Journal of Advances in Biology & Biotechnology

Volume 28, Issue 1, Page 503-512, 2025; Article no.JABB.129978
ISSN: 2394-1081

Assessment of Variability and Association among Green Forage Yield and Contributing Traits in Indigenous Genotypes of Grass Pea [*Lathyrus sativus* (L.)]

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.9734/jabb/2025/v28i11904

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/129978

Original Research Article

Received: 12/11/2024
Accepted: 14/01/2025
Published: 18/01/2025

ABSTRACT

Forty-four variable local accessions of grasspea including advanced lines and three checks were investigated. Observations were recorded from 5 selected plants of each genotypes in 3 replications. Estimates of GCV and PCV were high for leaflet width, number of primary branches and plant height indicating higher genetic variation in the genotypes studied. High heritability coupled with high genetic advance as percent of mean was observed forleaflet width, number of primary branches L/S ratio, plant height, length of primary branch, pods per plant.Significant

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Cite as: *Mishra, Anchal, Mayuri Sahu, and Harish Kumar Pandey. 2025. "Assessment of Variability and Association Among Green Forage Yield and Contributing Traits in Indigenous Genotypes of Grass Pea [Lathyrus Sativus (L.)]". Journal of Advances in Biology & Biotechnology 28 (1):503-12. https://doi.org/10.9734/jabb/2025/v28i11904.*

positive correlation of green forage yield per plant (g) with dry matter yield per plant (g), length of primary branch (cm), leaflet width (cm), at genotypic and phenotypic level respectively. In path analysis green forage yield was considered as dependent trait, Maximum positive direct effects was shown by DMY followed by days to first flowering, pods per plant, number of primary branch, plant height, leaflet width, leaflet length, length of primary branches.

Keywords: Correlation; germplasm; forage yield; Lathyrus sativus (L.); path analysis; variability.

1. INTRODUCTION

Grass pea (*Lathyrus sativus*), a vital fodder and feed crop which belongs to the Leguminosae family, within the Papilionideae subfamily and Vicieae tribe. It is characterized by a diploid chromosome number of 2n = 14. *Lathyrus* is good source of protein content and is better in nitrogen fixation, drought-tolerance and flood and soil salinity tolerance. *Lathyrus* species accommodate well in crop rotation, enhancing physical conditions of the soil; limiting disease and weed populations, and reducing total operational costs (Patto et al.2006). Popularly referred to as khesari, lakhadi, is tolerant of drought, hardy, nutritionally rich and has 362.3 kg cal. Energy, Water (%) 7.5-8.2, Starch (%) 48.0-52.3, Protein (%) 25.6-31.4, Fat (%) 0.58-0.80, Calcium (mg/kg) 3.8-4.3 (Rotter et al.1991).

Progress in the development of crop varieties depends heavily on genetic variability. To implement effective crop production programs, it is essentials to study genetic variation with estimates of phenotypic and genotypic variance paired with heritability and association analysis of different yield contributing traits is needed. Such basic statistic derivations provide knowledge of population mean, variance and standard deviation.

Association analysis enables breeders to understand the mutual component characters on which selection can be based for genetic improvement. Many economically important traits of plants are usually related to one another in one or several ways. Correlation coefficient and Path analysis is used to determine the degree and direction of association of independent variables with dependent traits In present study we are taking Green Matter Yield as dependent variable so studying about the relation of other independent variables with GMY is important.

2. MATERIALS AND METHODS

The material of research was obtained from AICRP On MULLaRP of Indira Gandhi Krishi Vishwavidyalaya, Raipur (Table 1) which consisted of forty-four diverse grass pea genotypes including released varieties and local germplasm of Chhattisgarh which are fit for fodder purpose. All these genotypes were planted in the Randomized Block Design (RCBD) with three replications at the Experimental plots of IGKV research farms, College of Agriculture, Raipur, Chhattisgarh, India during *Rabi*-2019-2020. The capital Raipur is located in the eastern part of the country situated in Chhattisgarh State, India, at 21ºl6’ N latitude and 81º36’N longitude and an altitude of 298.56 m above the mean sea level.

Recommended agronomic practices were followed to raise crop. The observations on plant height(cm), number of primary branch, length of primary branch(cm), leaflet length(cm), leaflet width(cm), peduncle length(cm), number of pods per plant, number of seeds per plant, 100 seed weight(g), day to first flowering, days to 50% flowering, days to maturity, dry matter yield(g), green matter yield(g), leaf/stem ratio were recorded on a five random plants from each genotype. Genotypic and phenotypic coefficients of variation were worked out as per the method suggested by Sivasubramanian and Madhavmenon (1973), heritability and genetic advance were calculated according to Johnson (1955). Correlation coefficient determined the positive and negative association among traits. Path coefficient analysis partitioned the observed genotypic correlation coefficient between yield and its components into direct and indirect effects.

3. RESULTS AND DISCUSSION

Genetic improvement in grass pea crop depends on extent of genetic variability for forage yield and its components. The present investigation aims to determine the magnitude and extent of variability and extent of association among 15 different traits including one dependent traits of green matter yield.

The analysis of variance (Table 2) for different traits exhibited significant differences among the genotypes for all the traits studied which indicates that considerable genetic variability is available in the genotypes studied. Plant height exhibited a range of 21 cm to 59 cm with a mean of 33.45cm. Number of primary branch ranged from 3.2-7.70 with a mean of 5.11. Length of primary branch ranged from 25.3 cm to 68 cm having mean of 41.06 cm. Leaflet length was measured with a range of 4.90 cm to 8.17 cm with a mean of 6.57 cm. Leaflet width was measured with a range of 0.57 cm to 2.23 cm with a mean of 0.93 cm. The range of peduncle length was varying from 2.1 to 3.80 cm with a mean 2.86 cm. The range of number of pods/plant was varying from 20 to 44 with a mean 30.31. The range of number of seeds/pod was varied from 2.66 to 4.03 with a mean 3.38. 100 seed weight was measured with a range of 5.04 g to 8.53 g with a mean of 6.32 g. Days to first flowering showed a mean value of 50.47 days within the range of 36.3 to 61.3 days. Days to 50% flowering ranged from 39.3 days to 69 days with in mean of 60.84 days. Days to maturity ranged from 102.33 to 108.33 days with in mean of 105.15 days. Dry matter yield ranged from 4.53g to 7.74g within mean of 6.22g. L/S ratio ranged from 0.61 to 1.20 within mean of 0.82. GMY ranged from 22.42 to 37.8 within mean of 30.32.

Selection efficiency mainly depends on the magnitude of genetic variability for quantitative traits. An assessment of heritable and non-heritable components of the total variability decides breeding procedure to be adopted. The nature and magnitude of variation for individual traits was assessed by phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean (Table 3). High GCV and PCV estimates were observed for leaflet width, number of primary branches and plant height indicating the higher genetic variation observed in the genotypes. The lowest amount of coefficient of variation at phenotypic level was recorded for days to maturity (0.993%). At genotypic level days to maturity was recorded for lowest amount (2.906%). Other characters showed moderate variability in terms of coefficient of variations at phenotypic and genotypic level.

These findings of GCV and PCV values are in close harmony with the result of Mekbib et al*.* (2018) for number of primary branches, length of primary branch, plant height and days to maturity, also similar conformity to the findings of previous workers Wuletaw and Endshaw (2002), Turk et al*.* (2007), Talukdar and Biswas (2008).

Heritability estimates along with genetic advance estimates would be more useful in predicting effectiveness of selection. High heritability coupled with high genetic advance as per cent of mean was observed for leaflet width, number of primary branch, L/S ratio, plant height, length of primary branch, pods per plant. These finding indicated that leaflet width, number of primary branch, L/S ratio, plant height, length of primary branch, pods per plant are governed by additive gene action and selection for this traits will be rewarding. The results are in harmony with findings of other workers such as Wuletaw and Endshaw (2002), Parihar et al*.* (2015).

Association analysis: Association analysis enables breeder to understand the mutual component characters on which selection can be based for genetic improvement. Many economically important traits of plants are usually related to one another in one or several ways.” In present study we are taking Green Matter Yield as dependent variable so studying about the relation of other independent variables

Table 1. List of 44 genotypes of grass pea used in study.

1	RLK-2	12	RLK-1397	23	RLK-1363	34	RLK-1301
2	RLK-74	13	RLK-1385	24	RLK-1379	35	PUSA-24
3	RLK-937	14	RLK-1317	25	RLK-1956	36	KL-5
4	RLK-11	15	RLK-1412	26	RLK-1312	37	MAHATEORA
5	RLK-127	16	RLK-202	27	RLK-895	38	PRATEEK
6	RLK-870	17	RLK-1392	28	RLK-345	39	JCL-19-3
7	RLK-481	18	RLK-1391	29	RLK-875	40	JCL-19-2
8	RLK-277	19	RLK-779	30	RLK-1472	41	JCL-19-4
9	RLK-1073	20	RLK-1158	31	RLK-917	42	JCL-19-1
10	RLK-407	21	RLK-1158	32	RLK-114	43	RATAN
11	RLK-472	22	RLK-860	33	RLK-1950	44	BIOL-5

(Source: AICRP on MULLaRP, COA, IGKV, Raipur.)

Table 2. Analysis of variance for Green forage yield and its attributing traits in Grass pea

Source of variation	Degree of freedom	Plant height (cm)	Number of primary branch	Length of primary branch (cm)	Leaf Length (cm)	Leaf width (cm)	Peduncle length	Pods/Plant	Seeds/pod
Replication	2	1.8409	2.6572	34.4545	0.8965	0.0090	0.8278	88.5075	0.3197
Treatment	43	187.5828**	5.0041**	209.6523**	2.7207**	0.4486**	0.6179**	110.2077**	0.3119**
Error	86	9.6393	0.3482	4.6095	0.0947	0.0045	0.0340	5.3060	0.1204

Source of variation	Degree of freedom	100 seed weight	Days to first flowering	Days to 50% flowering	Days to maturity	Dry matter yield	Leaf stem ratio	Green forage yield per plant (g)
Replication	2	0.0732	84.5681	55.7272	80.3939	0.0539	0.1443	300.0204
Treatment	43	1.3906**	42.9208**	93.82**	7.1543**	2.5791**	0.0987**	59.0232**
Error	86	0.0564	23.1883	20.2776	10.4249	0.192139	0.0009	1.5283

*** Significant at 1 % probability level, *Significant at 5 % probability level*

Table 3. Genetic variability parameters for green forage yield and its attributing traits in Grass pea

S.No.	Characters	Maximum	Minimum	Grand mean	S.D.	SE	CV (%)	PCV (%)	GCV (%)	H^2 (bs) %	GA	GA (as % of mean)
1	PH	59	21	33.45	7.907	1.7925	9.2804	24.821	23.021	86.0	18.858	56.368
2	NPB	7.70	3.2	5.11	1.291	0.3407	11.5292	26.933	24.340	81.7	2.972	58.073
3	LPB	68	25.3	41.06	8.359	1.2396	5.2279	20.798	20.131	93.7	21.125	51.438
4	LL	8.17	4.90	6.57	0.952	0.1778	4.6847	14.987	14.236	90.2	2.346	35.70
5	LW	2.23	0.57	0.93	0.386	0.0390	7.2131	41.759	41.131	97.0	0.90	96.954
6	PL	3.80	2.1	2.86	0.453	0.1065	6.437	16.681	15.391	85.1	1.075	37.489
7	P/P	44	20	30.31	6.061	1.3299	7.5996	20.937	19.509	86.8	14.546	47.991
8	S/P	4.13	2.66	3.38	0.322	0.2004	10.2496	12.678	7.461	34.6	0.393	11.593
9	100 SW	8.53	5.04	6.32	0.680	0.1372	3.7602	11.200	10.550	88.7	1.658	26.236
10	DFF	61.33	36.3	50.47	3.782	2.7802	9.5398	10.808	5.081	22.1	3.183	6.305
11	D50% F	69	39.3	60.84	5.592	2.5999	7.4014	11.000	8.138	54.7	9.670	15.894
12	DM	108.33	102.3	105.15	1.544	1.8641	3.0706	2.906	0.993	11.7	0.942	0.896
13	DMY	7.743	4.53	6.22	0.927	0.2531	7.0425	15.968	14.331	80.5	2.114	33.957
14	L/S	1.20	0.61	0.82	0.181	0.0177	3.7456	22.317	22.00	97.2	0.470	57.257
15	GMY	37.8	22.42	30.32	4.435	0.7138	4.0773	15.003	14.438	92.6	11.122	36.682

1 PH = Plant height (cm)
2 NPB= Number of primary branches
3 LPB= Length of primary branch
4 LL= Leaflet length (cm)
5 LW= Leaflet width (cm)
6 PL = Peduncle length (cm)
7 P/P = Pods per plant
8 S/P = Seeds per pod
9 100SW = 100 Seed weight (g)
10 DFF = Days to first flowering
11 D50%F = Days to 50% flowering
12 DM = Days to maturity
13 DMY = Dry matter yield (g)
14 L/S = Leaf stem ratio
15 GMY = Green matter yield (g)

Table 4. Genotypic and phenotypic correlation analysis for green forage yield and its attributing traits in Grasspea

Ch.		**NPB**	**LPB**	**LL**	**LW**	**PL**	**P/P**	**S/P**	**100SW**	**DFF**	**D50%F**	**DM**	**DMY**	**L/S**	**GMY**
PH	G	0.312**	0.495**	0.002	-0.007	0.104	0.083	0.061	0.133	-0.212*	0.092	-0.544**	0.168	0.084	0.261**
	P	0.24**	0.45**	0.018	-0.013	0.097	0.088	-0.015	0.122	-0.075	0.136	0.077	0.167	0.07	0.243**
NPB	G		0.036	-0.152	-0.217*	0.01	-0.16	-0.40**	-0.14	-0.348**	-0.291**	0.212*	-0.113	-0.156	0.165**
	P		0.025	-0.132	-0.190*	0.028	-0.15	-0.29**	-0.111	-0.154	-0.196*	0.014	-0.124	-0.136	0.17**
LPB	G			0.143	0.323**	0.199*	0.051	0.133	0.131	0.325**	0.253**	-0.299**	0.303**	0.126	0.376**
	P			0.121	0.312**	0.178*	0.041	0.077	0.122	0.135	0.208*	0.061	0.279**	0.123	0.348**
LL	G				-0.28**	0.016	0.044	-0.209*	0.22**	0.086	0.087	-0.212*	-0.062	-0.035	-0.028
	P				-0.28**	0.015	0.053	-0.145	0.197*	0.11	0.059	0.069	-0.043	-0.041	-0..031
LW	G					0.318**	0.142	-0.118	-0.099	0.302**	0.253**	0.176*	0.026	0.037	0.259**
	P					0.309**	0.139	-0.084	-0.092	0.115	0.177*	-0.11	0.033	0.034	0.243**
PL	G						0.091	0.014	0.091	0.313**	0.241**	-0.062	-0.178*	-0.155	0.118
	P						0.078	-0.038	0.107	0.128	0.171*	-0.098	-0.132	-0.149	0.101
P/P	G							0.082	0.40**	-0.146	0.258**	-0.114	-0.019	-0.03	0.09
	P							0.107	0.362**	-0.052	0.155	0.006	0.021	-0.02	0.068
S/P	G								0.082	-0.051	0.216*	0.490**	0.069	0.406**	-0.214*
	P								0.051	-0.035	0.056	-0.114	0.06	0.252**	-0.116
100	G									0.295**	0.091	-0.217*	0.101	0.024	0.052
SW	P									0.119	0.047	0.049	92	0.018	0.054
DFF	G										0.743**	-0.248**	0.043	0.272**	0.012
	P										0.251**	-0.048	0.011	0.139	0.025
D50	G											-0.027	-0.018	0.045	0.115
%	P											-0.021	-0.025	0.039	0.082
DM	G												-0.658**	0.356**	-0.54**
	P												0.155	-0.108	0.247**
DM	G													0.061	0.605**
Y	P													0.05	0.530**
L/S	G														0.045
	P														0.041

Table 5. Path coefficient analysis matrix of direct and indirect effects on green forage yield as dependent trait

	PH	**PB**	**LPB**	**LL**	**LW**	**PL**	**Pods/Plant**	**Seeds/Pod**	**100SW**	**DFF**	**D50%F**	**DM**	**DMY**	**L/S**	**r^2 with GMY**
PH	**0.301**	0.094	0.149	0.001	-0.002	0.031	0.025	0.019	0.040	-0.064	0.028	-0.164	0.051	0.025	0.261**
PB	0.108	**0.346**	0.013	-0.052	-0.075	0.004	-0.056	0.141	-0.049	-0.120	-0.101	0.073	-0.039	-0.054	0.165
LPB	0.084	0.006	**0.169**	0.024	0.055	0.034	0.009	0.022	0.022	0.055	0.043	-0.051	0.051	0.021	0.376**
LL	0.000	-0.033	0.031	**0.216**	-0.062	0.004	0.009	-0.045	0.048	0.019	0.019	-0.046	-0.013	-0.008	-0.028
LW	-0.002	-0.057	0.085	-0.076	**0.263**	0.084	0.037	-0.031	-0.026	0.079	0.067	0.046	0.007	0.010	0.259**
PL	0.005	0.001	0.009	0.001	0.015	**0.047**	0.004	0.001	0.004	0.015	0.011	-0.003	-0.008	-0.007	0.118
Pods/Plant	0.029	-0.057	0.018	0.016	0.050	0.032	**0.355**	0.029	0.144	-0.052	0.092	-0.041	-0.007	-0.011	0.090
Seeds/Pod	0.003	-0.022	0.007	-0.011	-0.006	0.001	0.004	**0.053**	0.004	-0.003	0.011	0.026	0.004	0.021	-0.214*
100SW	-0.036	0.038	-0.035	-0.060	0.027	-0.025	-0.109	-0.022	**-0.270**	-0.080	-0.025	0.058	-0.027	-0.007	0.052
DFF	-0.109	-0.179	0.168	0.044	0.156	0.161	-0.075	-0.026	0.152	**0.516**	0.383	-0.128	0.022	0.140	0.012
D50%F	-0.028	0.090	-0.078	-0.027	-0.078	-0.074	-0.079	-0.067	-0.028	-0.229	**-0.308**	0.008	0.006	-0.014	0.115
DM	-0.037	0.014	-0.020	-0.014	0.012	-0.004	-0.008	0.033	-0.015	-0.017	-0.002	**0.067**	-0.044	0.024	-0.548**
DMY	0.118	-0.079	0.212	-0.043	0.018	-0.125	-0.013	0.048	0.071	0.030	-0.013	-0.461	**0.700**	-0.043	0.605**
L/S	-0.009	0.016	-0.013	0.004	-0.004	0.016	0.003	-0.041	-0.003	-0.028	-0.005	-0.036	0.006	**0.013**	0.045

Residual = 0.701

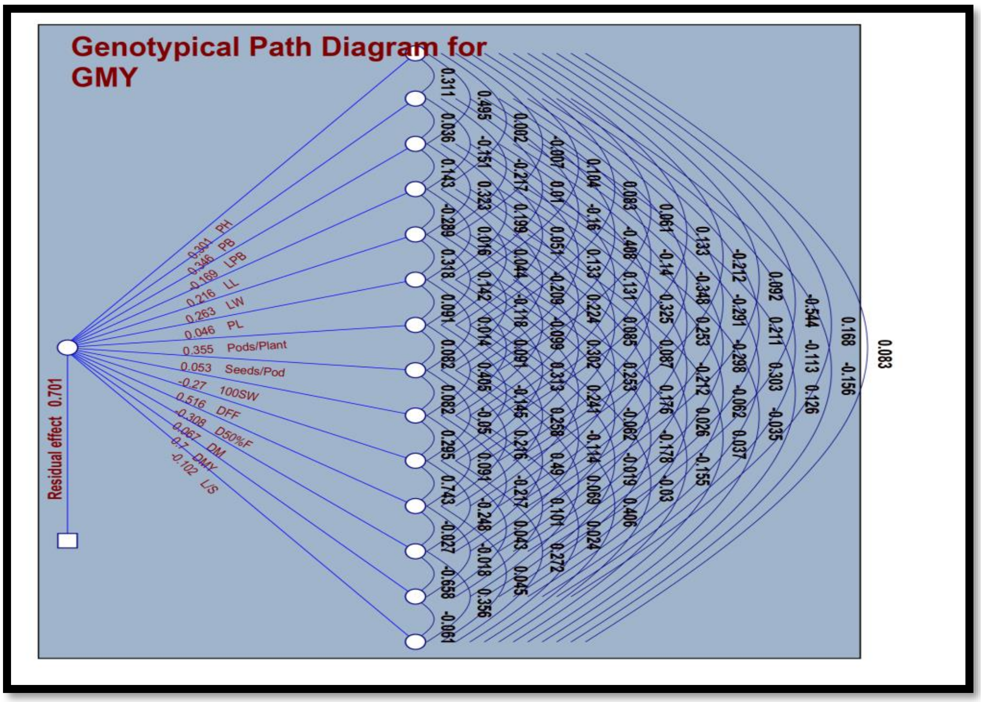

Fig. 1. Path diagram showing effects of independent traits on Green matter yield.

with GMY is important. Here, GMY is having positive significant correlation with DMY (0.605, 0.530) followed by length of primary branch (0.376, 0.348) and leaf width (0.259, 0.243) and negative significant correlation was found with days to maturity (-0.54) followed by seeds per pod (-0.214) at genotypic level (Table 4).

Besides this association analysis also revealed a positive but non-significant correlation with peduncle length (0.118,0.101), pods per plant (0.09,0.068), 100 seed weight (0.052,0.054), days to first flowering (0.012, 0.025), days to 50% flowering (0.115, 0.082) and leaf stem ratio (0.045, 0.041) and a negative but non-significant correlation with leaf length (-0.028, -0.031).

A positive genetic correlation between two desirable traits makes selection easy for improving both traits simultaneously while the reverse is the case for negative correlation (Udensi et al. 2012). Results which are found can be summarized by stating that the genotypic correlation values are higher than phenotypic correlation. Results revealed strong association of these traits with green forage yield per plant (g) and selection of these traits will be useful in improving green forage yield. Positive correlation between desirable traits is favourable because it helps in simultaneous improvement of both the characters. On the other hand, negative correlation will hinder the simultaneous expression of both characters with high values.

Path coefficient analysis was used to partition the observed correlation coefficients between green forage yield per plant (g) as dependent variable and its component traits into direct and indirect effects (Table 5) Maximum positive direct effects was shown by DMY (0.700) followed by days to first flowering (0.516), pods per plant (0.355), number of primary branch (0.346), plant height(0.301), leaflet width (0.263), leaflet length (0.216), length of primary branch (0.169), days to maturity (0.067), seeds per pod (0.053), peduncle length (0.047), leaf stem ratio (0.013) whereas negative direct effect were obtained *via* 100 seed weight (-0.270), days to 50% flowering (-0.308).

From the results we can concluded that there were existence of variability among the genotypes for the mentioned characters and sufficient scope for development of genotypes. It is concluded that “Significant amount of genetic variability was observed for most of the quantitative traits. The significant genetic variability in any breeding material is a prerequisite as it does not only provide a basis for selection but also provide some valuable information regarding selection of diverse parents for use in hybridization programme. The GCV and PCV values indicated that lot of variability exists among the genotypes at genotypic and phenotypic level and better chances of improvement is possible by selection. Study revealed that high genetic advance were recorded for the characters High genetic advance was recorded for the trait leaflet width, number of primary branch, L/S ratio, plant height, length of primary branch and pods per plant. These traits should be selected for further improvement for performance of genotypes because these traits accumulate more additive genes. High estimates of heritability with high genetic advance as percentage of mean was recorded for plant height (cm), number of primary branch, length of primary branch, leaflet length, leaflet width, pods per plant and L/S ratio, indicating predominance of additive gene action and selection based on these traits may be effective and sufficient improvement in seed yield may be achieve through selection of these traits. Significant positive correlation of green forage yield per plant (g) with dry matter yield per plant (g), length of primary branch (cm), leaflet width (cm), at genotypic and phenotypic level respectively. Positive association between desirable traits is favourable because it helps in simultaneous improvement in both the characters. In path analysis green forage yield was considered as dependent trait, Maximum positive direct effects was shown by DMY followed by days to first flowering, pods per plant, number of primary branch, plant height, leaflet width, leaflet length, length of primary branch. The analysis indicates true relationship between these characters and for green forage yield improvement direct selection for these traits will be rewarding revealed from the analysis. And therefore these characters should be considered as an important trait in selection criterion for enhancing the green forage yield. The improvement in green forage yield will be efficient if the selection is based on DMY followed by days to first flowering, pods per plant, number of primary branch, plant height, leaflet width, leaflet length, length of primary branch.

4. CONCLUSIONS

Base on this study, it can be concluded as follows**:**

- The GCV and PCV values revealed substantial variability among the genotypes at both genotypic and phenotypic level and it is indication of strong potential of improvement through selection.
- Traits like leaflet width, number of primary branch, L/S ratio, plant height, length of primary branch, pods per plant are governed by additive gene action and selection for this traits will be rewarding

A significant positive correlation of green forage yield per plant (g) was observed with dry matter yield per plant (g) length of primary branch (cm), leaflet width (cm), at genotypic and phenotypic level respectively. These findings suggest that selection based on these traits will be effective for further improvement of this forage crop.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

ACKNOWLEDGEMENT

The work on grasspea reported in this paper has been supported by research and teaching faculties of Department of Genetics and Plant Breeding, I.G.K.V.V. and I would like to thank Dr. Mayuri Sahu for her kind guidance and Mr. Harish Kumar Pandey for his support in statistical analysis.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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