

CHARACTER ASSOCIATION AND PATH ANALYSIS FOR SEED YIELD AND ITS COMPONENTS IN GRASS PEA (*Lathyrus sativus* L.)

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ABSTRACT

Present Experiment was conducted on Twentyone genotypes and these were evaluated during 2016-17 and 2017-18. the observations were recorded on different quantitative traits to estimate variability, heritability and genetic advance as % mean, character association and path analysis. In this study we find that High heritability with high genetic advance as % mean was observed for seed yield and number of pod plant⁻¹ which reveals simple selection is effective to develop these characters. Correlation studies revealed that seed yield plant⁻¹ showed the highly significant positive correlation at genotypic level with the traits viz., Days to 100% flowering, Days to 50% Pod maturity, Number of primary branches, Number of secondary branches, Number of seed Pod⁻¹ and Days to harvesting. The study of path analysis indicated that, at genotypic level. High positive direct effect towards seed yield was exhibited due to number of seeds pod⁻¹ followed by number pod plant⁻¹, number of secondary branches, days to 100% flowering, days to 50% pod maturity and days to harvesting. Therefore direct selection for these characters will help in development of high yielding varieties of grass pea.

INTRODUCTION

Lathyrus sativus L. (commonly known as grass pea or chickling pea) is a popular food and feed crop in certain Asian and African countries like Bangladesh, China, Ethiopia, India, Nepal and Pakistan because of its adaptation towards adverse growing condition as well as input requirement is very less. This crop has been reported to have high nutritive value as its seed is known for the sole source of calories of 351 cal/100g of seed with 58% carbohydrates, 28-32% protein, 0.6% fat and 3 g minerals per 100 g of seed. (Aykroyd and Doughty, 1964). It also contain calcium (110 mg), Iron (5.6 mg), phosphorus (500 mg) and vitamin B₁ (0.45 mg), B₂ (0.41 mg) and niacin (1.8 mg) per 100 g of seed besides containing tryptophan (0.4 - 0.5%) and nicotinic acid (Sharma and Padmanaban, 1969). To improve the productivity of such an important crop through breeding requires the knowledge of genetic variability of important traits of seed yield, heritability along with the genetic advance as percent mean provides an opportunity for selection of the trait. Generally seed yield is a complex trait and improvement of this trait requires knowledge of other seed yield contributing characters (Singh and Singh, 1995). Genetic variability is the most essential prerequisite for any successful crop improvement programme as it provides spectrum of variants for the effective selection, which can be achieved through the processes of hybridization, recombination, mutation and selection (Nair and Mehta, A. K. 2014). The correlation coefficient analysis measures the mutual relationship between various characters and it

determines the component traits on which selection can be relied upon the effect of improvement (Kadwey *et al.*, 2015). Estimation of correlation of coefficient reveals the interrelationship among the traits and Path analysis Splits the correlation into direct and indirect effects which express us to understand the cause and effect of related characters (Wright, 1921). Due to continuous increasing of human population, more and more food availability is required in coming years. Regarding this prospects, there is need of high yielding variety of Grasspea contributing good quality seed for the multiple purposes. Inception of the genetic improvement programme for seed yield and its component traits in any crop requires identification of suitable and adaptable genotypes for a particular agro climatic zone. By this way desired genes may be used directly as a base material for further improvement in order to break the existing yield plateau. Genetic evaluation of Grasspea genotypes for yield and quality traits is one of the important objectives of the any breeders deputed in Grasspea improvement programme. Knowledge about the genetic characteristics of a population is fundamental need in breeding programs. This strategy allows improvement and conservation of the genetic reliability of landrace/genetic resources (Kahraman and Onder 2009). The Present research aimed to assess the variability, Heritability, genetic advance, Correlation coefficients and path analysis for finding the selection criteria to improve the seed yield of Grasspea.

MATERIALS AND METHODS

The Present research work conducted during Rabi 2016 -17

and Rabi 2017-18. Twenty one genotypes were evaluated under this research work and the genotypes were listed in Table 1. The Research was conducted in two seasons at Agricultural Farm of Palli Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan, West Bengal. The farm is situated at 23°39' N 87°42' E and at 59 MSL. This region falls under sub-humid, subtropical, lateritic belt of West Bengal with hot summer and moderately cold and short winter. The experiment conducted in Randomized complete Block Design (RCBD) with Three Replications. The Observations taken on the Various Quantitative characters *viz.*, days to flower initiation, days to 50 % flowering, days to pod maturity, plant height, number of primary branches, number of secondary branches, number of pods plant⁻¹, pod length, number of seeds pod⁻¹, days to harvesting, root length and yield were recorded on five randomly selected competitive plants. Variability parameters, correlation and path analyses were worked out as per the standard methods. The possibility of improvement in any crop is measured by available variability in the crop. Path coefficient analysis will usually correlates coefficients into direct and indirect effects of various yield components, based on the assumption of mutual relationships among yield components. Statistically, path coefficient is a standardized partial regression coefficient, obtained from equations, where the yield-related variables are expressed as deviations from the means in units of standard deviation (Steel and Torrie,

1982). Determination of correlation and path coefficient between yield and yield criteria is important for the selection of favorable plant types for effective pea breeding programs. The objective for this type of study is to evaluate selection criteria in Grasspea breeding programs by means of Coefficient of variation, Correlation coefficient and Path coefficient analysis.

RESULTS AND DISCUSSION

From the experimental analysis The ANOVA revealed that, Highly significant amount of Variability present among traits (Table 2). PCV was slightly higher than GCV for some Characters which indicates the interaction of genotypes with the environment (Table 3). High GCV recorded for Number of Pod Plant⁻¹(27.95) , Seed yield (24.42) and Number of Seeds Pod⁻¹(23.17).

The character Days to Pod maturity recorded low GCV (2.28), and low PCV (3.59).Number of pods plant⁻¹ (31.53) showed the high PCV followed by seed yield (26.11). However, looking to the differences between GCV and PCV estimates, the maximum differences between PCV and GCV values was observed for number of primary branches followed by plant height . The GCV and PCV difference was of low magnitude for days to 50% flowering followed by Days to harvesting .

Table : 1 List of Genotypes

S.No	Genotype	S.No	Genotype	S.No	Genotype
1	Velva local	8	Mahatewra	15	Biol-212
2	Prateek	9	Nowda local	16	WBK-21-2-2
3	Nirmal	10	WBK-9-3	17	B-222
4	Waise	11	B-111	18	Shiruha local
5	WBK-13-1	12	WBK-5	19	WBK-20-5
6	WBK-11-3-1	13	PUSA-24	20	WBK-14-7
7	WBK-11-3	14	WBK-2	21	WBK-15-1

Table.2. Pooled analysis of variance (ANOVA) of various characters under study

Source	Df	Mean sum of square											
		Days to flower initiation	Days to 100% flowering	Days to 50% pod maturity	Plant Height (cm)	Primary branch	Secondary Branch	No.of Pods/plant	Pod length (cm)	No.of seeds/pod	Days to harvesting	Root length(cm)	seed yield(g)/plant
Genotypes	20	58.98***	68.07***	37.02***	46.56***	1.19***	2.56***	24.56***	0.07***	1.49***	109.29***	13.14***	65.40***
Error	100	2.17	1.83	7.27	12.8	0.21	0.25	1.07	0.02	0.04	4.5	0.54	1.52

*** the values are significant at P=0.05

Table 3: Phenotypic and genotypic coefficients of variability, heritability and genetic advance

	Grand mean	Min	Range Max	coefficient of variation %		Heritability (%)	Genetic advance	Genetic advance as percent of mean
				GCV	PCV			
Days to flower initiation	54.68	48.88	61.73	5.63	6.24	81.3	5.71	10.45
Days to 100% flowering	71.6	67.5	83	4.64	5.01	85.8	6.34	8.85
Days to 50% pod maturity	97.34	92	101.83	2.29	3.6	40.5	2.92	2.99
Plant height (cm)	32.06	26.86	36.18	7.34	13.4	30.5	2.7	8.42
No. of Primary branch	3.01	2.33	4	13.44	20.36	43.6	0.55	18.28
No. of Secondary Branch	3.12	2.16	4.67	19.84	25.6	60.1	0.99	31.69
No. of pods/plant	7.08	4.25	11.6	27.5	31.54	78.5	3.61	51.03
Pod length (cm)	2.6	2.43	2.85	3.49	6.38	29.8	0.1	3.92
No. of seeds/pod	2.12	1.26	2.87	23.18	25.41	83.2	0.92	43.53
Days to harvesting	102.17	92.16	109.33	4.08	4.63	77.77	7.57	7.4
Root length (cm)	8.18	6.4	10.9	17.76	19.9	79.7	2.66	32.67
seed yield (gm)/plant	13.36	8.57	20.93	24.42	26.11	87.4	6.28	47.04

Table 4 : Genotypic(G) and Phenotypic (P) correlation coefficient for the characters under study

	Days to flower initiation	Days to flower in	Days to 100% flowering	Days to 50% pod maturity	Plant height (cm)	No. of primary branches	No. of secondary branches	No. of pod/plant	Pod length	No. of seeds /pod	Days to harvesting	Root length (cm)	Seed yield (g)
Days to flower initiation	G	1	0.4323	-0.2863	-0.053	0.0449	0.3806	-0.117	-0.2117	-0.1148	0.0984	0.0601	-0.2565
	P	1	0.3942***	-0.1454	-0.0223	0.0352	0.2378**	-0.1084	-0.1328	-0.1265	0.0714	0.0057	-0.2197
Days to 100% flowering	G	1	1	-0.4148	-0.3686	0.2847	0.2933	-0.1253	0.055	0.0981	0.1197	-0.0404	0.0182
	P	1	1	-0.2167*	-0.2343***	0.1425	0.2447**	-0.086	0.0473	0.0833	0.1452	-0.0397	0.0203
Days to 50% pod maturity	G	1	1	1	0.0602	-0.1079	-0.3497	0.0303	-0.2066	0.2102	0.4754	0.1763	0.2145
	P	1	1	1	0.0057	-0.0107	-0.1808*	-0.1062	-0.0804	0.1051	0.2997***	0.1058	0.1213
Plant height (cm)	G	1	1	1	1	-0.5624	0.2357	0.5312	0.053	-0.1196	-0.276	0.3947	-0.1577
	P	1	1	1	1	-0.2185*	0.0812	0.3121***	0.1482	-0.0637	-0.1469	0.2032*	-0.1351
No. of primary branches	G	1	1	1	1	1	0.1067	-0.2474	0.4254	0.5081	0.0487	-0.6588	0.1129
	P	1	1	1	1	1	0.0234	-0.1423	0.2052*	0.2479**	-0.0015	-0.3035***	0.0587
No. of secondary branches	G	1	1	1	1	1	1	-0.0938	-0.3403	0.1981	0.1248	-0.2003	0.2544
	P	1	1	1	1	1	1	-0.0211	-0.1488	0.1689	0.1070	-0.0862	0.1632
No. of pod/plant	G	1	1	1	1	1	1	1	0.5641	-0.2976	-0.0475	0.0451	-0.0641
	P	1	1	1	1	1	1	1	0.2926***	-0.2385**	-0.0426	0.035	-0.032
Pod length (cm)	G	1	1	1	1	1	1	1	1	-0.1274	-0.2534	-0.3694	-0.2221
	P	1	1	1	1	1	1	1	1	-0.0542	-0.1425	-0.1705	-0.073
No. of seeds/pod	G	1	1	1	1	1	1	1	1	1	0.2055	-0.0953	0.3179
	P	1	1	1	1	1	1	1	1	1	0.1529	-0.0495	0.2742
Days to harvesting	G	1	1	1	1	1	1	1	1	1	1	-0.1842	0.4774
	P	1	1	1	1	1	1	1	1	1	1	-0.1694	0.3997
Root length (cm)	G	1	1	1	1	1	1	1	1	1	1	1	-0.3641
	P	1	1	1	1	1	1	1	1	1	1	1	-0.3169

*, **, Significant at P=0.05 and 0.01, respectively

Table.5: 1 Phenotypic Path Coefficient Analysis for the characters

	Days to flower initiation	Days to 100% flowering	Days to 50% pod maturity	Plant height (cm)	No. of primary branches	No. of secondary branches	No. of pod/plant	Pod length (cm)	No. of seeds/pod	Days to harvesting	Root length (cm)	Correlation with seed yield
Days to flower initiation	-0.2592	0.0066	-0.0042	0.0011	-0.0016	0.0319	0.0049	0.012	-0.0214	0.0217	-0.0015	-0.2197
Days to 100% flowering	-0.0905	0.0189	-0.0063	0.0114	-0.0065	0.0328	-0.0039	-0.0043	0.0141	0.044	0.0106	0.0203
Days to 50% pod maturity	0.0377	-0.0041	0.0289	-0.0003	0.0005	-0.0242	-0.0048	0.0072	0.0177	0.0909	-0.0283	0.1213
Plant height (cm)	0.0058	-0.0044	0.0002	-0.0486	0.01	0.0109	0.014	-0.0134	-0.0107	-0.0445	-0.0544	-0.1351
No. of primary branches	-0.0091	0.0027	-0.0003	0.0106	-0.0459	0.0031	-0.0064	-0.0185	0.0418	-0.0005	0.0812	0.0587
No. of secondary branches	-0.0617	0.0046	-0.0052	-0.0039	-0.0011	0.134	-0.0009	0.0134	0.0285	0.0325	0.0231	0.1632
No. of pod/plant	0.0281	-0.0016	-0.0031	-0.0152	0.0065	-0.0028	0.045	-0.0264	-0.0402	-0.0129	-0.0094	-0.032
Pod length (cm)	0.0344	0.0009	-0.0023	-0.0072	-0.0094	-0.0199	0.0132	-0.0902	-0.0091	-0.0432	0.0456	-0.073
No. of seeds/pod	0.0328	0.0016	0.003	0.0031	-0.0114	0.0226	-0.0107	0.0049	0.1687	0.0464	0.0132	0.2742
Days to harvesting	-0.0185	0.0027	0.0087	0.0071	0.0001	0.0143	-0.0019	0.0128	0.0258	0.3032	0.0453	0.3997
Root length (cm)	-0.0015	-0.0007	0.0031	-0.0099	0.0139	-0.0116	0.0016	0.0154	-0.0083	-0.0514	-0.2675	-0.3169

Residual = 0.8092; values indicated as bold represent direct effects

Table. 5.2. Genotypic path coefficient analysis of for the characters

	Days to flower initiation	Days to 100% flowering	Days to 50% pod maturity	Plant height (cm)	No. of primary branches	No. of secondary branches	No. of pod/plant	Pod length (cm)	No. of seeds/pod	Days to harvesting	Root length (cm)	Correlation with seed yield
Days to flower initiation	-0.334	0.0789	-0.0382	0.011	-0.0194	0.074	-0.0271	0.0604	-0.0392	0.0123	-0.0352	-0.2565
Days to 100% flowering	-0.1454	0.1813	-0.0554	0.0766	-0.1234	0.057	-0.029	-0.0157	0.0335	0.015	0.0236	0.0182
Days to 50% pod maturity	0.0956	-0.0752	0.1335	-0.0125	0.0468	-0.068	0.007	0.0589	0.0718	0.0596	-0.1031	0.2145
Plant height (cm)	0.0177	-0.0668	0.008	-0.2078	0.2437	0.0458	0.1232	-0.0151	-0.0409	-0.0346	-0.2309	-0.1577
No. of primary branches	-0.015	0.0516	-0.0144	0.1169	-0.4333	0.0207	-0.0573	-0.1214	0.1736	0.0061	0.3853	0.1129
No. of secondary branches	-0.1271	0.0532	-0.0467	-0.049	-0.0462	0.1944	-0.0218	0.0971	0.0677	0.0156	0.1171	0.2544
No. of pod/plant	0.0391	-0.0227	0.004	-0.1104	0.1072	-0.0182	0.2318	-0.1609	-0.1017	-0.006	-0.0264	-0.0641
Pod length (cm)	0.0707	0.01	-0.0276	-0.011	-0.1844	-0.0662	0.1308	-0.2852	-0.0435	-0.0318	0.2161	-0.2221
No. of seeds/pod	0.0383	0.0178	0.0281	0.0249	-0.2202	0.0385	-0.069	0.0363	0.3417	0.0258	0.0557	0.3179
Days to harvesting	-0.0329	0.0217	0.0635	0.0573	-0.0211	0.0243	-0.011	0.0723	0.0702	0.1254	0.1078	0.4774
Root length (cm)	-0.0201	-0.0073	0.0235	-0.082	0.2855	-0.0389	0.0105	0.1054	-0.326	-0.0231	-0.5849	-0.3641

Residual = 0.4851; values indicated as bold represent direct effects

Estimation of Heritability helps to Predict the Transmission of Characters From Parents to off Spring (Falconer,1981). The highest magnitude of heritability was observed for seed yield (87.40%) followed by days to 100% flowering (85.80%). Number of seeds pod⁻¹ (83.40%), days to flower initiation (81.30%) and root length (79.70%). High heritability alone may not lead to valid conclusions unless it is accompanied with the Genetic advance as percent mean (Johnson and Robinson, 1955). Similar finding regarding heritability was observed by several scientists (seed yield was observed by Ranjan *et al.* (2007), Turk *et al.* (2007), Chakrapani (2008), Kahalkar (2010) and Kamdi *et al.* (2015) : seed pod⁻¹ was observed by Dixit (2000) and Turk *et al.* (2007) : pod plant⁻¹ was observed by Islam *et al.* (1989), Pandey (2000)).

High heritability coupled with high genetic advance indicates that most likely the heritability is due to additive gene effects and selection may be effective (Johnson *et al.*, 1955) and High heritability coupled with Genetic Advance as % mean was recorded for Number of Pods Plant⁻¹. Similar Findings has been reported by Sharma *et al.* (1997), Mourya (1998).

Correlation Studies (Table 4) indicated that Seed yield Plant⁻¹ at Genotypic level showed that highly significant Positive correlation with the traits viz., Days to 100% flowering, Days to 50% Pod maturity, Number of Primary Branches, Number of secondary Branches, Number of seeds pod⁻¹, Days to Harvesting. Some traits found to be negatively correlated with seed yield that are Days to flower initiation, Plant height, Number of Pod Plant⁻¹, Pod length, Root length. These association studies are similar to findings which are reported

by Kumar and Dubey (1997), Pandey *et al.* (2000). Similar findings regarding Plant height was observed by Ratna *et al.* (2015) that Plant height negatively correlated with seed yield at Genotypic level.

The Correlation studies describes only nature and degree of relationship of seed yield contributing characters but it will not provide the details of direct and indirect effects. Path Coefficient analysis (Table 5.1 and 5.2) is a statistical method to split the correlation coefficients into Direct and Indirect effects of independent variables on dependent variable. The study of path analysis indicated that, at genotypic level highest positive direct effect towards seed yield was exhibited due to number of seeds pod⁻¹ followed by number pod plant⁻¹, number of secondary branches, days to 100% flowering, days to 50% pod maturity and days to harvesting. Therefore direct selection for these characters will help in development of high yielding varieties of grass pea. Similar findings on seed yield plant⁻¹ through number of seed pod⁻¹ was observed by Pandey *et al.* (1996) and Pandey *et al.* (2000) and through number of pod⁻¹ was observed by Kavunchu (1985), Ali *et al.* (1986), Das and Kundagrami (2002) and sinha and singh (2005).

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