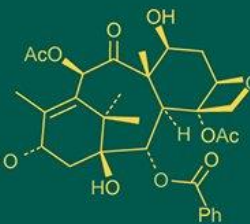
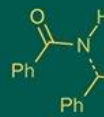
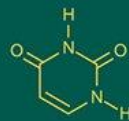
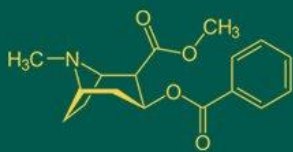


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Genetic variability, Heritability, correlation and path coefficient analysis of *Lathyrus* (*Lathyrus sativus*) mutants for yield and yield contributing traits

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Abstract

The present investigation entitled "Genetic variability, Heritability, correlation and path coefficient analysis of *Lathyrus* (*Lathyrus sativus*) mutants for yield and yield contributing traits" was conducted to assess the relationships among seed yield and its contributing traits, estimate genetic parameters, and identify promising mutant genotypes of *Lathyrus sativus*. The total 24 mutant lines along with the parent check NLK-73 and check Ratan were evaluated in a Randomized Block Design with three replications during Rabi season of 2024-25 at the College of Agriculture, Nagpur. Nine traits, viz., days to 1st flower, days to 50% flowering, days to maturity, plant height (cm), number of branches per plant⁻¹, number of pods per plant⁻¹, 100-seed weight (g), seed yield per plant⁻¹ and ODAP content (%) were recorded. Analysis of variance revealed significant differences among genotypes for all the studied traits, indicating the presence of substantial genetic variability. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits, suggesting environmental influence on trait expression. High heritability coupled with high genetic advance was observed for ODAP content, seed yield per plant, number of pods per plant, number of branches per plant, and 100-seed weight, indicating the predominance of additive gene action and the effectiveness of selection. Correlation analysis revealed that number of pods per plant, number of branches per plant, and 100 seed weight were positively associated with seed yield, whereas ODAP content showed a negative association. Path coefficient analysis indicated that number of pods per plant, plant height, 100 seed weight, and ODAP content exerted high direct effects on seed yield. Based on genetic variability, correlation, path analysis, and overall performance, the mutant lines NLM-1, NLM-7, and NLM-13 were identified as promising genotypes for future breeding programmes aimed at improving seed yield while maintaining desirable quality traits in *Lathyrus sativus*.

Keywords: *Lathyrus sativus*, mutants, genetic variability, correlation, path analysis, seed yield

Introduction

Lathyrus (*Lathyrus sativus* L.), commonly known as grass pea, chickling vetch or khesari dal, is an important food legume belonging to the family Fabaceae. It is a self-pollinated crop with 2n = 14 chromosomes and is well adapted to marginal production environments. The crop is valued for its high nutritional quality, particularly its protein content, and serves as an important source of food and fodder in several regions. *Lathyrus* is considered a climate-resilient pulse crop because of its ability to withstand adverse environmental conditions such as drought, salinity and waterlogging. Its adaptability to low-rainfall and stress-prone areas makes it an important crop for sustainable agriculture and food security.

Despite its nutritional and agronomic importance, the utilization and wider acceptance of *Lathyrus* have been restricted mainly due to the presence of the neurotoxic non-protein amino acid β -N-oxalyl-L- α , β -diaminopropionic acid (β -ODAP), which is associated with neurolathyrism when consumed in excessive amounts over a prolonged period. Traditional varieties of grass pea may contain considerable levels of β -ODAP. Therefore, the major objectives of *Lathyrus* improvement programmes include the development of high-yielding genotypes with reduced neurotoxin content, while maintaining desirable agronomic and nutritional characteristics.

Mutation breeding is an effective approach for creating additional genetic variability and generating novel alleles that can be utilized in crop improvement programmes. Induced mutations can broaden the genetic base of existing germplasm and provide useful variability for important traits such as yield, maturity, plant architecture and seed characteristics. In *Lathyrus*, the development and evaluation of mutant populations therefore provide opportunities to identify superior genotypes with improved yield potential and desirable quality attributes, including reduced β -ODAP content.

Seed yield is a complex quantitative character governed by several component traits and is strongly influenced by environmental conditions. Consequently, direct selection for yield alone may not always be effective. The presence of genetic variability and the relationships among yield and its contributing characters are therefore of considerable importance in formulating an effective breeding strategy. Evaluation of traits such as flowering and maturity duration, plant height, number of branches, number of pods, number of seeds per pod, seed weight and other yield-related attributes can provide useful information for identifying superior mutant genotypes.

Correlation analysis is an important statistical tool for determining the degree and direction of association between yield and its component characters. The knowledge of genotypic and phenotypic correlations helps breeders understand whether improvement in one trait is likely to be associated with improvement or deterioration in another trait. Positive association between yield and its component traits may facilitate indirect selection, whereas negative associations may indicate the presence of undesirable relationships that need to be considered during selection. Thus, correlation analysis provides a useful basis for identifying traits that can be effectively used as selection criteria for improving seed yield in *Lathyrus* mutants.

However, correlation coefficients alone do not explain whether the observed association between two traits is due to a direct influence of one trait on yield or arises indirectly through other associated characters. Path coefficient analysis provides a more detailed understanding by partitioning the correlation coefficients into direct and indirect effects of component traits on seed yield. This analysis helps identify characters having a strong direct contribution to yield and distinguishes them from traits whose association with yield is mainly due to indirect effects through other characters. Therefore, path analysis is particularly useful for determining the relative importance of yield-contributing traits and for developing an effective selection strategy in breeding programmes.

In *Lathyrus* mutants, information on the association among yield and yield-contributing traits, together with their direct and indirect effects on seed yield, can assist in the identification of promising mutant genotypes. Such information is valuable for selecting desirable mutants and for planning future breeding programmes aimed at improving productivity and other important traits. Therefore, the present investigation entitled “Studies on Correlation and Path Analysis in *Lathyrus* Mutants” was undertaken to assess the association among yield and yield-contributing traits and to determine the direct and indirect effects of component characters on seed yield, with the ultimate objective of identifying promising mutants for utilization in *Lathyrus* improvement programmes.

Materials and Methods

The experimental material comprised 24 low ODAP *Lathyrus* mutant genotypes in the M_6 generation, along with the parent NLK-73 and check Ratan. The mutant genotypes were developed from *Lathyrus* cultivar NLK-73 through induced mutation and selected in successive generations based on desirable traits, particularly low ODAP content, higher seed yield and earliness. The experiment was conducted during Rabi 2024-25 at the Research Farm of the Agricultural Botany Section, College of Agriculture, Nagpur. The experiment was laid out in a Randomized Block Design (RBD) with three replications. A total of 26 treatments comprising 24 mutant genotypes, the parent NLK-73 and check Ratan were evaluated. The plot size was 1.36 m $\times$ 3.00 m, with a spacing of 45 cm $\times$ 10 cm, three rows per plot and 60 plants per plot. The crop was sown on 24 November 2024 and harvested according to the maturity of individual genotypes. Five plants from each genotype were randomly selected for recording observations on days to first flower, days to 50 percent flowering, days to maturity, plant height (cm), number of branches plant⁻¹, number of pods plant⁻¹, 100 seed weight (g), seed yield plant⁻¹ (g) and seed ODAP content (%).

Results and Discussion

Genetic variability parameters

The analysis of variance revealed highly significant differences among the mutant lines for all the characters studied, indicating the presence of substantial genetic variability for effective selection and genetic improvement. The existence of significant variation among genotypes suggests ample scope for identifying superior mutants for yield and associated traits.

The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) indicated that PCV values were consistently higher than the corresponding GCV values for all traits, suggesting the influence of environmental factors on phenotypic expression. However, the narrow differences between GCV and PCV for most characters indicated that the observed variability was predominantly genetic. Higher GCV and PCV were recorded for ODAP content, seed yield per plant and number of pods per plant, indicating greater genetic variability and better prospects for improvement through selection. In contrast, days to maturity, days to first flowering and days to 50% flowering exhibited comparatively lower GCV and PCV values, suggesting limited variability for these traits. Similar observations have been reported by Kumar *et al.* (2020) [8], Gujar *et al.* (2022) [3], Kanwar *et al.* (2023) [5] and Mekonen *et al.* (2024) [10].

Heritability and genetic advance

Heritability estimates ranged from 45.82% to 96.36%, while genetic advance as percent of mean ranged from 3.09% to 25.20%. The highest heritability was observed for ODAP content (96.36%), followed by 100 seed weight (71.51%) and days to first flowering (70.15%), indicating that these traits were largely governed by genetic factors. Seed yield per plant, number of pods per plant and number of branches per plant exhibited moderate heritability coupled with relatively high genetic advance, suggesting the involvement of additive gene action and the possibility of effective improvement through direct selection. High heritability together with high genetic advance for ODAP content indicated that this trait can be efficiently improved by simple phenotypic selection.

Similar findings have been reported by Jesberson *et al.* (2018)^[4], Chetariya *et al.* (2019)^[1], Kumar *et al.* (2020)^[8] and Mekonen *et al.* (2024)^[10].

Correlation analysis

Correlation analysis demonstrated that seed yield per plant exhibited strong positive associations with plant height, number of pods per plant, number of branches per plant and 100 seed weight at both genotypic and phenotypic levels. Among these traits, plant height and number of pods per plant showed the strongest positive correlations with seed yield, indicating that selection for these traits would indirectly improve grain yield. Conversely, days to first flowering, days to 50% flowering, days to maturity and ODAP content showed negative associations with seed yield, suggesting that early flowering, early maturity and reduced ODAP content favour higher productivity. The magnitude of genotypic correlations was generally higher than the corresponding phenotypic correlations, indicating that genetic factors had a greater influence than environmental effects on trait association. These findings agree with reports of Talukdar (2009)^[12], Jesberson *et al.* (2018)^[4], Deshmukh (2020)^[2] and Kour *et al.* (2023)^[7].

Path coefficient analysis

Path coefficient analysis partitioned the correlation coefficients into direct and indirect effects and revealed the actual contribution of different traits towards seed yield. Plant height exhibited a high positive direct effect on seed yield, indicating that improvement in plant height would directly enhance yield. Days to maturity also showed a positive direct effect; however, its overall correlation with seed yield remained negative because of unfavourable indirect effects through other characters. ODAP content exerted the highest negative direct effect, demonstrating that increased ODAP concentration adversely affected seed yield. Number of pods per plant displayed a very high positive correlation with seed yield despite its negative direct effect, suggesting that its influence was mainly mediated through favourable indirect effects via other yield components. Overall, plant height, number of pods per plant, number of branches per plant and 100-seed weight emerged as important traits for indirect selection, while lower ODAP content and early flowering should receive priority during breeding for high-yielding and nutritionally improved lathyrus genotypes. Similar conclusions were reported by Kumari and Prasad (2005)^[9], Kate *et al.* (2017)^[6], Jesberson *et al.* (2018)^[4] and Parihar *et al.* (2019)^[11].

Table 1: Analysis of variance (mean sum of squares) for different characters under study in lathyrus

Sources of variation	D.F.	Mean sum of squares								
		Days to 1 st flower	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches plant ⁻¹	Number of pods plant ⁻¹	100 seed weight (g)	Seed yield plant ⁻¹ (g)	ODAP content (%)
Replications	2	0.25	2.73	3.01	28.97	0.03	24.13	0.07	0.69	0.00001
Genotypes	25	6.89**	12.06**	11.93**	63.43**	0.42**	99.08**	0.79**	28.68**	0.00301**
Error	50	0.86	2.74	3.37	16.25	0.10	24.27	0.18	6.53	0.00004

Note *, ** = Significant at 5% and 1% level respectively.

Table 2: Estimates of genetic variability, heritability, genetic advance and response to selection as percent of mean

Character	Range		Mean	GCV%	PCV%	h ² (bs) (%)	G.A	GAM (%)
	Max	Min						
Days to first flower	50.35	45.01	47.78	2.97	3.55	70.15	2.27	4.75
Days to 50% flowering	60.73	53.80	57.32	3.08	4.22	53.15	3.24	5.65
Days to maturity	110.82	103.79	108.15	1.56	2.31	45.82	3.34	3.09
Plant height (cm)	73.32	55.43	63.28	6.27	8.94	49.18	7.58	11.98
No. of branches plant ⁻¹	4.67	3.47	3.97	8.15	11.46	50.54	0.61	15.36
No. of pods plant ⁻¹	61.28	29.62	49.49	10.09	14.17	50.68	9.40	19.00
100 seed weight (g)	8.49	6.25	7.76	6.22	7.36	71.51	0.77	9.86
Seed yield plant ⁻¹ (g)	25.08	14.22	19.84	13.69	18.80	53.06	5.00	25.20
ODAP content (%)	0.247	0.146	0.196	15.94	16.24	96.36	0.04	21.77

Table 3: Genotypic and phenotypic correlation of different traits with seed yield plant⁻¹

Character		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of pods plant ⁻¹	100 seed weight (g)	ODAP content (%)	Seed yield plant ⁻¹ (g)
Days to first flower	G	0.99**	0.98**	-0.93**	-0.69**	-0.82**	-0.29	0.43*	-0.82**
	P	0.82**	0.60**	-0.56**	-0.48*	-0.51**	-0.19	0.35	-0.51**
Days to 50% flowering	G		0.80**	-0.77**	-0.77**	-0.64**	-0.54**	0.36	-0.56**
	P		0.51**	-0.57**	-0.62**	-0.39*	-0.44*	0.31	-0.35
Days to maturity	G			-0.42*	-0.69**	-0.42*	0.02	0.43*	-0.37
	P			-0.26	-0.48*	-0.25	0.02	0.34	-0.28
Plant height (cm)	G				-0.78**	0.97**	0.40*	-0.65**	0.98**
	P				0.43*	0.50**	0.29	-0.50**	0.67**
No. of branches plant ⁻¹	G					0.36	0.40*	-0.40*	0.47*
	P					0.28	0.33	-0.35	0.28
No. of pods plant ⁻¹	G						0.89**	-0.72**	0.98**
	P						0.61**	-0.53**	0.61**
100 seed weight (g)	G							-0.51**	0.39*
	P							-0.48*	0.34
ODAP content (%)	G								-0.95**
	P								-0.79**

Table 4: Direct and indirect effect of eight variables on yield of lathyrus mutant

Sr. No.	Character	Days to first flower	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches plant ⁻¹	No. of pods plant ⁻¹	100 seed weight (gm)	ODAP content	Genotypic correlation with seed yield plant ⁻¹
1	Days to first flower	-0.307	-0.376	-0.303	0.288	0.213	0.252	0.091	-0.133	-0.820
2	Days to 50% flowering	-1.229	-1.004	-0.810	0.779	0.777	0.645	0.545	-0.369	-0.569
3	Days to maturity	1.105	0.902	1.119	-0.472	-0.776	-0.470	0.024	0.484	-0.374
4	Plant height (cm)	-0.724	-0.599	-0.325	0.772	0.605	0.830	0.310	-0.508	1.089
5	No. of branches plant ⁻¹	0.293	0.326	0.292	-0.331	-0.422	-0.152	-0.172	0.169	0.479
6	No. of pods plant ⁻¹	0.412	0.323	0.210	-0.539	-0.181	-0.502	-0.450	0.362	0.980
7	100 seed weight (gm)	0.175	0.322	-0.012	-0.238	-0.242	-0.532	-0.593	0.303	0.398
8	ODAP content	-0.544	-0.463	-0.545	0.830	0.505	0.910	0.644	-1.260	-0.950

*Values in the bold are the direct effect Residual effect =-0.5131

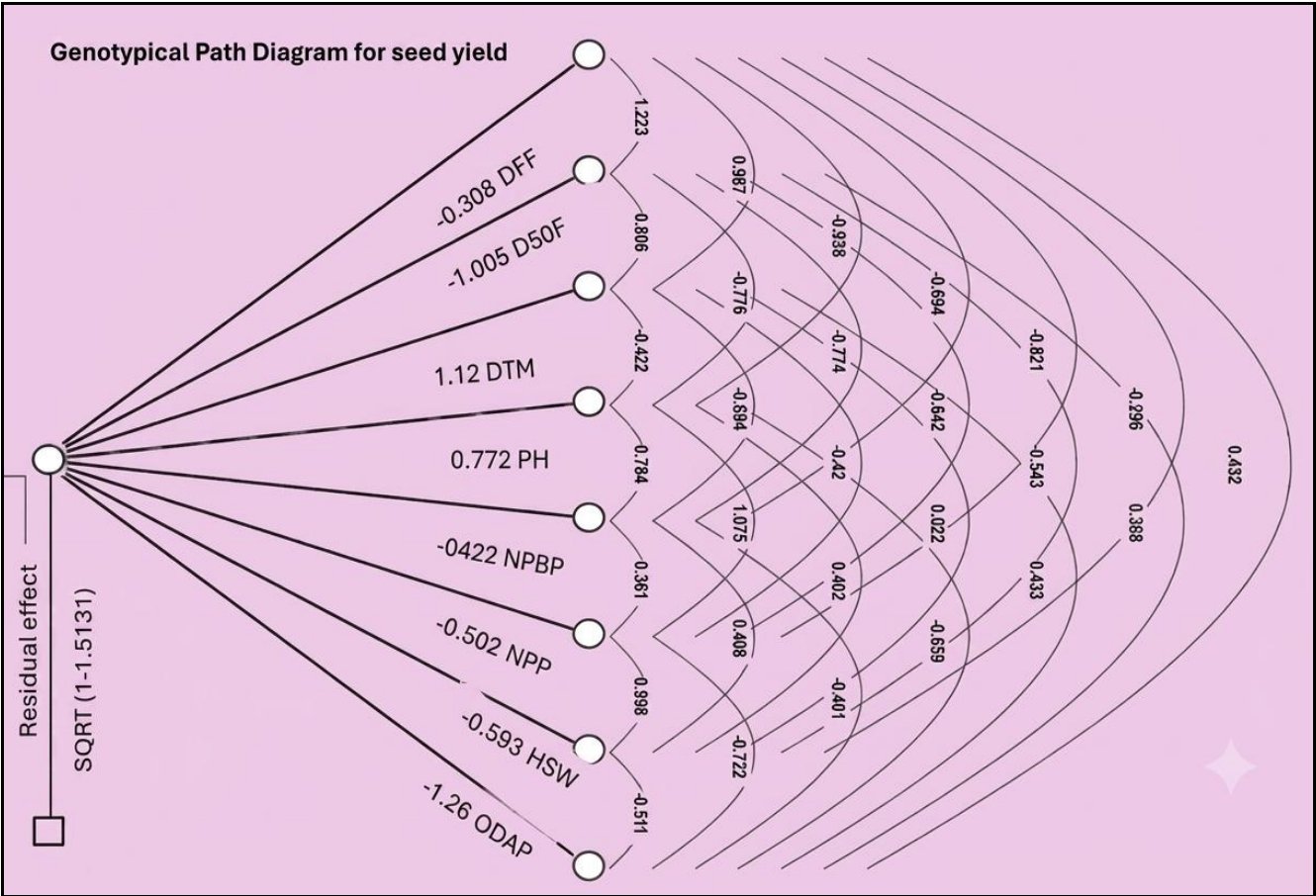


Fig 1: Path diagram for seed yield

Conclusion

The present investigation revealed substantial genetic variability among the lathyrus mutant lines for yield and its associated characters. High GCV, PCV, heritability and genetic advance for seed yield, number of pods per plant and ODAP content indicated considerable scope for improvement through selection. Correlation analysis identified plant height, number of pods per plant, number of branches per plant and 100 seed weight as important yield contributing traits, whereas early flowering, early maturity and lower ODAP content were desirable for simultaneous improvement of productivity and grain quality. Path coefficient analysis further confirmed that plant height exerted a high positive direct effect on seed yield, while number of pods per plant influenced yield mainly through indirect effects. Therefore, these characters should be emphasized as major selection criteria in future breeding programmes aimed at developing high-yielding, early maturing and low ODAP lathyrus.

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