing and molecular markers would strengthen the assessment of genetic diversity and facilitate efficient utilization in future breeding programmes.

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References

1. Pandey RL. Descriptors for *Lathyrus* spp. Biodiversity International. 2000.
2. Ramya KR, Tripathi K, Singh R, Pandey A, Pamarthi RK, Rajendran NR, Gore PG, Panda RR, Barpete S, Gomashe S, Bhatt KC. Insights into morphological and molecular diversity in grass-pea (*Lathyrus sativus* L.) germplasm. Genetic Resources and Crop Evolution. 2024;72:543–555.
3. Indumathi S, Parikh M, Saxena RR, Bhariya SK, Nagaraju D, Sharmila K. Morphological variability in a diverse collection of grass pea (*Lathyrus sativus* L.) germplasm accessions. Journal of Advances in Biology & Biotechnology. 2026;29(1):1144–1153.
4. Lassoued S, Giosafatto CVL, Mariniello L, Neila TF. Morphological characterization and in vitro digestibility of seven *Lathyrus sativus* (grass pea) accessions originating from Eurasia, Africa, and Canada. European Food Research and Technology. 2023;249:2419–2432.

5. Sahu M, Mishra A, Pandey H. Characterization and assessment of genetic diversity in local and improved accessions of grass pea (*Lathyrus sativus* L.) for green forage yield traits. Range Management and Agroforestry. 2022;43(2):237–246.

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