

Print ISSN : 0972-8813  
e-ISSN : 2582-2780

[Vol. 21(3) September-December 2023]

# Pantnagar Journal of Research

(Formerly International Journal of Basic and  
Applied Agricultural Research ISSN : 2349-8765)



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## To study of correlation and path coefficients analysis for pod yield in garden pea [*Pisum sativum* L. var. *hortense*]

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**ABSTRACT:** In this experiment crosses was made in 2018-2019 using diallel mating design (excluding reciprocal crosses) and the data investigated in 2019-2020 at Vegetable Research Farm of Chandra Shekhar Azad University of Agriculture and Technology Kanpur, India. The experimental material comprised 8 diverse genotypes of vegetable pea obtained from Vegetable Science Department of Chandra Shekhar Azad University of Agriculture and Technology. The 28 crosses along with their 8 parents / diverse genotypes were grown in Randomized Block Design with three replications. Results of Correlation study revealed that pod yield per plant exhibited highly significant and positive correlation with plant height, number of branches per plant, days to 50% flowering, pod length, shelling percentage and pod width. The highest positive and direct effect on pod yield per plant was exerted by intermodal length followed by number of grain per pod and pod length. These are used in breeding programme in future prospects point of view.

**Key words:** Correlation, diallel analysis, garden pea, path coefficients analysis

Garden Pea [*Pisum sativum* L. var. *hortense*] is a self-pollinated crop belongs to family leguminosae sub family Fabaceae. It is normal diploid crop with chromosome number  $2n=2x=14$ . Based on genetic diversity its primary centre of origin is Mediterranean region, Western Asia, Central Asia and as secondary centre of origin it is of Near East and Ethiopia India ranks third in area after China and USSR under pea (vegetable and pulse pea) cultivation. In India total area covered by peas is 45, 40,000 hectare with the green pod yield production of 54, 22,000 metric tons its productivity is 8.6 metric tons per hectare. The present experiment was conducted to revealed nature of gene action Correlation, path coefficients analysis in Diallel mating design to identify potent parents and superior hybrid combination in Vegetable Pea. Garden Pea is an oldest domesticated grain legume in the world. It is cultivated during winter season in India which is a major source of protein (6.8%-7.2%) for human consumption. The present study was undertaken to study association analysis of pod yield with other quantitative traits and to estimate direct and indirect effects of various traits on pod yield.

## MATERIALS AND METHODS

The experimental material comprised 8 diverse genotypes of vegetable pea viz., AP-3, KS-280, KS-282, KS-111 and AP-1 obtained from Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur. Kashi Mukta, Kashi Nandani and Pant Uphar were obtained from IIVR, Varanasi and GBPUA&T, Pant Nagar. A set of 28 crosses were attempted during *rabi* 2018- 2019. Quite good number of crosses were attempted to produce sufficient F1 seed in each cross. The 28 crosses along with their 8 parents were grown in Randomized Block Design with 3 replications during *rabi* 2019-2020. The field chosen was as homogenous as possible. Recommended agronomic practices were adopted to raise a good crop. Each treatment was sown in single row plot of 4 m length. The inter and intra rows spacing was kept 25 cm and 15 cm, respectively. All the recommended agronomic practices were followed to raise a healthy crop. The data were recorded on randomly selected plants for each genotype on twelve morphological characters viz., days to 50 % flowering, plant height

(cm), number of branches per plant, Inter-nodal length (cm), first fruiting node, number of pod per cluster, number of pods, green pod yield per plant, pod length, pod width, number of seed per pod and shelling %.

Analysis of variance (ANOVA) was performed to estimate the variations among the genotypes using CPCS1 programme. Genetic parameters (Variance components, Genotypic and phenotypic coefficients of variation, correlations and path coefficients) were estimated the following formula was used for calculating the genotypic and phenotypic coefficients of correlation.

$$\text{Genotypic correlation } [r_{xy}(g)] = \frac{\text{Cov. } xy(g)}{\sqrt{[Vx(g) Vy(g)]}}$$

$$\text{Phenotypic correlation } [r_{xy}(p)] = \frac{\text{Cov. } xy(p)}{\sqrt{[Vx(p) Vy(p)]}}$$

Where,  
Cov. xy (g) and Cov. xy (p) = genotypic and phenotypic covariances, respectively. These were obtained as:

$$\text{Cov. } xy(p) = \frac{\text{Cov.}xy(g)+\text{Cov.}xy(e)}{r}$$

$$\text{Cov. } xy(g) = \frac{\text{Cov.}xy(p)-\text{Cov.}xy(e)}{r}$$

Vx (g) and Vy (g) = genotypic variance for the characters x and y, respectively.

Vx (p) and Vy (p) = phenotypic variance for the characters x and y, respectively.

Vx(e) and Vy(e) = error variance for characters x and y, respectively.

### Path coefficient analysis

Path coefficient analysis was carried out according to Dewey and Lu (1959). Path coefficients were estimated by solving the following simultaneous equation indicating the basic relationship between correlation and path coefficient. The equations used are as follows:

$$r_{ij} = P_{iy} + \sum_{j=1}^{10} r_{ij} P_{iy} \text{ for } i = 1, 2, \dots, 10$$

$$r_{ij} = \sum_{j=1}^{10} r_{ij} P_{iy} \text{ for } r_{ij} = 1$$

The above equations can be written in the form of matrix.

$$[A]_{10 \times 1} = [B]_{10 \times 1} [C]_{10 \times 1}$$

Where, A is column vector of correlations  $r_{ij}$ ; B is the correlation matrix of  $r_{ij}$  and C is the column vector of direct effect,  $P_{iy}$

Residual factor was calculated as follows:

$$P_{xyss} = \sqrt{1 - R^2}$$

$$R^2 = \sum_j P_{iy} r_{ij}$$

Where,

The  $r_{ij}$  i.e.  $r_{1,1}$  to  $r_{9,10}$  denote correlations between all possible combinations of independent characters  $P_{1y}$  to  $P_{10y}$  denote direct effects of various characters on character y.

$r_{iy}$  = Correlation coefficient between  $i^{th}$  and y characters.

$P_{iy}$  = Direct effect of  $i^{th}$  character on y.

## RESULTS AND DISCUSSION

The analysis of variance for parent and  $F_1$ 's for all 12 characters was carried out for testing the significance among the treatments. The mean square for all the traits are presented in (Table 1). The variance due to treatments were further partitioned in to components namely replication, parents,  $F_1$ 's and parents Vs  $F_1$ 's. Highly significant differences for all the characters were observed among parents and  $F_1$ 's. The variances were also noted for parents v/s  $F_1$ 's for days to 50% flowering, plant height, inter-nodal length, number of pods per plant, number of first fruiting node, number of grain per pod, pod yield per plant while the characters namely, number of branches per plant, number of pods per cluster, pod width and shelling (%) were non-significant. The significant variance indicating better scope for further improvement of breeding material by selection of promising genotype in crop improvement programme. The significant variance also observed by earlier workers viz., Singh *et al.*

Table 1: Analysis of Variance for parents and F<sub>1</sub> for 12 yield character derived from in 8x8 diallel cross in Garden pea

Source of variation	D.F.	Mean Square											
		Days to 50% flowering	Plant height (cm)	No of branch/plant	Inter-nodal length (cm)	No. of pod/cluster	No. of pod/plant	No of fruiting node	No of First grain/pod	Pod length (cm)	Pod width (cm)	Shelling %	Pod yield/plant(g)
Replication	2	4.77	3.22	0.01	0.77**	0.009	0.22	0.86**	0.009	0.424**	0.04 *	3.211	65.04**
Treatments	35	90.44**	1482.80 **	0.09**	3.05 **	0.06**	15.16**	6.41**	1.812**	1.540**	0.04**	74.26 **	500.39**
Parents	7	43.08 **	2420.47 **	0.07**	1.92**	0.05 *	31.85**	4.17***	2.26**	4.014**	0.06 **	63.08**	831.09**
F <sub>1</sub> s	27	86.89**	1284.36**	0.10**	3.40**	0.07**	9.14**	6.72**	1.63**	0.757**	0.04**	79.91**	417.86**
Parent Vs. F <sub>1</sub> s	1	518.00**	276.85***	0.02	1.67 **	0.001	60.76**	13.67 **	3.54**	5.379**	0.01	0.15	413.60**
Error	70	1.23	5.65	0.008	0.06	0.016	0.08	0.08	0.029	0.038	0.006	5.75	4.670
Total	107	30.48	488.79	0.035	1.06	0.032	5.01	2.16	0.61	0.536	0.020	28.11	167.951

Table 2: Phenotypic correlation for twelve characters in 8x8 diallel crosses in Garden pea

Attributes	Days to 50% flowering	Plant height (cm)	No of branch/plant	Inter-nodal length (cm)	No. of pod/cluster	No. of pod/plant	No of fruiting node	No of First grain/pod	Pod length (cm)	Pod width (cm)	Shelling %	Pod yield/plant(g)
Days to 50% flowering	1.000	0.397**	0.012	0.521**	-0.013	0.196*	0.001	-0.322**	-0.209*	-0.018	0.000	0.280**
Plant height (cm)		1.000	0.194*	0.743**	-0.047	-0.001	-0.010	0.060	-0.096	0.231*	0.036	0.364**
No of branch per plant			1.000	0.249**	-0.322**	0.292**	-0.331**	0.082	-0.011	0.301**	-0.136	-0.073
Inter-nodal length (cm)				1.000	0.214*	-0.226*	-0.130	-0.102	0.038	0.130	0.129	0.329**
No of pod per cluster					1.000	-0.346**	-0.312**	-0.027	0.412**	-0.129	0.197*	-0.315**
No. of pod per plant						1.000	0.067	0.041	-0.112	0.152	-0.200*	0.026
No of First fruiting node							1.000	0.156	-0.156	0.029	-0.022	0.202*
No of grains per pod								1.000	0.267**	0.061	-0.078	0.008
Pod length(cm)									1.000	-0.116	0.116	0.144
Pod width(cm)										1.000	-0.430**	0.129
Shelling %											1.000	0.125

Phenotypic correlation is given under parenthesis, \*significant at 5% level,\*\*significant at 1% level

Table 3: Direct and indirect effect of twelve characters on pod yield in 8x8 diallel crosses in Garden pea as independent variable at genotype level

Attributes	Days to 50% flowering	Plant height (cm)	No of branch/plant	Inter-nodal length (cm)	No. of pod/cluster	No. of pod/plant	No of first fruiting node	No of grain/pod	Pod length (cm)	Pod width (cm)	Shelling %	Pod yield/plant(g)
Days to 50% flowering	0.0946	-0.0171	-0.0071	0.2909	0.0111	0.0152	-0.0001	-0.0045	-0.0978	-0.0049	-0.0001	0.280**
Plant height (cm)	0.0376	-0.0431	-0.1129	0.4144	0.0391	-0.0001	0.0012	0.0008	-0.0449	0.0635	0.0079	0.364**
No of branch per plant	0.0012	-0.0083	-0.5825	0.1391	0.2679	0.0227	0.0380	0.0011	-0.0051	0.0826	-0.0295	-0.073
Inter-nodal length (cm)	0.0493	-0.0320	-0.1452	0.5579	-0.1781	-0.0175	0.0150	-0.0014	0.0177	0.0356	0.0280	0.329**
No of pod per cluster	-0.0013	0.0020	0.1876	0.1195	-0.8318	-0.0269	0.0358	-0.0004	0.1930	-0.0355	0.0428	-0.315**
No. of pod per plant	0.0185	0.0001	-0.1703	-0.1260	0.2880	0.0776	-0.0077	0.0006	-0.0527	0.0416	-0.0435	0.026
No of First fruiting node	0.0001	0.0004	0.1927	-0.0728	0.2595	0.0052	-0.1149	0.0022	-0.0733	0.0079	-0.0048	0.202*
No of grains per pod	-0.0305	-0.0026	-0.0480	-0.0571	0.0225	0.0032	-0.0179	0.0139	0.1249	0.0166	-0.0169	0.008
Pod length(cm)	-0.0197	0.0041	0.0063	0.0211	-0.3424	-0.0087	0.0180	0.0037	0.4688	-0.0319	0.0252	0.144
Pod width(cm)	-0.0017	-0.0100	-0.1751	0.0723	0.1074	0.0118	-0.0033	0.0008	-0.0544	0.2747	-0.0933	0.129
Shelling %	0.0000	-0.0016	0.0790	0.0720	-0.1640	-0.0155	0.0026	-0.0011	0.0544	-0.1181	0.2171	0.125

Residual effect (0.625), \*significant at 5% level, \*\*significant at 1% level

(2017), Lal *et al.* (2018) and Gupta *et al.* (2020) for all the characters in table pea.

**Correlation coefficients**

The grain yield or seed yield, in almost all the crops, is referred as main character, which results from multiplicative interactions of several other componential characters termed as yield contributing characters. Thus, identification of important yield components and information about their inter-relationship with other is very useful for developing efficient breeding strategy in developing high yielding varieties. In this respect, the correlation coefficient, which provides symmetrical measurement of degree of association between two variables or characters, help us to understand the nature and magnitude of association among yield and yield components. In the present investigation is presented in (Table 2) it was found that the genotypic correlation coefficients between different characters were generally similar in sign and nature to the corresponding phenotypic correlation coefficients. However, in general genotypic correlations were higher in magnitude from the corresponding phenotypic values which indicated that these correlations were due to pleiotropic effect of gene rather than linkages. Similar, results have been reported by Nawab *et al.* (2008), Sharma *et al.* (2009) and Singh *et al.* (2011). Pod yield per plant exhibited highly significant and positive correlation with plant height, number of branches per plant, days to 50% flowering; positive association with pod length, shelling percentage, pod width, Shelling percentage exhibited highly significant and positive correlation with pod width; positive association with number of pod per cluster, intermodal length. The positive and significant relationship between pod width, number of branches per plant; plant height, intermodal length and number of pod per plant. Pod length showed highly significant and positive association with number of pod per cluster and number of grain per pod; positive association with intermodal length and number of branches per plant. Number of grain per pod showed positive association with number of first fruiting node, intermodal length, number of branch per plant; negative and significant association with days to 50% flowering. Number of



first fruiting node positive correlation with days to 50% flowering. Number of pods per plant showed highly significant and positive correlation with number of branches per plant; negative and significant with intermodal length and number of pod per cluster. Number of pod per cluster exhibited non-significant and positive correlation with inter-nodal length. Number of branch per plant, with days to 50 per cent flowering and plant height. These findings are in accordance with earlier reported by Sharma *et al.* (2007) and Parihar *et al.* (2014)

#### Path coefficient analysis

Path-coefficient analysis is simple regression coefficient which split the correlation coefficient values into direct and indirect effects. It provides ample information helpful for effective indirect selection. It also provides very clear picture of character association for formulating efficient selection strategy. Path coefficient analysis differs from simple correlation in that to point out the cause and their relative importance, whereas, the later measures simply the mutual association ignoring the causation. In the present study path coefficient analysis are presented in Table 3 The highest positive and direct effect on pod yield per plant was exerted by inter-nodal length followed by number of grain per pod, pod length whereas very low positive and direct effect on pod yield per plant was exerted by days to 50 % flowering, number of pod per plant and number of grains per pod. It is supported by Kumar *et al.* (2014), Singh *et al.* (2019). Highly positive and indirect effect on pod yield per plant was exerted by shelling percentage via number of pod per cluster, pod length and plant height; pod width via number of branch per plant, plant height ; pod length via number of pod per cluster, number of grain per pod, inter-nodal length; number of grain per pod via number of first fruiting node, number of branch per plant; number of first fruiting node via number of branch per plant, number of pod per cluster; number of pod per plant via number of branch per plant and days to 50 % flowering; number of pod per cluster via number of branch per plant and plant height; inter-node length via plant height ,days to 50 % flowering. The finding of Singh *et al.* (2019) supported this result.

#### CONCLUSION

On the results of Correlation study revealed that pod yield per plant exhibited highly significant and positive correlation with plant height, number of branches per plant, days to 50% flowering, pod length, shelling percentage and pod width. The highest positive and direct effect on pod yield per plant was exerted by intermodal length followed by number of grain per pod and pod length. it can be utilized for further crop improvement programme and may be used for selection of transgressive segregants.

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Received: September 20, 2023

Accepted: December 9, 2023