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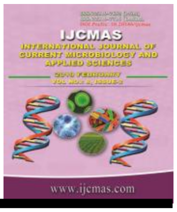

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Character Association and Path Analysis in Diverse Genotypes of Pea (*Pisum sativum* L.)

Shalini Singh[1]*, B. Singh[1], V. Rakesh Sharma[2], Vinay Verma[1] and Mukesh Kumar[1]

[1]*Department of Horticulture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut - 250 110 (U.P.), India*
[2]*CSIR- NBRI, Rana Pratap Marg, Lucknow -226 001 (U.P), India*

**Corresponding author*

ABSTRACT

Fifty-five pea (*Pisum sativum* L.) genotypes were evaluated using eleven morphological traits to assess the interrelationship among yield and yield-related attributes and their direct and indirect effects on seed yield. Based on the correlation coefficient analysis, seed yield per plant showed positive and significant association with green pod yield per plant, shell weight per plant, number of pods per plant and length of pod both at genotypic and phenotypic levels. Path coefficient analysis revealed that direct positive effect on seed yield per plant was exhibited by green pod yield per plant, number of first fruiting node, length of pod, days to 50% flowering and plant height. Hence, from correlation and path analysis it can be inferred that green pod yield per plant and pod length revealed significant and positive correlation and direct positive effect on seed yield and these traits shall be used as key indices towards the direct selection of genotypes for the successful breeding programme for yield improvement of pea germplasm.

Keywords

Genotypes of pea,
Pisum sativum L.
Path analysis

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Introduction

Pea (*Pisum sativum* L.) also called as “Matar” is an important legume vegetable for temperate and sub-tropical regions of the world and its center of origin is Mediterranean region of Southern Europe and Western Asia. It is an important crop because of its diversity of utilization and extensive production areas (Boros and Wawer, 2009). It is grown for its fresh green seeds, edible pods, dried seeds and foliage (Duke, 1981). Being number one of the processed vegetables, it can be used for off-season consumption in its fresh, canned frozen or dehydrated forms (Santalla *et al.*, 2001). It is a rich source of health benefiting Phyto-nutrients, minerals, vitamins and antioxidants and is known for its superior quality protein like high levels of lysine making it an appropriate dietary complement to cereals (Gul *et al.*, 2006; Dhama *et al.*, 2010). It also plays an important role in nitrogen fixation. Short duration and early varieties of pea have the potential to provide premium returns to the farmers as they can fetch a better price and can be used for multi-cropping (Anant *et al.*, 2006).

Pea occupies 5.43 lakh hectare area in India with production of 54.32 lakh tons (NHB, 2017-18) and shares 21 percent production of the world. Uttar Pradesh is a major field pea producing state in India producing about 60% of the country's produce. The productivity of pea is quite low to fit the required demand and this may be mainly due to lack of high yielding varieties and resistance to biotic and abiotic stress (Kumar *et al.,* 2015). To meet the current demand, there is an urgent need of germplasm evaluation for genetic improvement of pea germplasm to develop desired high yielding genotypes. Yield improvement cannot be solely achieved through direct selection because yield is a complex character, which is dependent on various yield-related traits and environmental conditions. The efficiency of selection in any breeding programme is enhanced with the knowledge of the association of yield components and their relative contribution shown by path analysis. It guides the breeder to realize the actual yield components and furnish an effective basis of phenotypic selection. Correlation analysis helps in the evaluation of relationship existing between yield and its components.

Determination of the traits having the greatest influence on yield can be done through path coefficient analysis which permits the partitioning of correlation coefficients into direct and indirect effects, giving the relative importance of each of the causal factors. This knowledge of path coefficient is a decision support tool that helps researchers to determine the contribution of each variable to the response variable and each variable *via* other variables to that response variable (Akinnola, 2012). The present study was undertaken to determine the inter-relationship among the components and the direct and indirect influences of each of the component characters towards the pea yield in order to predict an appropriate plant type to be used as base material for further pea breeding programme.

Materials and Methods

A total of fifty-five genotypes of garden pea were evaluated using eleven morphological traits at Horticultural Research Centre, SVPUA&T, Meerut during Rabi season, 2015. The details of the genotypes along with their availability of sources are given in table 1. The experiment was laid out in RBD with three replications. All the genotypes selected for the research were planted in row-to-row and plant-to-plant spacing of 60 cm and 10 cm, respectively. All the recommended horticultural practices and plant protection measures were followed uniformly from time to time to raise a healthy crop. After eliminating the border and unhealthy plants five plants were randomly selected in each genotype per replication for observations. Observations were recorded for eleven morphological traits viz., days to 50 % flowering, plant height (cm), number of first fruiting node, length of first fruiting node (cm), number of pods per plant, length of pod (cm), width of pod (cm), number of seeds per pod, green pod yield per plant (g), shell weight per plant (g) and seed yield per plant (g). The mean values were subjected to statistical analysis to work out phenotypic and genotypic correlation coefficient (Johnson *et al.,* 1955). Path coefficient analysis was performed according to Dewey and Lu (1959) to compute the direct and indirect effects of the traits on the total yield per plant.

Results and Discussion

A total of fifty-five pea genotypes were evaluated using eleven morphological traits. Based on analysis of variance, all the eleven characters studied showed significant differences, indicating the presence of sufficient variability among the genotypes.

Since, yield is a complex and polygenic character, the genetic improvement of yield can merely achieve through indirect selection of other associated character. Thus, character association study was conducted in order to know how various characters are correlated with yield and intercorrelated among each other. Character correlations were made at both genotypic and phenotypic levels as shown in table 2. In general, the magnitude of genotypic correlation coefficient was higher than their corresponding phenotypic correlation coefficient. This indicated a strong inherent relationship in different pair of characters dependent on environment influence which modifies the expression of genotype, thus altering the phenotypic expression (Nandpuri *et al.,* 1973). These results are similar to the findings of Nawab *et al.,* (2009) and Pal and Singh (2012).

The correlation studies revealed that seed yield per plant showed significant and positive correlation with green pod yield per plant, shell weight per plant, number of pods per plant and length of pod both at genotypic and phenotypic level, which suggested the possibilities of improving seed yield by simultaneous improvement of these traits. Similar trend was reported by Yadav *et al.,* (2010); Devi *et al.,* (2010) for green pod yield per plant, number of pods per plant and pod length; Tiwari and Lavanya (2012) and Kumar *et al.,* (2014) for pod length. Negative correlation was observed at genotypic and phenotypic level for plant height, length of first fruiting node and days to 50% flowering, indicating that these characters shall be taken into consideration for the earliness of the crop.

In the inter correlation among the characters, green pod yield per plant exhibited positive significant association with number of pods per plant and length of pod at both genotypic and phenotypic level. The results are in close harmony with the findings of Pal and Singh (2012); Karnwal *et al.,* (2013) and Kumar *et al.,* (2015). In addition, plant height showed positive and significant correlation with days to 50% flowering at genotypic and phenotypic level. Therefore, knowledge on the inter correlation association of the traits may be considered as the most reliable selections indices for effective improvement in pea.

The genotypic and phenotypic correlations were further analyzed by path coefficient technique because correlation coefficients are the indication of simple association between variables. In addition, knowledge on presence of association among component characters reveals that some of them may serve as indicator of yield. This involves partitioning of the correlations into direct and indirect effects via alternative characters or pathways. In the present investigation, path coefficient analysis revealed that green pod yield per plant exhibited very high direct positive effect on seed yield per plant both at genotypic and phenotypic level. In addition, significant positive direct effect on seed yield per plant was also observed by number of first fruiting node, length of pod, days to 50% flowering and plant height (Table 3). Therefore, direct selection of these traits might bring an overall improvement in the crop yield as these characters played an important role in increasing seed yield per plant. These results were in agreement with the findings of Rai *et al.,* (2006) for days to 50% flowering and plant height; Sharma *et al.,* (2007) for plant height and length of pod; Singh *et al.,* (2011) for plant height; Kumar *et al.,* (2013); for pod length and days to 50% flowering and Siddika *et al.,* (2013) for days to 50% flowering. However, in negative direction significant direct effect on seed yield per plant was exhibited by shell weight per plant, length of first fruiting node, number of seeds per pod, width of pod and number of pods per plant. The high indirect effect also showed that most of the characters influenced the seed yield through number of pods per plant and number of seeds per pod. These results are in preponderance with the findings of Rasaei *et al.*, (2011).

Table.1 List of garden pea genotypes evaluated for the present study

S/N	Genotypes Names	Source of collection	S/N	Genotypes Names	Source of collection
1.	VRP-3	I.I.V.R., Varanasi	31.	VRP-174	I.I.V.R., Varanasi
2.	VRP-13	I.I.V.R., Varanasi	32.	VRP-95	I.I.V.R., Varanasi
3.	VRP-26	I.I.V.R., Varanasi	33.	VRP-49	I.I.V.R., Varanasi
4.	VRP-194	I.I.V.R., Varanasi	34.	VRP-276	I.I.V.R., Varanasi
5.	VRP-222	I.I.V.R., Varanasi	35.	VRP-82	I.I.V.R., Varanasi
6.	VRP-375	I.I.V.R., Varanasi	36	VRP-145	I.I.V.R., Varanasi
7.	VRP-324	I.I.V.R., Varanasi	37.	VRP-343	I.I.V.R., Varanasi
8.	VRP-115	I.I.V.R., Varanasi	38.	VRP-131	I.I.V.R., Varanasi
9.	VRP-69	I.I.V.R., Varanasi	39.	VRP-248	I.I.V.R., Varanasi
10.	VRP-313	I.I.V.R., Varanasi	40.	VRP-64	I.I.V.R., Varanasi
11.	VRP-311	I.I.V.R., Varanasi	41.	VRPM-15	I.I.V.R., Varanasi
12.	VRP-73	I.I.V.R., Varanasi	42	VP-233	I.I.V.R., Varanasi
13.	VRP-228	I.I.V.R., Varanasi	43.	EC-97280	N.B.P.G.R., New Delhi
14.	VRP-321	I.I.V.R., Varanasi	44.	EC-8372	N.B.P.G.R., New Delhi
15.	VRP-320	I.I.V.R., Varanasi	45	EC-8724	N.B.P.G.R., New Delhi
16.	VRP-355	I.I.V.R., Varanasi	46.	EC-71944	N.B.P.G.R., New Delhi
17.	VRP-16	I.I.V.R., Varanasi	47.	MO-23	I.I.V.R., Varanasi
18.	VRP-22	I.I.V.R., Varanasi	48.	MO-19	I.I.V.R., Varanasi
19.	VRP-122	I.I.V.R., Varanasi	49.	KS-228	I.I.V.R., Varanasi
20.	VRP-383	I.I.V.R., Varanasi	50.	DPP-94/8-06	I.I.V.R., Varanasi
21.	VRP-284	I.I.V.R., Varanasi	51.	UDAY	I.I.V.R., Varanasi
22.	VRP-65	I.I.V.R., Varanasi	52	MUKTI	I.I.V.R., Varanasi
23.	VRP-223	I.I.V.R., Varanasi	53.	SHAKTI	I.I.V.R., Varanasi
24.	VRP-402	I.I.V.R., Varanasi	54.	SAMRIDHI	I.I.V.R., Varanasi
25.	VRP-382	I.I.V.R., Varanasi	55.	NANDINI	I.I.V.R., Varanasi
26.	VRP-176	I.I.V.R., Varanasi			
27.	VRP-273	I.I.V.R., Varanasi			
28.	VRP-327	I.I.V.R., Varanasi			
29.	VRP-107	I.I.V.R., Varanasi			
30.	VRP-156	I.I.V.R., Varanasi			

Table.2 Estimates of genotypic and phenotypic correlation co-efficient between different characters of pea

		X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**X9**	**X10**	**X11**
X1	G	1.000	0.392**	0.081	0.115	0.092	-0.368**	-0.250**	0.162*	-0.150	-0.068	**-0.204****
	P	1.000	0.377**	0.085	0.109	0.090	-0.355**	-0.233**	0.157*	-0.145	-0.069	**-0.192***
X2	G			0.068	0.526**	-0.071	-0.246**	-0.131	0.261**	-0.256**	-0.203**	**-0.293****
	P			0.069	0.508**	-0.070	-0.243**	-0.125	0.256**	-0.251**	-0.200*	**-0.287****
X3	G				0.703**	0.018	-0.129	-0.001	0.133	-0.049	0.011	**-0.117**
	P				0.686**	0.015	-0.124	-0.017	0.130	-0.046	0.008	**-0.105**
X4	G					-0.069	-0.078	-0.070	0.162*	-0.143	-0.082	**-0.214****
	P					-0.070	-0.075	-0.067	0.150	-0.136	-0.079	**-0.205****
X5	G						-0.085	-0.179*	-0.149	0.835**	0.859**	**0.745****
	P						-0.083	-0.166*	-0.147	0.832**	0.851**	**0.737****
X6	G							0.311**	0.245**	0.343**	0.266**	**0.394****
	P							0.284**	0.236**	0.336**	0.258**	**0.383****
X7	G								-0.004	-0.008	-0.043	**0.026**
	P								-0.007	-0.011	-0.042	**0.020**
X8	G									0.002	-0.111	**0.100**
	P									0.000	-0.105	**0.095**
X9	G										0.958**	**0.961****
	P										0.948**	**0.955****
X10	G											**0.843****
	P											**0.822****
X11	G											**1.000**
	P											**1.000**

***significant at 5% level; **significant at 1% level, X1-Days to 50% flowering, X2-Plant height(cm), X3-Number of first fruiting node, X4-Length of first fruiting node (cm), X5-Number of pods per plant, X6-Length of pod (cm), X7-Width of pod (cm), X8-Number of seeds per pod, X9-Green pod yield per plant (g), X10-Shell weight per plant (g), X-11-Seed weight per plant (g), G-Genotypic level, P-Phenotypic Level**

Table.3 Direct and indirect effect of different characters of different traits

		X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	G	**0.022**	0.007	0.002	-0.005	0.000	-0.008	0.001	-0.003	-0.284	0.067	**-0.204****
	P	**0.006**	-0.0013	0.0003	-0.0043	-0.0006	-0.0040	-0.0001	0.0026	-0.2438	0.0530	**-0.192***
X2	G	0.008	**0.018**	0.002	-0.025	0.000	-0.006	0.000	-0.005	-0.485	0.199	**-0.293****
	P	0.002	**-0.0035**	0.0002	-0.0200	0.0005	-0.0027	0.0000	0.0042	-0.4214	0.1536	**-0.287****
X3	G	0.002	0.001	**0.023**	-0.034	0.000	-0.003	0.000	-0.003	-0.093	-0.011	**-0.117**
	P	0.0005	-0.0002	**0.0035**	-0.0270	-0.0001	-0.0014	0.0000	0.0021	-0.0764	-0.0064	**-0.105**
X4	G	0.002	0.010	0.016	**-0.048**	0.000	-0.002	0.000	-0.003	-0.270	0.080	**-0.214****
	P	0.0006	-0.0018	0.0024	**-0.0393**	0.0005	-0.0008	0.0000	0.0024	-0.2291	0.0604	**-0.205****
X5	G	0.002	-0.001	0.000	0.003	**-0.002**	-0.002	0.001	0.003	1.580	-0.839	**0.745****
	P	0.0005	0.0002	0.0001	0.0028	**-0.0064**	-0.0009	-0.0001	-0.0024	1.3965	-0.6534	**0.737****
X6	G	-0.008	-0.005	-0.003	0.004	0.000	**0.023**	-0.001	-0.005	0.649	-0.260	**0.394****
	P	-0.0020	0.0008	-0.0004	0.0029	0.0005	**0.0112**	0.0001	0.0038	0.5645	-0.1985	**0.383****
X7	G	-0.005	-0.002	0.000	0.003	0.000	0.007	**-0.003**	0.000	-0.016	0.042	**0.026**
	P	-0.0013	0.0004	-0.0001	0.0027	0.0011	0.0032	**0.0003**	-0.0001	-0.0187	0.0320	**0.020**
X8	G	0.004	0.005	0.003	-0.008	0.000	0.006	0.000	**-0.021**	0.003	0.108	**0.100**
	P	0.0009	-0.0009	0.0005	-0.0059	0.0009	0.0026	0.0000	**0.0162**	-0.0006	0.0809	**0.095**
X9	G	-0.003	-0.005	-0.001	0.007	-0.002	0.008	0.000	0.000	**1.893**	-0.936	**0.961****
	P	-0.0008	0.0009	-0.0002	0.0054	-0.0053	0.0038	0.0000	0.0000	**1.6787**	-0.7277	**0.955****
X10	G	-0.001	-0.004	0.000	0.004	-0.002	0.006	0.000	0.002	1.814	**-0.977**	**0.843****
	P	-0.0004	0.0007	0.0000	0.0031	-0.0054	0.0029	0.0000	-0.0017	1.5906	**-0.7680**	**0.822****

***significant at 5% level; **significant at 1% level, X1-Days to 50% flowering, X2-Plant height(cm), X3-Number of first fruiting node, X4-Length of first fruiting node (cm), X5-Number of pods per plant, X6-Length of pod (cm), X7-Width of pod (cm), X8-Number of seeds per pod, X9-Green pod yield per plant (g), X10-Shell weight per plant (g), X11-R with Seed yield per plant (g) G-Genotypic level, P-Phenotypic Level**

To what extent causal factors accounts for the variability of the dependent factor is determined by residual effect. In this study, the residual effect of path coefficient analysis was 0.0191and 0.0197 on seed yield per plant at genotypic and phenotypic levels, respectively. This indicated that, for the genetic analysis of pea, the eleven characters taken under study were sufficient. Path coefficient analysis provides information of direct and indirect effect of any character, whether the observed correlation is due to the direct influence or due to other variables. Based on the above results, the characters like green pod yield per plant, shell weight per plant, number of pods per plant and pod length were the important seed yield determinants. Among these, green pod yield per plant and pod length were positively and significantly correlated with seed yield per plant and also showed direct effect on seed yield per plant. Thus, plant breeders should focus on above mentioned characters during selection of elite genotypes. Based on mean performance the genotypes *viz*., VRP-383, VRP-311, VRP-320 and Kashi shakti exhibited high values for characters that showed significant positive correlation with seed yield per plant and these genotypes can be further used for the genetic improvement of pea germplasm.

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