Variability and Character Association Study for Horticultural Traits in Vegetable Pea (*Pisum sativum* var. *hortense* L.) under East-Indian Climatic Conditions

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ABSTRACT

Vegetable pea is a very widely grown and popular vegetable crop. It is the second most important food legume worldwide after French bean. The average productivity of garden pea is low in Bihar (6.31t/ha) when compared with National average (9.98t/ha). To improve the productivity, it is essential to identify and breed new garden pea genotypes. For the improvement of any crop genetic variability is the basic requirement. Abundant genetic variation is present in *Pisum sativum* (Blixt 1974). For the improvement of genetic behavior of the crop understanding of genetic variability exist in that crop for different characters and is an essential tool for identification of suitable genes and their nature of association. The investigation was comprised of 28 Vegetable pea genotypes and the experiment was conducted at the Experimental farm of the Department of Horticulture (Vegetable and Floriculture), Bihar Agricultural College, BAU, Bihar during 2018-19. All the morphological and biochemical data were recorded. Results indicated that PCV and GCV were high for first flower node, number of primary branches, internodal length, ascorbic acid and total sugar. These high estimates indicated that there is substantial variability ensuring ample scope for improvement of these traits through simple selection. At both phenotypic and genotypic levels pod yield per plant had shown a positive and significant correlation with pod length, seeds per pod, shelling (%), plant height, and pods per plant. Selection on the basis of these traits might lead to higher yield.

Keywords Variability, Correlation, Yield, Garden pea.

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INTRODUCTION

Vegetable pea (*Pisum sativum* var. *hortense* L.), a member of Leguminosae (Fabaceae) family, and is a very widely grown and popular vegetable crop. It is the second most important food legume worldwide after *Phaseolus vulgaris* (Taran *et al.* 2005). It is a rich source of protein, amino acids and carbohydrates. Peas are highly nutritive and are rich source of digestible proteins (7%), along with carbohydrates and minerals. It is used as a fresh vegetable or in soup, canned, processed or dehydrated. Worldwide vege-

table pea occupies an area of 2.66 million hectares, production of 20.67 million tonnes and productivity of 7.75 t/ha. In India, area of 0.053 million hectares, production 5.345 million tonnes and productivity of 10.08 t/ha. In Bihar, it occupies an area 10,510 ha with a production of 66,360 tonnes and the productivity is 6.31 t/ha (Horticultural Statistics at a Glance 2017). The average productivity of vegetable pea is low in Bihar (6.31t/ha) when compared with National (10.08t/ha) and world average (7.5 t/ ha). Hence the investigation was carried out to identify high yielding genotypes for Bihar condition.

For the improvement of any crop genetic variability is the basic requirement (Azmat *et al.* 2011). Abundant genetic variation is available in *Pisum sativum* (Blixt 1974). For the improvement of genetic behaviour of the crop understanding of genetic variability exist in that crop for different characters and is an essential tool for identification of suitable genes and their nature of adherence (Nwangburuka *et al.* 2011). Heritability indicates the proportion of phenotypic variance that is due to genotypes which is heritable. It serves as a useful guide to breeders as the selection for trait having high heritability. The genetic advance is an improvement in the genetic value of new population as compared to original one. It will be possible to decide various breeding program for improvement of different characters based on the study of heritability and genetic advance (Kumari *et al.* 2012). Correlation measures the mutual relationship between different plant characters and determines the component characters on which selection can be based for improvement in yield. The objective of this study was to identify the nature and quantum of genetic variability and to study character association between yield and related traits in Vegetable pea.

MATERIALS AND METHODS

The experimental material for the present study comprised of 28 genotypes of vegetable pea (*Pisum sativum* var. *hortense* L.). These genotypes were evaluated during *rabi* season at the Experimental farm of the Department of Horticulture (Vegetable and Floriculture), Bihar Agricultural College, BAU, Sabour, Bhagalpur, Bihar during 2018-19. The experiment was laid out in Complete Randomized Block Design with three replications. The pea seeds were sown at a spacing of 30 cm × 10 cm during the first week of October. Recommended package of practices were followed for healthy growth of the crop. The observations were recorded on randomly taken five plants of each genotype in each replication followed by computing their means for the horticultural and quality traits. The data were statistically analyzed as per the standard procedure for analysis of variance (Panse and Sukhatme 1967), Phenotypic and genotypic variance as per Burton (1953), Heritability (broad sense) as per Lush (1949), Genetic advance as per Lush (1949) and Johnson *et al.* (1955) and correlation coefficients (Al-Jibouri *et al.* 1958).

RESULTS AND DISCUSSION

The estimates of variability parameters revealed that in general, phenotypic coefficient of variation (PCV) were higher in magnitude than the corresponding genotypic coefficient of variation (GCV) for all the characters studied in present investigation. Variability parameters revealed that high magnitude of PCV and GCV respectively were observed for the traits like first flower node (35.28 and 31.80), number of primary branches (56.03 and 54.45), internodal length (33.94 and 33.08), ascorbic acid (32.17 and 32.12) and total sugar (41.54 and 41.34) (Table 1). Earlier researchers also observed high amount of PCV and GCV values for number of primary branches per plant (Singh *et al.* 2014); intermodal length (Guleria *et al.* 2009) and total sugar (Kumar *et al.* 2015). Results indicated the differences in the genetic material used and change in the growing conditions. It necessitates the use of selection procedure in the current genetic material for respective traits very cautiously. Moderate amount of PCV and GCV were observed for days to first flower (20.03 and 18.12), days to 50% flowering (18.91 and 16.78), nodes per plant (22.05 and 20.35), seeds per pod (21.09 and 18.53), shelling percentage (11.58 and 10.44), number of pickings (20.01 and 15.37), pod length (14.69 and 13.61), pods per plant (28.37 and 25.44), pod yield per plant (24.94 and 21.22) and total soluble solids (22.54 and 18.96) respectively. Whereas low amount of PCV and GCV were observed for days to first picking (8.16 and 7.75) and protein content (9.15 and 9.13) respectively. Similar findings of low estimates of PCV and GCV

Table 1. Estimates of parameters of variability for different characters in Vegetable pea.

Traits	Range	Population mean	GCV	PCV	h^2_{bs}	GAM (%)
Growth parameters						
Days to first flower	38.80-68.20	51.53	18.12	20.03	81.84	33.76
Days to 50% flowering	43.67-75.33	60.69	16.78	18.91	78.75	30.67
First flower node	4.77-13.27	8.07	31.8	35.28	81.24	59.04
Days to first picking	71.18-102.41	86.20	7.75	8.16	90.26	15.17
No. of primary branches	1.40-8.27	2.62	54.45	56.03	94.43	100
Internodal length (cm)	2.09-7.86	3.54	33.08	33.94	94.95	66.39
Nodes per plant	16.96-37.32	24.84	20.35	22.05	85.16	38.68
Plant height (cm)	48.93-150.80	71.06	29.99	30.56	96.32	60.64
Yield contributing traits						
Pod length (cm)	6.09-10.66	8.50	13.61	14.69	85.79	25.97
Seeds per pod	3.73-8.50	5.82	18.53	21.09	77.12	33.51
Shelling (%)	36.13-58.17	47.20	10.44	11.58	81.27	19.39
Pods per plant	12.09-33.73	18.34	25.44	28.37	80.47	47.02
No. of pickings	2.00-4.00	3.10	15.37	20.01	58.97	24.31
Pod yield per plant (g)	55.56-117.34	80.37	21.22	24.94	70.81	32.87
Quality characters						
TSS (°Brix)	7.50-19.36	13.86	18.96	22.54	94.09	36.34
Ascorbic acid (mg/100g)	10.36-30.01	18.26	32.12	32.17	99.68	66.06
Protein (%)	24.65-36.01	30.01	9.13	9.15	99.54	18.77
Total sugars (%)	2.95-10.94	4.52	41.34	41.54	99.01	84.73

were also reported by Barcchiya *et al.* (2018) for protein content and Pathak and Jamwal (2002) for days to first picking.

In the present study, high heritability estimates (>60%) were recorded for all the characters which were studied such as days to first flower (81.84), first flower node (81.24), days to 50% flowering (78.75), days to first picking(90.26), number of primary branches (94.43), nodes per plant (85.16), plant height (96.32), pod length (85.79), shelling percentage (81.27), seeds per pod (77.12), pods per plant (80.47), pod yield per plant (70.81), total soluble solids (94.09), ascorbic acid (99.68), protein content (99.54) and total sugar (99.01) except no. of pickings. The results indicate that almost all of the variability in a trait comes from genetic differences, with very small influence of environmental factors. High heritability estimates were also reported for days to first flowering, days to 50% flowering and primary branches per plant (Ali *et al*. 2018), first flower node (Kumar *et al*. 2015), days to first picking (Sharma and

Bora 2011), plant height and pod per plant (Ceyhan *et al.* 2012), seeds per pod and pod yield per plant (Gupta *et al.* 2018).

For a useful selection program, just the knowledge of heritability is not sufficient and therefore it is helpful to study genetic advance all along with heritability. The high genetic advance expressed as percent of mean (>30%) was observed for days to first flower (33.76), days to 50% flowering (30.67), first flower node (59.04), number of primary branches (100), nodes per plant (38.68), internodal length (66.39), plant height (60.64), seeds per pod (33.51), pods per plant (47.02), pod yield per plant (32.87), TSS (36.34), ascorbic acid (66.06) and total sugars (84.73) (Table 1). High degree of genetic advance was also revealed for days to first flower, pod yield per and plant height by Gudadinni *et al.* (2017); for days to 50% flowering and number of primary branches per plant by Ali *et al*. (2018); for seeds per pod and pods per plant by Gupta *et al*. (2018).

High heritability together with high genetic advance was observed for days to first flower (81.84 and 33.76), days to 50% flowering (78.75 and 30.67), first flower node (81.24 and 59.04), number of primary branches (94.43 and 100), internodal length (94.95 and 66.39), nodes per plant (85.16 and 38.68), plant height (96.32 and 60.64), seeds per pod (77.12 and 33.51), pods per plant (80.47 and 47.02), pod yield per plant (70.81 and 32.87), TSS (94.09 and 36.34), ascorbic acid (99.68 and 66.06) and total sugars (99.01 and 84.73). The higher estimates of heritability and GAM suggesting the role of additive dominance and thereby use of simple selection for improvement of these characters. These higher estimates of broad

sense heritability and genetic advance as per cent of mean were in consonance with the results obtained by Ali *et al.* (2018) for days to first flower and Gupta *et al.* (2018) for days to 50% flowering.

Correlation coefficients

Genotypic correlation coefficients were higher in magnitude than their respective phenotypic correlation coefficients for most of the characters studied (Table 2). In the present study, pod yield per plant exhibited a positive and significant correlation at both phenotypic and genotypic levels with pod length, seeds per pod, shelling (%), plant height and pods

Table 2. Estimation of phenotypic (P) and genotypic (G) correlation coefficient for different horticultural traits in garden pea.

Trait		Days to first flower	Days to 50% flowering	First flower node	Pod length (cm)	Seeds/pod	Shelling (%)	TSS (°B)	Days to first picking)	Plant height (cm)
Days to 50% flowering	P	0.89**								
	G	0.97**								
First flower node	P	0.79**	0.73**							
	G	0.95**	0.82**							
Pod length (cm)	P	0.03	-0.06	0.06						
	G	0.03	-0.05	0.15						
Seeds / pod	P	-0.15	-0.14	-0.16	0.54**					
	G	-0.16	-0.15	-0.15	0.67**					
Shelling (%)	P	-0.03	-0.01	0.00	0.20	0.34**				
	G	-0.04	0.00	0.03	0.22*	0.42**				
TSS (°B)	P	-0.08	-0.03	-0.01	0.15	-0.10	-0.11			
	G	-0.06	-0.04	-0.01	0.17	-0.12	-0.11			
Days to first picking	P	0.42**	0.50**	0.33**	-0.23*	-0.22*	-0.12	-0.17		
	G	0.57**	0.63**	0.39**	-0.23*	-0.27*	-0.11	-0.21		
Plant height (cm)	P	0.30**	0.32**	0.32**	-0.31**	-0.11	-0.09	-0.41**	0.35**	
	G	0.35**	0.37**	0.36**	-0.33*	-0.14	-0.1	-0.43**	0.37**	
No. of primary branches	P	0.13	0.24*	0.07	-0.30**	-0.27*	-0.07	-0.06	0.33**	0.16
	G	0.13	0.24*	0.07	-0.32**	-0.33**	-0.08	-0.07	0.37**	0.17
Nodes / plant	P	0.44**	0.48**	0.30**	-0.16	-0.14	-0.30**	0.10	0.47**	0.39**
	G	0.49**	0.52**	0.27*	-0.14	-0.15	-0.35**	0.09	0.51**	0.41**
Pods / plant	P	0.09	0.14	-0.04	-0.45*	-0.05	0.00	-0.40**	0.28**	0.61**
	G	0.09	0.15	-0.07	-0.51	-0.11	0.03	-0.46**	0.32**	0.68**
No. of pickings	P	0.26*	0.30**	0.07	-0.28**	-0.19	-0.13	-0.06	0.28**	0.31**
	G	0.39**	0.42**	0.11	-0.43**	-0.23*	-0.16	-0.08	0.41**	0.42**
Total sugar (%)	P	0.03	0.11	-0.1	0.07	0.15	0.02	0.15	-0.07	-0.23*
	G	0.03	0.12	-0.11	0.07	0.18	0.02	0.16	-0.08	-0.24*
Intermodal length (cm)	P	-0.11	-0.14	0.02	-0.14	0.00	0.21	-0.46*	-0.04	0.53**
	G	-0.11	-0.12	0.07	-0.16	0.00	0.24*	-0.47**	-0.02	0.55**
Ascorbic acid (mg/100g)	P	0.13	0.15	0.18	0.06	0.11	0.10	-0.10	0.21	0.12
	G	0.14	0.16	0.19	0.07	0.12	0.11	-0.10	0.22*	0.12
Protein (%)	P	0.40**	0.39**	0.39**	0.05	-0.06	0.20	-0.09	0.23*	0.03
	G	0.43**	0.44**	0.43**	0.06	-0.07	0.22*	-0.09	0.24*	0.03
Yield / plant (g)	P	0.03	0.01	0.06	0.31**	0.25*	0.22*	-0.13	0.09	0.24*
	G	0.04	0.02	0.06	0.40**	0.36**	0.31**	-0.14	0.09	0.32**

Table 2. Continued.

Trait		No. of primary branches	Nodes / plant	Pods / plant	No. of pickings	Total sugar (%)	Intermodal length (cm)	Ascorbic acid (mg/100g)	Protein (%)
Days to 50% flowering	P								
	G								
First flower node	P								
	G								
Pod length (cm)	P								
	G								
Seeds / pod	P								
	G								
Shelling (%)	P								
	G								
TSS (˚B)	P								
	G								
Days to first picking	P								
	G								
Plant height (cm)	P								
	G								
No. of primary branches	P								
	G								
Nodes / plant	P	0.06							
	G	0.06							
Pods / plant	P	0.17	0.22*						
	G	0.19	0.27*						
No. of pickings	P	0.41*	0.35**	0.42**					
	G	0.52**	0.47**	0.50**					
Total sugar (%)	P	0.02	0.10	-0.29**	0.05				
	G	0.03	0.10	-0.32**	0.07				
Intermodal length (cm)	P	0.13	-0.52**	0.32**	0.01	-0.29**			
	G	0.14	-0.52**	0.38**	0.04	-0.30**			
Ascorbic acid(mg/100g)	P	0.09	-0.06	-0.10	-0.22*	0.06	0.13		
	G	0.10	-0.06	-0.11	-0.28**	0.06	0.14		
Protein (%)	P	0.11	0.04	-0.03	-0.100	0.22*	-0.05	0.48**	
	G	0.11	0.04	-0.04	-0.14	0.22*	-0.06	0.48**	
Yield / plant (g)	P	-0.18	0.04	0.35**	-0.07	-0.27*	0.18	0.07	0.03
	G	-0.24*	0.06	0.49**	-0.11	-0.31**	0.20	0.09	0.04

*Significant at P ≤ 0.05.

per plant. Results indicated that these are major traits contributing towards increased yield. Pod yield per plant had revealed negative and significant association at both genotypic and phenotypic levels with number of primary branches and total sugar.

Among the growth parameters, days to first flower had significant positive association with days to 50% flowering, first flower node, days to first picking, plant height, nodes per plant, no. of pickings, protein content, pod length, no. of primary branches, pods per plant, total sugar, ascorbic acid and yield per plant both at genotypic and phenotypic

level thereby implying for indirect selection of these traits for earliness. Kumar and Sharma (2006) also reported significant positive relationship of days to first flower with days to first picking in their study. While negative association was observed with seeds per pod, shelling (%) and internodal length.

Days to 50% flowering was significantly and positively correlated with first flower node, days to first picking, plant height, no. of primary branches, no. of pickings and protein content both at phenotypic and genotypic level. Earlier workers also reported significant and positive association of days to 50% flowering

with days to first picking (Katoch *et al*. 2018) and no. of primary branches (Gautam *et al*. 2017). Contrary to the present findings, Singh and Yadav (2005) found negative correlation between days to 50 % flowering and no. of primary branches per plant.

Pod length was significantly and positively correlated with seeds per pod and pod yield per plant both at genotypic and phenotypic level indicating the strong relationship of these traits for direct selection while going for improvement of yield indirectly. Pod length was significantly and negatively correlated with days to first picking, plant height, no. of primary branches and no. of pickings. Similar findings were also observed by previous workers for significant and positive association of pod length with pod yield per plant (Kumar *et al*. 2004) and seeds per pod (Katoch *et al.* 2018).

A significant positive association was noticed for seeds per pod with TSS and pod yield per plant both at genotypic and phenotypic level. Seeds per pod also were significantly and negatively associated with days to first picking and no. of primary branches per plant. Shelling (%) was significantly and positively correlated with pod yield per plant, internodal length, total sugar, ascorbic acid and protein content while negatively correlated with nodes per plant, TSS, plant height, pods per plant, no. of pickings and protein content. A significant positive association was noticed for plant height with nodes per plant, pods per plant, no. of pickings, internodal length, pod yield per plant, no. of primary branches, ascorbic acid and protein content and negative association with total sugars.

CONCLUSION

High heritability accompanied with high genetic advance as percent of mean were recorded for days to first flower, days to 50% flowering, first flower node, no. of primary branches, internodal length, nodes per plant, plant height, seeds per pod, pods per plant, pod yield per plant, TSS, ascorbic acid and total sugar. Due to additive gene action improvement of these traits could be effective by phenotypic selection. High heritability coupled with high genetic advance is more helpful in predicting the genetic gain under selection. High heritability along with moderate genetic advance

was observed for days to first picking, pod length, shelling (%), number of pickings and proteins. This may be attributed to non additive gene action. Pod yield per plant had shown a positive and significant correlation at both phenotypic and genotypic levels for pod length, seeds per pod, shelling (%), plant height and pods per plant. Selection on the basis of these traits might lead to higher yield in vegetable pea.

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