Short Research Article

Correlation and Path Coefficient Analysis of Yield Components in Advanced Lines of Grasspea (Lathyrus sativus L.)

Jaspreet Kour* and Neha Agarwal

Dept. of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh (495 001), India

Article History

Manuscript No. ARISE 61 Received in 30th April, 2016 Received in revised form 28th July, 2016 Accepted in final form 1st August, 2016

Correspondence to

*E-mail: kourjassi.kour@gmail.com

Keywords

Grasspea, correlation coefficient, path correlation

Abstract

The present study was undertaken with eighteen advanced lines with their five parents were grown during rabi 2011 in Randomized Complete Block Design (RBD) with three replications in plot size of 4×0.45 m² at row spacing of 30 cm apart. The observations for 15 biometric characters viz., length of the first bearing node (cm), days to 50% flowering, days to maturity, number of pods plant⁻¹, number of seeds pod⁻¹, number of seeds plant⁻¹, seed yield plant⁻¹ (g), 100 seed weight (g), plant biomass plant⁻¹ (g), harvest index (%), swelling index, seed protein content (%) and ODAP content (%) at flowering, pod filling and maturity stages were recorded on five plant basis in each plot in each replication. Positive genotypic correlation was shown by harvest index, number of seeds plant⁻¹, plant biomass plant⁻¹ and number of pods plant⁻¹. Yield was positive and significantly correlated with seed ODAP content, biomass plant⁻¹, harvest index, days to maturity, number of seeds pod-1, length of first bearing node and number of pods plant⁻¹. Seed ODAP content, biomass plant⁻¹, harvest index, days to maturity, number of seeds pod-1, length of first bearing node and number of pods plant⁻¹ contributed maximum positive and direct effect on yield indicating these traits should be given emphasis while selecting high yielding cultivars. Our results indicated from the present study that traits showing strong and positive correlation with seed yield may be given priority while characters showing negative correlation should avoid during selection of superior genotypes for improving seed yield in grasspea.

1. Introduction

Grasspea (Lathyrus sativus L.), an annual pulse crop belonging to the family Fabaceae grows well under adverse environmental conditions and its many cultivars possess different attributes endowed with many properties that combine to make it an attractive food crop in drought-stricken, rain-fed areas where soil quality is poor and extreme environmental conditions prevail. (Palmer et al., 1989). Compared with other legumes, the grass pea is resistant to many pests including storage insects (Palmer et al., 1989). These properties make it an attraction crop for plant breeders. During last few years, intensive research work has been initiated to improve yield as well as the quality of grasspea. Grain yield in grasspea is a complex entity determined by the interplay of a number of attributes. Adequate knowledge of interrelation of factors influencing such complex characters is essential for designing an effective plant breeding programme. Studies of correlation of agronomic and morphological characters are helpful in

the identification of the components of a complex character such as yield but they do not provide precise information on the relative importance of direct and indirect influences of each of the componential characters. The technique of path coefficient analysis developed by Wright (1921) has been extensively used by conventional breeders. This analysis helps to identify different components affect yield. The present paper elucidates the interrelationship of factors influencing grain yield of advanced breeding lines through correlation and path coefficient analysis.

2. Materials and Methods

Eighteen advanced lines with their five parents (listed in Table 1) were grown during rabi 2011 in Randomized Complete Block Design (RBD) with three replications in plot size of 4×0.45 m² at row spacing of 30 cm apart. The observations for 15 biometric characters viz., length of the first bearing node (cm), days to 50% flowering, days to maturity, number

S1.	Genotype	Genera-	Source	Sl.	Genotype
No.		tion		No.	
1.	Mahateora	Parent	AICPIR, MUL- LARP, IGKV, Raipur	14.	Prateek×Ratan
2.	Prateek	Parent	AICPIR, MUL- LARP, IGKV, Raipur	15.	Pusa- 24×Mahateora
3.	Pusa 24	Parent	IARI, New Delhi	16.	Pusa-24×Prate
4.	Ratan	Parent	IARI, New Delhi		
5.	RLS 3004	Parent	IGKV, Raipur	17.	Mahateora×
6.	$Ratan{\times}Mahateora$	\mathbf{F}_{7}	AICPIR, MUL-		RLS-3004
			LARP, IGKV, Raipur	18.	$Prateek \times$
7.	Ratan×Pusa-24	\mathbf{F}_7	AICPIR, MUL-		Mahateora
8.	Prateek×	E	LARP, IGKV, Raipur	19.	$Prateek \times$
0.	RLS-3004	F_7	AICPIR, MUL- LARP, IGKV, Raipur		RLS- 3004
9.	Pusa-	F_7	AICPIR, MUL-	20.	Prateek×Ratan
	24×RLS-3004	- 7	LARP, IGKV, Raipur	0.1	B
10.	Ratan×RLS-3004	\mathbf{F}_{7}	AICPIR, MUL-	21.	Ratan×Mahate
		,	LARP, IGKV, Raipur	22	Druge 24v Drugter
11.	Prateek×Pusa-24	\mathbf{F}_{7}	AICPIR, MUL-	22.	Pusa 24×Prate
		_	LARP, IGKV, Raipur	23.	RLS- 3004×Pr
12.	Mahateora×Ratan	F_7	AICPIR, MUL- LARP, IGKV, Raipur	23.	teek
1.0	D (D (1				took
13.	Ratan×Prateek	F_7	AICPIR, MUL- LARP, IGKV, Raipur	and it	s components ar

of pods plant¹, number of seeds pod⁻¹, number of seeds plant¹, seed yield plant⁻¹(g), 100 seed weight (g), plant biomass plant⁻¹ (g), harvest index (%), swelling index, seed protein content (%) and ODAP content (%) at flowering, pod filling and maturity stages were recorded on five plant basis in each plot in each replication. Observations of flowering and maturity recorded on plot basis as per the descriptors for *Lathyrus* spp. (IPGRI, 2000). These observations were averaged and then subjected to statistical analysis. The genotypic correlation coefficients were estimated following the method of Singh and Chowdhury (1977). The genotypic correlation coefficients were partitioned into path coefficient using the technique outlined by Dewey and Lu (1959).

3. Results and Discussion

The different characters were analyzed for the evaluation of correlations (here genotypic correlation is mentioned). The correlation coefficients were partitioned into components of direct and indirect effects through path analysis.

3.1. Correlation analysis

The genotypic correlation coefficients between plant yield

Sl.	Genotype	Genera-	Source
No.		tion	
14.	Prateek×Ratan	F_6	AICPIR, MUL-
		Ť	LARP, IGKV, Raipur
15.	Pusa-	F_6	AICPIR, MUL-
	24×Mahateora		LARP, IGKV, Raipur
16.	Pusa-24×Prateek	F_6	AICPIR, MUL-
			LARP, IGKV, Raipur
17.	Mahateora×	F_6	AICPIR, MUL-
	RLS-3004		LARP, IGKV, Raipur
18.	Prateek×	F_6	AICPIR, MUL-
	Mahateora	v	LARP, IGKV, Raipur
19.	Prateek×	F_{5}	AICPIR, MUL-
	RLS- 3004	5	LARP, IGKV, Raipur
20.	Prateek×Ratan	F_{5}	AICPIR, MUL-
		-	LARP, IGKV, Raipur
21.	Ratan×Mahateora	F_{5}	AICPIR, MUL-
		-	LARP, IGKV, Raipur
22.	Pusa 24×Prateek	F_5	AICPIR, MUL-
		5	LARP, IGKV, Raipur
23.	RLS-3004×Pra-	F_{5}	AICPIR, MUL-
	teek	3	LARP, IGKV, Raipur

re presented in Table 2. Seed yield plant-1 exhibited highly significant positive correlation with harvest index (0.880**, 0.749**) followed by number of seeds plant⁻¹ $(0.689^{**}, 0.652^{**})$, plant biomass plant⁻¹ $(0.661^{**}, 0.620^{**})$ and number of pods plant⁻¹ (0.621**, 0.570**) at both the genotypic and phenotypic levels, respectively. These findings are further supported by the findings of Ali et al. (1986); Pandey et al. (2000); Larbi et al. (2010) reported for yield and attributes in grasspea.

3.2. Path coefficient analysis

The estimates of direct and indirect effects of the fourteen yield attributes on plant yield are presented in Table 3. The highest positive direct effect towards grain yield was exhibited due to seed ODAP content (1.159) followed by biomass plant⁻¹ (0.655), harvest index (0.546), days to maturity (0.281), number of seeds pod-1 (0.175), length of first bearing node (0.123) and number of pods plant⁻¹ (0.047). However, the negative direct effect on grain yield was noted due to ODAP content at pod filling stage (-1.127), followed by ODAP content at flowering stage (-0.581), days to 50% flowering (-0.311), 100 seed weight (-0.250), swelling index (-0.230), seed protein content (-0.082) and number of seeds plant⁻¹ (-0.039). Hence these traits showing positive correlation may be considered as important while planning for grasspea improvement seed yield are in accordance with the findings of Pandey et al. programme. The above findings of positive direct effects on

(1996), Pandey et al. (2000); Kahalkar (2010).

Sl.	Characters		Days	Days to	Length of	No. of	No. of	No. of	Seeds	100
No.			to 50%	maturity	first bear-	pods	seeds	seeds	yield	seed
			flowering		ing node	plant-1	pod ⁻¹	plant ⁻¹	plant-1	weight
					(cm)				(g)	(g)
1.	Days to 50% flowering	G	1.000	0.659**	0.103	-0.037	-0.699**	-0.216	-0.184	-0.197
2.	Days to maturity	G		1.000	1.057**	-0.029	-0.954**	-0.190	-0.838	0.401
3.	Length of first bearing node (cm)	G			1.000	0.2.85	-0.944**	0.101	0.121	-1.125**
4.	No. of pods plant-1	G				1.000	-0.017	0.898**	0.621**	-0.203
5.	No. of seeds pod-1	G					1.000	0.276	0.104	-0.371
6.	No. of seeds plant ⁻¹	G						1.000	0.689**	-0.166
7.	Seedsyield plant ¹ (g)	G							1.000	-0.210
8.	100 seed weight (g)	G								1.000
9.	Plant biomass plant ⁻¹	G								
10.	Harvest index (%)	G								
11.	Swelling index	G								
12.	Seed protein content %	G								
13.	ODAP at flowering stage	G								
14.	ODAP at pod filling stage	G								
15.	ODAP in seed	G								

^{*}Significant at (*p*=0.05); **at (*p*=0.01)

Table 2: Continue...

Sl.	Characters		Plant	Harvest	Swelling	Seed pro-	ODAP at	ODAP at	ODAP in
No.			biomass	index	index	tein con-	flowering	pod fill-	seed
			plant-1	(%)		tent %	stage	ing stage	
1.	Days to 50% flowering	G	-0.113	0.018	-0.168	-0.0652	0.352	-0.145	0.008
2.	Days to maturit	G	-0.323	-0.490*	-0.040	-0.495*	0.366	0.208	0.474^{*}
3.	Length of first bearing node	G	0.719**	-0.287	0.786^{**}	-0.163	1.051**	0.043	0.105
	(cm)								
4.	No. of pods plant-1	G	0.908^{**}	0.248	0.060	-0.016	0.086	-0.463*	-0.574**
5.	No. of seeds pod-1	G	-0.207	0.459^{*}	0.101	-0.055	0.169	-0.612**	-0.580**
6.	No. of seeds plant ⁻¹	G	0.858**	0.415^{*}	0.086	0.024	0.176	-0.616**	-0.681**
7.	Seedsyield plant ⁻¹ (g)	G	0.661**	0.880^{**}	0.002	-0.029	-0.003	-0.265	-0.262
8.	100 seed weight (g)	G	-0.237	0.243	-0.296	-0.124	-0.506	0.374	0.353
9.	Plant biomass plant-1	G	1.000	0.249	0.188	0.053	0.085	-0.440*	-0.512*
10.	Harvest index (%)	G		1.000	-0.101	0.017	0.072	-0.203	0.004
11.	Swelling index	G			1.000	0.198	0.113	-0.308	-0.284
12.	Seed protein content %	G				1.000	0.027	0.083	0.087
13.	ODAP at flowering stage	G					1.000	0.237	-0.027
14.	ODAP at pod filling stage	G						1.000	0.990**
15.	ODAP in seed	G							1.000

Sl.	Characters		Days	Days to	Length of	No. of	No. of	No. of	100 seed
No.			to 50%	matu-	first bearing	pods	seeds	seeds	weight
			flowering	rity	node (cm)	plant-1	pod ⁻¹	plant-1	(g)
1.	Days to 50% flowering	G	-0.311	0.185	0.013	-0002	-0.122	0.008	0.049
2.	Days to maturity	G	-0.205	0.281	0.130	-0.001	-0.167	0.007	-0.100
3.	Length of first bearing node (cm)	G	-0.032	0.297	0.123	0.013	-0.165	-0.004	0.281
4.	No. of pods plant ⁻¹	G	0.012	-0.008	0.035	0.047	-0.003	-0.035	0.051
5.	No. of seeds pod-1	G	0.217	-0.268	-0.116	-0.001	0.175	-0.011	0.093
6.	No. of seeds plant ¹	G	0.067	-0.053	0.012	0.042	0.048	-0.039	0.042
7.	100 seed weight (g)	G	0.061	0.113	-0.138	-0.009	-0.065	0.006	-0.250
8.	Plant biomass plant-1 (g)	G	0.035	-0.091	0.088	0.042	-0.036	-0.033	0.059
9.	Harvest Index (%)	G	-0.006	-0.138	-0.035	0.012	0.080	-0.016	0.061
10.	Swelling index	G	0.052	-0.011	0.097	0.003	0.018	-0.003	0.074
11.	Seed protein content %	G	0.203	-0.139	-0.020	-0.001	-0.010	-0.001	0.031
12.	ODAP content	G	-0.110	0.103	0.129	0.004	0.030	-0.007	0.127
	at flowering stage								
13.	ODAP content at pod filling stage	G	0.045	0.058	0.005	-0.022	-0.107	0.024	-0.094
14.	ODAP content in seed	G	-0.002	0.133	0.013	-0.027	-0.101	0.026	-0.088

*Significant at (*p*=0.05); **at (*p*=0.01)

Sl.	Characters		Plant	Har-	Swell-	Seed	ODAP	ODAP	ODAP	Seed yield
No.			biomass	vest	ing	protein	content	content at	content	plant ⁻¹ (g)
			plant-1	index	index	content	at flow-	pod filling	in	
			(g)	(%)		%	ering	stage	seed	
							stage			
1.	Days to 50% flowering	G	-0.074	0.010	0.039	0.053	-0.205	0.163	0.009	-0.183
2.	Days to maturity	G	-0.212	-0.268	0.009	0.041	0.213	-0.234	0.549	-0.383
3.	Length of first bearing node (cm)	G	0.471	-0.157	0181	0.013	-0.611	-0.049	0.122	0.2839
4.	No. of pods plant ⁻¹	G	0.594	0.136	-0.014	0.001	-0.050	0.521	-0.666	0.621**
5.	No. of seeds pod-1	G	-0.135	0.251	-0.023	0.005	-0.098	0.689	-0.673	0.105
6.	No. of seeds plant-1	G	0.561	0.227	-0.020	-0.002	-0.102	0.694	-0.789	0.689**
7.	100 seed weight (g)	G	-0.155	-0.133	0.068	0.010	0.294	-0.421	0.409	-0.210**
8.	Plant biomass plant ⁻¹ (g)	G	0.655	0.136	-0.043	-0.004	-0.049	0.496	-0.594	0.661**
9.	Harvest Index (%)	G	0.163	0.546	0.023	-0.001	-0.042	0.228	0.004	0.880^{**}
10.	Swelling index	G	0.123	-0.055	-0.230	-0.016	-0.065	0.347	-0.330	0.002
11.	Seed protein content %	G	0.034	0.010	-0.046	-0.082	-0.015	-0.094	0.100	-0.03
12.	ODAP content	G	0.056	0.039	-0.026	-0.002	-0.581	0.267	-0.031	-0.002
	at flowering stage									
13.	ODAP content at pod	G	-0.288	-0.111	0.071	-0.007	0.138	-1.12	1.148	-0.267
	filling stage									
14.	ODAP content in seed	G	-0.335	0.002	0.066	-0.007	0.016	-1.116	1.159	-0.261

Residual effect: 0.0500; Diagonal bold values indicate direct effect (for Genotypic Path)

4. Conclusion

Traits showing strong and positive correlation with seed yield might be given priority while characters showing negative correlation should be avoided during selection of superior genotypes for improving seed yield in grasspea.

5. References

- Ali, M.S., Shaikh, M.A.Q., Islam, M.S., Saha, C.S., 1986. Induction of mutants in grasspea (L. sativus) and their character association. Bangladesh Journal of Nuclear Agriculture. 50-57.
- Dewey, D.R., Lu, K.H., 1959. A correlation and Pathcoefficient analysis of components of crested wheat grass seed production. Agronomy Journal 51, 515–518.
- IPGRI., 2000. Descriptors for Lathyrus spp. International Plant Genetic Resources Institute, Rome, Italy, 4-49.
- Kahalkar, R.J., 2010. Genetic analysis of grain yield, its component and neurotoxin content in selected genotypes of grasspea (Lathyrus sativus). M.Sc. (Ag) Thesis. Department of Plant Breeding and Genetics, IGKV, Raipur, C.G.., India.
- Larbi, A., Abd El-Moneima, A.M., Nakkoula, H., Jammalb B., Hassana, S., 2010. Intra-species variations in yield

- and quality in Lathyrus species: Grasspea (L. sativus L.) Animal Feed Science and Technology 161, 9–18.
- Palmer, V.S., Kaul, A.K., Spencer, P.S., 1989. International Network for the Improvement of Lathyrus sativus and the Eradication of Lathyrism (INILSEL): A TWMRF initiatie, 219–223. In: Spencer, P. (Ed.), The Grass Pea: Threat to Promise. Proceedings of the International Network for the Improvement of Lathyrus sativus and the Eradication of the Lahyrism. Third World Medical Research Foundation, New York.
- Pandey, R.L., Chitale, M.W., Sharma, R.N., Geda, A.K., 2000. Evaluation and characterization of germplasm of grasspea (Lathyrus sativus). Journal of Medicinal Aromatic Plant Science 19(1), 14-16.
- Pandey, R.L., Chitale, M.W., Sharma, R.N., Rastogi, N., 1996. Status of Lathyrus research in India. In: Arora, R.K., Mathur, P.N., Riley, K.W., Adhum, Y. (Eds.), Lathyrus and Lathyrus genetic resource in Asia. In: Proceedings of Regional Workshop, 45–52.
- Singh, R.K., Chowdhury, B.D., 1977. Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi, India.
- Wright, S., 1921. Correlation and causation. Journal of Agricultural Research 20, 557–585.