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Analysis of Trait Association and Genetic Diversity in Garden Pea (*Pisum sativum* L.) Genotypes under Middle Gangetic Plain Region of India

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ABSTRACT

Background: Garden pea is a cool season vegetable crop cultivated extensively throughout the world. Besides nutritional quality it also boosts soils through the fixation of atmospheric nitrogen. The most important task of pea breeding is to develop varieties with high and stable production, different maturity types and resistance against biotic and abiotic stresses. To fulfil these objectives, analysis of genetic diversity is the prerequisite to choose genetically diverse parents for a successful hybridization program and to know the source of genes for a particular trait within the available germplasm.

Methods: A study was conducted at ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi during 2015, using principle component analysis, correlation analysis and stepwise regression analysis approaches to assess the genetic diversity present in 160 pea genotypes for the identification of diverse parents for use in crop improvement.

Result: Based on the phenotypic data, three superior genotypes VRPD-2, VRPR-15 and VRP-292 were identified on the basis of pod yield, number of pods per plant, ten pod weight, pod length and number of seeds per pod whereas three other genotypes VRPE-45-1, VRPE-55 and VRPE-36 were found early flowering. Principle Component Analysis revealed that first four principle components contributed to 85% of the total variation so these four were given due importance for further explanation. Stepwise multiple regression analysis revealed that number of pods per plant, ten pod weight and number of internode for first pod were the best predictors of pod yield per plant.

Key words: Correlation, Diversity, Pea, Principle components, Regression.

INTRODUCTION

Vegetable-pea or garden pea (*Pisum sativum* L.) is one of the most consumed vegetable legumes, grown in 0.5 m ha with 4.84 mt production having a very high productivity of nearly 9.7 t/ha. India is only second to China producing nearly 24% of world production. Pea is balanced with macro and micro nutritional profile and is low in fat but high in fiber, protein, ascorbic acid, ß-carotene, thiamine, riboflavin and iron (National Food Administration, 2002). These nutritional properties make it a valuable food capable of meeting the global dietary needs of >900 million undernourished people (Devi *et al.* 2018a).

Germplasm diversity play an important role in the survival and adaptation of a crop under changing environmental conditions, selection of diverse desirable parents, to exploit heterosis and to generate desirable recombinants. In order to make use of existing variability for efficient use in breeding program, it is necessary to characterize the variability of available germplasm for both qualitative and quantitative traits and determine correlations among traits of interest. Multivariate techniques such as D^2 statistics, principal component analysis and discriminate function analysis are very useful techniques for the identification and selection of diverse parental lines (Sanwal *et al.* 2015). Therefore, the present study was planned to evaluate the pea genotypes for diversity and association of different traits to evolve/suggest suitable breeding strategies for developing high yielding pea cultivars.

MATERIALS AND METHODS

The present investigation was undertaken at the Experimental Farm of ICAR-Indian Institute of Vegetable Research, Varanasi (82°52′37″ E and 25°18′21″ N; 83 m above the mean sea level) from November to April, 2015-16. Agro-climatically, the experimental site represents the Middle Gangetic Plain Region of India, characterized by humid sub-tropical climate with an average rainfall of 998 mm. A total of 160 genotypes of pea collected from different parts of India were grown in a Completely Randomized Block Design (RBD) with three replications followed by recommended cultural practices to raise a healthy crop. The plot for each

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genotype consisted of 5 rows of 3 m length each, spaced at 30 cm; while the plants were spaced at 5 cm distance. Observation were recorded for plant height (cm), days to 50% flowering, first pod node number, pod length (cm), number of pods/plant, number of seeds/pod, 10- pod weight (g), pod yield/plant (g) and shelling percent. Ten competitive plants were randomly selected from the middle row of each plot in each replication to record observations on the quantitative traits. Means of all observations were calculated for quantitative traits and subjected to principal component analysis (PCA). The principal components with eigen values >1.0 were selected as proposed by Jeffers (1967). Simple correlation and stepwise regression were carried out by using SPSS software version 16.0. Stepwise regression analysis was conducted with pod yield per plant as response variable and other traits as predictor variables. Genotypic and phenotypic coefficients of variations were also estimated according to Burton and Devane (1953). Heritability in broad sense and Genetic advance as percent of mean were worked out as per the procedures of Falconer (1981) and Johnson *et al.* (1955), respectively.

RESULTS AND DISCUSSION

Mean performance of different traits

The 160 genotypes of pea were evaluated for variability for nine traits. The variability for plant height ranged from 21.3 to 215.8 cm with mean value 72.8±2.9; for days to 50% flowering from 27.0 to 85.0 days with mean of 45.4 ±1.1 days; for number of internode for first pod ranged between 6.3 to 20.0 with mean 10.9±0.2; whereas for pod length the values ranged from 4.5 to 10.3 cm with a mean of 7.8±0.09 cm and for number of pods/plant it was from 3.3 to 21.2 with a mean of 9.9±0.3 (Table 1). Similarly, 10-pod weight varied between 20.0 to 100.0 g with a mean of 59.70±1.50. Number of seeds/ pod was in the range of 3.21 to 9.51 with mean 6.35±0.08 and pod yield/plant varied from 19.8 to 138.16 g with a mean of 54.4±1.6 g. Shelling percent was in the range of 30.0 to 60.0 with a mean value of 47.3±0.4 (Table 1). A wide range of variations were also reported for plant height (Million, 2012) and pod yield (Ashraf *et al.* 2011; Achakzai and Bangulzai, 2006; Murtaza *et al.* 2007). Significant differences were observed for pod yield/plant among the different genotypes. Maximum pod yield was observed in the genotype VRPD-2 (138.1 g) followed by VRPR-15 (133.0 g) and VRP-292 (100.3 g). These genotypes also performed well for number of pods /plant, 10-pod weight, pod length and number of seeds/pod indicating these traits may contribute to pod yield. Days to 50% flowering showed a wide variation among the genotypes studied. Genotypes DCP-2 (85 days), VRP-48 (73 days), VRP-215 (69 days) took maximum number of days for flowering while VRPE-45-1 (27 days), VRPE-55 (27 days) and VRPE-36 (28 days) took minimum number of days for flowering. Based on the comparison between days taken to flowering and high yield it can be concluded that medium days to flowering genotypes can be hybridized with high yielding genotypes for the selection of desirable segregants. Similar studies for the evaluation of genotypes for different traits were also conducted by Sanwal *et al.* (2018), Devi *et al.* (2018b) and *Ali et al.* (2018). Coefficient of variation (CV) is the most commonly used statistical measures to evaluate the precision of experiments. In field experiments, CV value less than 10% means high precision, 10-20% good precision, 20-30% low precision and above 30% very low precision (Gomes, 2009). In present study, for plant height, days to 50% flowering, number of internode for first pod, pod length, ten-pod weight and shelling percent recorded low CV values whereas number of pod/plant, number of seeds/pod, pod yield/plant recorded medium CV values indicating the precision of the experiment.

Estimation of correlation coefficients

Correlation analysis defines the relationships between dependent traits and its independent traits. Correlation studies played a very important role in genetic improvement of cultivars (Sanwal *et al.* 2015 and Kumar and Sharma, 2006). Plant height, number of internode for first pod, number of pods/plant, 10-pod weight, number of seeds/pod and shelling percent showed significantly positive correlation with pod yield/plant whereas days to 50% flowering exhibited negative correlation with pod yield/plant (Table 2). This indicated that mid-season genotypes have better yielding capacity as compared to early genotypes. Similarly, green pod yield/plant showed a positive and significant correlation with days to 50% flowering, average pod weight and number of pod/plant suggesting improvement of yield through these traits (Devi *et al.* 2018b). Number of pods/plant showed a significant positive correlation with plant height, days to 50% flowering, number of internode for first pod, pod yield/plant, shelling percent and significant negative correlation with pod length, 10-pod weight and number of seeds/pod (Table 2). These relationships can be used for developing targeted breeding strategies for improving pod yield of pea (Devi *et al.* 2018b).

Genetic parameters

Information on the nature and magnitude of variability is of great significance for starting any breeding programme. Presence of considerable variation in parental material has maximum chances of evolving desirable plant types. The variability can be assessed by various statistics such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance. Phenotypic coefficient of variation was slightly higher than their respective genotypic coefficient of variation for all the characters indicating the role of environment for the traits studied. High PCV and GCV were observed for plant height, days to 50% flowering, number of internode for first pod, number of pods/plant, 10 pod weight and shelling percent whereas moderate PCV and GCV was observed for pod length, number of seeds/ pod and pod

Table 1: Mean values of the 160 pea genotypes for the nine quantitative traits.

Trait	Abbreviation	Min.	Max.	Mean	CV (%)
Plant height	PH	21.33	215.83	72.81±2.90	4.59
Days to 50% flowering	DF	27.0	85.0	45.41 ±1.10	2.18
Number of internode for First pod	IFP	6.33	16.0	10.86±0.22	5.51
Pod length	PL	4.50	10.28	7.84±0.09	5.66
Number of pods/plant	NPP	3.33	21.16	9.90±0.33	12.37
10-pod weight	TPW	20.0	100.0	59.70±1.50	1.45
Number of seeds/pod	NSP	3.21	9.51	6.35±0.08	11.65
Pod yield/plant	PYP	19.81	138.06	54.40±1.56	12.53
Shelling percent	SP	30.0	60.0	47.33±0.40	2.02

Table 2: Simple correlation coefficients among nine quantitative traits in 160 pea genotypes.

Trait	PH	DF	IFP	PL	NPP	TPW	NSP	PYP
DF	0.63***							
IFP	0.56***	0.64***						
PL	-0.55***	-0.53***	-0.08					
NPP	0.64***	0.61***	0.41***	-0.51***				
TPW	-0.60***	-0.60***	-0.28***	0.73***	-0.60***			
NSP	-0.36***	-0.46***	-0.20***	0.52***	-0.37***	0.70***		
PYP	0.29***	-0.29***	0.34***	0.03	0.69***	0.30***	0.14**	
SP	-0.03	-0.01	-0.09	-0.05	0.14**	-0.07	0.04	0.11*

Abbreviation of traits provided in Table 1.

* Significant at $p<0.05$**;** ** Significant at $p<0.01$**;** *** Significant at $p<0.001$ level.

Table 3: Coefficient of phenotypic and genotypic variability, heritability and genetic advance for different character.

Characters	Coefficient of variability (%)		Heritability	Genetic advance
	Phenotypic	Genotypic	(Broad Sense %)	(as % of Mean)
PH	50.45	50.24	99	103.06
DF	29.28	29.20	99	59.98
IFP	26.18	25.59	96	51.54
PL	15.02	13.92	86	26.56
NPP	43.77	41.99	92	82.97
TPW	31.49	31.46	99	64.73
NSP	19.11	15.15	63	24.74
PYP	10.80	10.61	89	69.09
SP	37.70	35.56	97	21.48

yield/plant (Table 3). Similar results were also reported for number of pods/plant, days to first flowering and pod yield/plant by Gudadinni *et al.* (2017); for pod length, number of pods/plant and number of seeds/pod by Kumar *et al.* (2015); for pod number/plant by Jeberson *et al*. (2016); and for plant height by Tambolkar *et al*. (2016). Heritability measures the extent of genetic control of a particular trait and its transmission to progeny and hence has direct bearing on selection efficiency of traits concerned. Heritability and genetic advance should be considered together for effective selection (Johnson *et al.* 1955). High heritability coupled with high genetic advance was observed for plant height, days to 50% flowering, number of internode for first pod, number of pods/plant, 10-pod weight and shelling percent, pod length, number of seeds/pod and pod yield/plant which indicated the presence of additive gene action in governing these traits which can be exploited by simple selection methods.

Principal component analysis

In the present study, the first four principal components accounted for more than 85% of total variation (Table 3). The principal components having eigen value less than 1 were treated as non-significant so first three principal components explaining more than 77% of total variation were used for further explanation. The percentages of cumulative variation by first three principal components are 46%, 64.76% and 77.50% respectively. For evaluation and characterization of cultivars, more than 75% of the total variation is acceptable (Singh *et al*. 2017). Pod length (0.88), 10-pod weight (0.91), number of seeds/pod (0.79) showed positive loading in PC1 and other traits displayed negative loading. Traits with large value nearer to unit value have

Table 4: Eigen values and percentage variations for the first four principal components obtained from factor analysis of 160 pea genotypes.

Factor	1	2	3	4
Eigenvalue	4.14	1.70	1.12	0.73
Variance cumulative (%)	46.0	64.76	77.50	85.30
Traits	Factor loading			
PH	-0.53	0.55	0.37	-0.06
DF	-0.51	0.67	0.26	0.01
IFP	-0.04	0.95**	0.16	-0.05
PL	0.88**	0.01	-0.17	-0.01
NPP	-0.50	0.27	0.78**	0.10
TPW	0.91**	-0.24	-0.03	-0.07
NSP	0.79**	-0.20	0.15	0.04
PYP	0.18	0.20	0.94**	0.04
SP	-0.02	-0.05	0.07	0.99**

Abbreviation of traits provided in Table 1.

** Significant factor loadings (considered for values above 0.70).

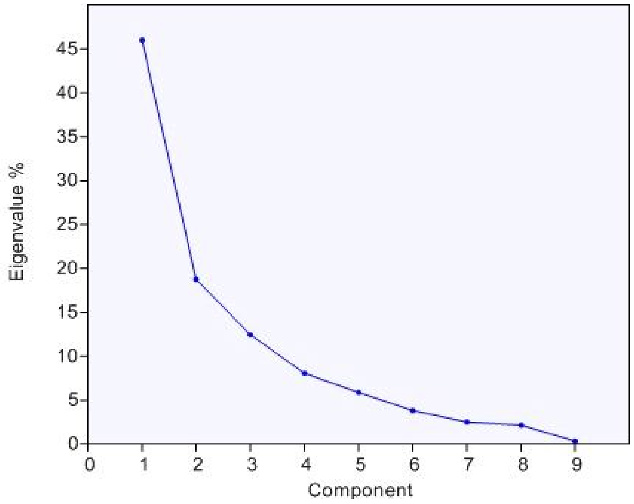

Fig 1: The scree plot based on principal component analysis (PCA) of nine quantitative and qualitative traits in 160 pea genotypes.

more impact on grouping than those with lower value nearer to zero (Chahal and Gosal, 2002). The positive and negative sign of the loadings shows the direction of association between variables and components. In PC 2, plant height (0.55), days to 50% flowering (0.67) and number of internode for first pod (0.95), showed positive loading and the remaining traits showed negative loading. PC 3 had positive contribution by number of pods/plant (0.78) and pod yield/ plant (0.94) (Table 4). These traits contributed maximum towards the genetic divergence. Based on the PCA analysis it can be concluded that yield and its contributing traits were present in PC 1 and PC 3. High value of identified traits suggested that selection of genotypes on the basis of first and third components may lead to increased yield and pod characteristics.

Kumar *et al.* (2018) found that 75% of the total variation was explained by first three PCs and high value for 100-seed weight and pods/plant were observed in PC 2. Umar *et al.* (2014) observed that first principal component explained 40.29% of the total variation and have positive relation with pod length and width. Similarly, Sanwal *et al.* (2015) analysed the contribution of different character towards the expression of genetic divergence and identified 10-pod weight contributed maximum (58.29%) followed by days to 50% flowering (23.83%), plant height (11.31%) and shelling percent (4.95%). These four characters contributed more than 98% to the total genetic divergence in the genotypes studied. Scree plot represents the percent variation of eigen value with each principal components. PC 1 explained the maximum variation of 46.0% with eigen value 4.14 followed by PC 2 had variation 18.76% and eigen value 1.70 and PC3 with variation 12.74% and eigen value 1.12 (Fig 1). Principal components having eigen value more than one exhibited more variability among the pea genotypes for the selection of distantly related parents. So selection of genotypes from PC1 will be beneficial as this PC exhibited maximum variation in comparison to other PCs. The biplots between PC 1 and PC 2 represent the diversity among traits as well genotypes (Fig 2). The results showed that almost all the genotypes and traits had high degree of variation. Similar reports in pea were reported by Nadiya *et al.* (2018) and Arif *et al.* (2020).

Regression analysis

In regression analysis the pod yield/plant was taken as dependent variable and other traits were considered as independent variable. Analysis of variance showed significant variation for number of pods/plant, 10 pod weight and number of internode for first pod in response to pod yield/plant. The results of stepwise multiple regression analysis indicated that number of pods/plant was found as best predictor which was able to explain 47.9% of variance of the dependable variable i.e., pod yield/plant. 10-pod weight was the second best predictor which together with number of pods/plant can predict as much as 89.6 % of the variance and number of internode for first pod was third best predictor which along with number of pods/plant and

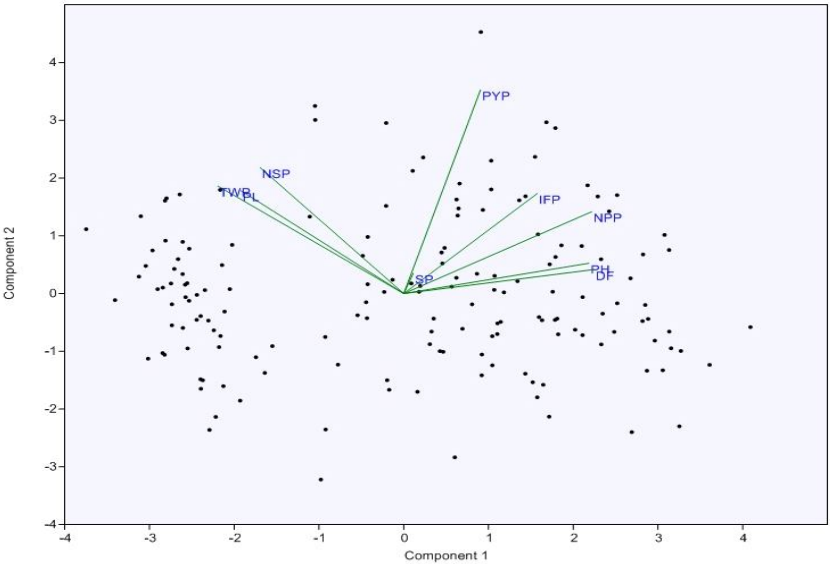

Fig 2: Biplot of first two principal components generated from PCA of nine quantitative and qualitative traits in 160 pea genotypes. Green lines represent each variable pointing in the direction of its maximum change across the diagram.

Table 5: Regression analysis showing variation in response Pod yield per plant over eight quantitative traits in 160 pea genotypes.

Source of variation	df	Sum of Squares	Mean Square	F value
Regression	3	55896.78	18632.26	490.04***
Residual	156	5931.47	38.02	
Total	159	61828.25		
Final regression model (PYP) = -56.72 + 5.33 (NPP) + 0.85 (TPW) + 0.68 IFP				

** Significant at p<0.001.

10-pod weight predicted 90.4% of the total variance of the pod yield/plant (Table 5). Due to low contribution, the other traits were not included in the model. Stepwise multiple regression analysis results found significantly positive correlation of number of pods/plant with number of seeds/ plant under heat tolerant (69.1%), heat susceptible (79.9%) and overall categories (87.7%) of different pea genotypes (Mohapatra *et al.* 2020). A significant role of plant height (21%) and stem diameter (7%) as predictable variables was observed for lodging resistance in pea (Kujur *et al.* 2014).

CONCLUSION

The present study revealed significant variation for all the studied traits among the genotypes. Pod yield was positively and significantly correlated with most of the traits studied. The results of principle component analysis revealed that first four principle components contributed 85% of the total variation and these results can be used in future pea breeding programs aimed to develop early maturing pea genotypes along with higher yield traits and selection of diverse genotypes from any segregating populations. Number of pods per plant, ten-pod weight and number of internode for first pod were the best predictors for pod yield /plant and these traits should be considered at the time of selection.

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Contribution of authors

SKS- planned and executed the research work; HK- analysis and interpretation of data, JD- conducted the experiments and edited the manuscript, BS- overall guidance and execution of experimental facilities.

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