CORRELATION AND PATH COEFFICIENT ANALYSIS FOR YIELD AND COMPONENT TRAITS IN PEA (*PISUM SATIVUM* L.)

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Abstract

Twenty eight pea genotypes were evaluated for their genetic variability attributes under sub-tropical conditions of Himachal Pradesh during *Rabi*, 2021. The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high for plant height and pod weight. High heritability along with high genetic advance was observed in days to first flower, node at which first flower appear, days to 50 % flowering, pod length, pod weight, number of primary branches per plant, plant height, number of pods per plant and number of seeds per pod. Pod yield was positively and significantly correlated with pod length, pod weight, pod width, pod girth, number of pods per plant, number of seeds per pod, shelling percentage and TSS. The pod length exhibited highly positive and direct effect on pod yield followed by pod weight and plant height. Therefore, selection based on these traits could be effective for higher pod yield in pea genotypes.

Introduction

Pea (*Pisum sativum* L.) belongs to the family Fabaceae and has a diploid chromosome number of $2n = 2x = 14$. It is a highly nutritive crop with a high percentage of digestible protein (23-33%), carbohydrates (42.65%), fibres (13.4%), vitamin-A, calcium and magnesium and antioxidant compounds (Urbano *et al.* 2003). It is also high in lysine, an important amino acid which is absent in cereals.

Pea is an important crop for the vegetable growers of Himachal Pradesh, covering an area of 25.99 thousand hectare with a production of 328.80 thousand metric tonnes and a productivity of 12.65 t/ha. In spite of such economic importance, pea production per unit area remains low in the country due to a lack of high yielding varieties with poor or no disease resistance. Hence, there is an urgent need to evaluate a large number of genotypes and identify high yielding and superior pea varieties that can be released commercially as such or incorporated into future crop breeding programme to improve yield and other horticultural traits.

Yield is influenced by a number of genetic factors that interact with the environment. Therefore, the success of any breeding programme is determined by the genetic variability of the base population as well as selection efficiency (Kumari *et al.* 2008). Heritability indicates the proportion of phenotypic variance that is due to genotypes which is heritable. It is a useful guide for breeders because selection for a trait with high heritability will be effective and improvement will be achieved through selection. The selection procedures can be improved further by learning about the correlations between different characters and gaining a better understanding of the relationship between these traits and yield through path coefficient analysis. Therefore, the study was undertaken to find out the genetic variability, association among yield contributing traits and effects of each of the component traits towards yield.

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Materials and Methods

Twenty eight pea genotypes was studied at the Experimental Research Farm of the Department of Vegetable Science, College of Horticulture and Forestry, Neri, Hamirpur (HP) situated at an elevation of 650 m above mean sea level with $31^{o}41'47.6"$ N latitude and $72^{o}28'6.3"$ E longitude. Among twenty eight genotypes, twenty were collected from NBPGR, New Delhi and one each from IARI, New Delhi; CSAUA&T, Kanpur; IARI Regional Station, Katrain; PAU, Ludhiana and four were the local collection. Seeds were sown in the field in October, 2021 at a spacing of 60 X 10 cm in a plot size of 1.8 X 0.8 m. Each genotype was sown in a Randomized Complete Block Design (RCBD) with three replications. The standard cultural practices as recommended in the Package of Practices of Vegetable Crops were followed to raise a healthy crop. The observations were recorded on ten randomly selected plants of each genotype in each replication for the trait. The mean values were statistically analysed in order to compute ANOVA for all of the characters, as suggested by Panse and Sukhatme (1997). The phenotypic and genotypic coefficients of variation were calculated as per the formula given by Burton and De Vane (1953). The genotypic and phenotypic correlations were assessed using the method proposed by Al-Jibouri *et al.* (1958). The effects were obtained following the methods of Dewey and Lu (1959).

Results and Discussion

The analysis of variance revealed that there were significant differences between genotypes for all of the horticultural traits. Variability among 28 genotypes of pea for each of the traits measured in terms of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance as percent of mean are given in Table 1. For all the characters studied, the phenotypic coefficient of variation was greater than the genotypic coefficient of variation, indicating the influence of environmental factors on character expression. However, the difference between PCV and GCV is minute revealing less influence of environmental factors on these traits offering ample scope for improvement. The phenotypic and genotypic coefficient of variation ranged from 8.01 to 40.96 % and 7.60 to 39.59 %, respectively. Maximum phenotypic and genotypic coefficient of variation was observed for pod weight. High phenotypic and genotypic coefficients of variation were also observed for plant height and number of primary branches per plant reflecting presence of high genetic variability among all the genotypes for these traits and offered better scope for improvement (Table 1). These findings are in close confirmity with the results obtained by Singh *et al.* (2011), Kumar *et al.* (2014), Jeberson *et al.* (2016), Gautam *et al.* (2017), Khan *et al.* (2017) and Devi *et al.* (2018). Moderate phenotypic and genotypic coefficients of variation were recorded for the traits pod yield, number of pods per plant, pod length, number of seeds per pod, node at which first flower appear, total soluble solids, days to 50 % flowering and days to first flower which was in consonance with the findings of Kumar *et al.* (2015), Khan *et al.* (2017), Devi *et al.* (2018) and Singh *et al.* (2019).

In the present investigation the magnitude of broad sense heritability ranged from 67.83 to 99.13 % and high heritability was shown by all the traits except total soluble solids, pod yield per plot and shelling percentage (Table 1). High heritability along with high genetic advance as percentage of mean was recorded for traits such as days to first flower, node at which first flower appear, days to 50 % flowering, pod length, pod weight, number of primary branches per plant, plant height, number of pods per plant and number of seeds per pod indicating that most likely the heritability for these characters is due to additive gene effects, which in turn offers good scope for effective selection. High heritability coupled with moderate genetic advance was recorded in pod width, pod girth and days to marketable maturity which may be attributed to additive and non-

additive gene effects. The reported findings were consistent with Kumar *et al.* (2015), Devi *et al.* (2017), Gautam *et al.* (2017), Azam *et al.* (2020) and Bahadur and Devi (2021). Moderate heritability accompanied with moderate genetic advance was observed for the characters shelling percentage and total soluble solids which is in agreement with the findings of Kumar *et al.* (2015) and Devi *et al.* (2017). These traits were influenced by effects of environment and selection would be ineffective due to non-additive gene action.

Results of a correlation analysis showed that genotypic correlation coefficients were higher in magnitude than phenotypic correlation coefficients indicating the inherent association between various characters (Table 2). Present study indicated that the genotypic and phenotypic correlation coefficients among different characters showed that pod yield had positive and significant association with pod length, pod weight, pod width, pod girth, number of pods per plant, number of seeds per pod, shelling percentage and total soluble solids. This reflects the strong genetic association between the above characters and pod yield hence selection on the basis of these traits might lead to higher pod yield in pea. These results are similar with the findings of Katoch *et al.* (2016), Gautam *et al.* (2017) and Devi *et al.* (2018). Kumar *et al.* (2015) and Devi *et al.* (2017) also reported positive correlation of pod yield with number of pods per plant, pod length, number of seeds per pod, shelling percentage and total soluble solids suggesting these are major yield contributing traits. Negative correlations at genotypic and phenotypic levels were recorded for the traits days to first flower, node at which first flower appear, days to 50% flowering and days to marketable maturity, indicating that these characteristics should be considered for crop earliness which are in accordance with the findings of Kumar *et al.* (2014).

The path coefficient analysis quantifies the direct and indirect impact of various independent variables on a dependent variable (Table 3). It plays an important role in effective crop improvement programme by identifying various yield contributing traits and providing accurate information about indirect selection. Path coefficient analysis at genotypic level indicated that the maximum positive direct effect on pod yield was observed by trait pod length. Further, pod weight, plant height, node at which first flower appear, number of pods per plant, total soluble solids, days to marketable maturity, pod width, days to 50 % flowering and shelling percentage also had positive direct effect on pod yield which indicated that these were the main traits contributing to yield which was in agreement with the findings of Kumar *et al.* (2014), Kumar *et al.* (2015), Katoch *et al.* (2016), Devi *et al.* (2017), Gautam *et al.* (2017), Bhardwaj *et al.* (2020) and Naeem *et al.* (2020). While, negative direct effects was observed for the traits pod girth, days to first flower, number of seeds per pod and number of primary branches per plant. Rai *et al.* (2006) assessed path analysis in pea and showed significant positive direct effects of number of pods per plant and plant height towards yield per plant which is in accordance with the present study. Devi *et al.* (2017) in their studies also revealed that direct effects were higher for pod length, number of pods per plant, days to 50 % flowering, total soluble solids and pod width.

Based on the performance of the genotypes it is concluded that the genotypes Pusa Pragati, LC-P-1 and LC-P-2 were recorded superior in pod yield and other important horticultural traits. Correlation study revealed highly significant and positive correlation of pod yield with pod length, pod weight, pod width, pod girth, number of pods per plant, shelling percentage and total soluble solids. Pod length exhibit the highest positive direct effect towards pod yield followed by pod weight, plant height, node at which first flower appear, number of pods per plant, total soluble solids, days to marketable maturity, pod width, days to 50% flowering and shelling percentage. So, selection based on these traits will be worthwhile for any breeding programme.

Table 1. Estimation of different genetic parameters for various horticultural traits in pea (*Pisum sativum* L.).

Horticultural traits	Mean	Range	Coefficient of variation (%)		Heritability (%)	Genetic advance as % mean
			Phenotypic	Genotypic		
Days to first flower (DFF)	73.74	54.67-91.00	11.22	10.63	89.65	20.73
Node at which first flower appear (NFF)	12.02	7.47-15.67	15.59	14.83	90.58	29.08
Days to 50 % flowering (DFPF)	79.56	61.33-98.00	11.59	10.79	86.57	20.67
Pod length (cm) (PL)	7.83	6.55-11.07	16.15	16.07	99.03	32.95
Pod weight (g) (PW)	4.67	3.12-9.77	40.96	39.59	93.39	78.81
Pod width (cm) (PW)	1.21	1.07-1.46	8.84	7.97	81.25	14.80
Pod girth (cm) (PG)	3.98	3.56-4.74	8.16	7.60	86.77	14.59
Number of primary branches per plant (NPBPP)	11.35	6.25-16.42	21.89	19.89	82.54	37.23
Plant height (cm) (PH)	175.24	90.08-223.33	27.89	27.77	99.13	56.96
Number of pods per plant (NPPP)	32.72	25.50-45.83	16.50	15.49	88.06	29.94
Number of seeds per pod (NSPP)	6.49	5.00-9.00	15.87	14.22	80.26	26.25
Shelling percentage (%) (SP)	52.25	41.16-60.30	9.93	8.84	79.41	16.24
Days to marketable maturity (DMM)	132.53	108.67-143.33	8.01	7.86	96.33	15.89
Total soluble solids (^{0}B) (TSS)	13.39	10.34-16.46	14.25	11.74	67.83	19.92
Pod yield (kg/plot) (PY)	2.29	1.49-3.13	19.22	16.29	71.91	28.46

Table 2. Genotypic and phenotypic coefficients of correlation among various horticultural traits in pea.

Traits		DFF	NFF	DFPF	PL	PW	PW	PG	NPBPP	PH	NPPP	NSPP	SP	DMM	TSS	PY
DFF	G	1														
	P	1														
NFF	G	0.946**	1													
	P	0.870**	1													
DFPF	G	0.995**	0.922**	1												
	P	0.893**	0.843**	1												
PL	G	-0.749**	-0.837**	-0.670**	1											
	P	-0.705**	-0.788**	-0.615**	1											
PW	G	-0.828**	-0.888**	-0.722**	0.972**	1										
	P	-0.741**	-0.804**	-0.649**	0.945**	1										
PW	G	-0.645**	-0.707**	-0.525**	0.837**	0.852**	1									
	P	-0.540**	-0.598**	-0.431**	0.774**	0.782**	1									
PG	G	-0.678**	-0.739**	-0.578**	0.885**	0.913**	0.955**	1								
	P	-0.606**	-0.648**	-0.509**	0.825**	0.868**	0.839**	1								
NPBPP	G	0.076	0.192	0.004	-0.388**	-0.403**	-0.163	-0.375**	1							
	P	0.056	0.171	0.046	-0.352**	-0.354**	-0.172	-0.319**	1							
PH	G	0.415*	0.484**	0.350*	-0.653**	-0.616**	-0.360**	-0.441**	0.700**	1						
	P	0.390**	0.455**	0.314*	-0.648**	-0.597**	-0.328**	-0.418**	0.636**	1						
NPPP	G	-0.126	-0.098	-0.223*	-0.112	-0.093	-0.120	-0.176	0.425**	0.437**	1					
	P	-0.126	-0.083	-0.215*	-0.106	-0.072	-0.095	-0.149	0.355**	0.405**	1					
NSPP	G	-0.665**	-0.698**	-0.602**	0.797**	0.809**	0.590**	0.596**	-0.270*	-0.435**	-0.085	1				
	P	-0.531**	-0.581**	-0.497**	0.718**	0.720**	0.508**	0.493**	-0.185	-0.385**	-0.069	1				
SP	G	-0.474**	-0.463**	-0.476**	0.512**	0.480**	0.416**	0.471**	-0.028	-0.230*	0.333**	0.170	1			
	P	-0.424**	-0.381**	-0.405**	0.453**	0.415**	0.335**	0.399**	0.002	-0.202	0.316**	0.151	1			
DMM	G	0.909**	0.884**	0.829**	-0.890**	-0.926**	-0.757**	-0.772**	0.240*	0.570**	0.095	-0.865**	-0.427**	1		
	P	0.844**	0.831**	0.761**	-0.871**	-0.879**	-0.669**	-0.714**	0.212	0.556**	0.079	-0.759**	-0.391**	1		
TSS	G	-0.643**	-0.674**	-0.611**	0.657**	0.648**	0.621**	0.560**	-0.038	-0.388**	-0.113	0.598**	0.434**	-0.673**	1	
	P	-0.533**	-0.563**	-0.432**	0.539**	0.496**	0.456**	0.458**	0.045	-0.328*	-0.120	0.372**	0.308**	-0.553**	1	
PY	G	-0.834**	-0.828**	-0.834**	0.677**	0.714**	0.582**	0.594**	0.181	-0.059	0.585**	0.657**	0.636**	-0.732**	0.632**	1
	P	-0.643**	-0.673**	-0.642**	0.578**	0.610**	0.445**	0.476**	0.162	-0.060	0.475**	0.504**	0.459**	-0.639**	0.446**	1

*, **Significant at 5% and 1% level respectively. Abbreviations are similar as in Table 1.

Table 3. Genotypic path coefficient analysis for effects of various traits on pod yield per plot in pea.

Traits	DFF	NFF	DFPF	PL	PW	PW	PG	NPBPP	PH	NPPP	NSPP	SP	DMM	TSS	GCPY
DFF	**-0.857**	0.448	0.033	-0.765	-0.811	-0.120	0.732	-0.018	0.331	-0.037	0.175	-0.012	0.230	-0.163	-0.834[**]
NFF	-0.811	**0.474**	0.031	-0.855	-0.869	-0.132	0.798	-0.045	0.386	-0.029	0.183	-0.012	0.224	-0.171	-0.828[**]
DFPF	-0.853	0.437	**0.033**	-0.685	-0.707	-0.098	0.624	-0.001	0.280	-0.065	0.158	-0.012	0.210	-0.155	-0.834[**]
PL	0.642	-0.396	-0.022	**1.021**	0.951	0.156	-0.956	0.090	-0.521	-0.033	-0.209	0.013	-0.226	0.167	0.677[**]
PW	0.710	-0.421	-0.024	0.992	**0.979**	0.159	-0.986	0.094	-0.491	-0.027	-0.213	0.012	-0.235	0.165	0.714[**]
PW	0.553	-0.335	-0.017	0.855	0.834	**0.186**	-1.031	0.038	-0.287	-0.035	-0.155	0.010	-0.192	0.158	0.582[**]
PG	0.581	-0.350	-0.019	0.905	0.894	0.178	**-1.080**	0.088	-0.352	-0.052	-0.157	0.012	-0.196	0.142	0.594[**]
NPBPP	-0.065	0.091	0.000	-0.396	-0.395	-0.030	0.405	**-0.233**	0.558	0.125	0.071	-0.001	0.061	-0.010	0.181
PH	-0.356	0.229	0.012	-0.667	-0.603	-0.067	0.477	-0.163	**0.797**	0.128	0.114	-0.006	0.144	-0.098	-0.059
NPPP	0.108	-0.046	-0.007	-0.115	-0.091	-0.022	0.189	-0.099	0.349	**0.294**	0.022	0.008	0.024	-0.029	0.585[**]
NSPP	0.570	-0.330	-0.020	0.814	0.792	0.110	-0.644	0.063	-0.347	-0.025	**-0.263**	0.004	-0.219	0.152	0.657[**]
SP	0.407	-0.219	-0.016	0.522	0.470	0.078	-0.508	0.006	-0.184	0.098	-0.045	**0.025**	-0.108	0.110	0.636[**]
DMM	-0.779	0.419	0.028	-0.910	-0.907	-0.141	0.834	-0.056	0.454	0.028	0.227	-0.011	**0.253**	-0.171	-0.732[**]
TSS	0.551	-0.319	-0.020	0.671	0.635	0.116	-0.605	0.009	-0.309	-0.033	-0.157	0.010	-0.171	**0.254**	0.632[**]

Residual effect = 0.05365. Abbreviations are similar as in Table 1.

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