RESEARCH PAPER

Assessment of genetic divergence and association of horticultural traits with yields in garden pea on Shivalik hills of Uttarakhand

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Abstract : An experiment was undertaken to assess the genetic divergence, correlation co-efficient and path analysis among various horticultural traits in thirty-two genotypes of garden pea based on seventeen traits. The present investigation was revealed that all the pea germplasms significantly different for the traits phenotypic and genotypic correlation co-efficients among different characters showed that pod yield per plant had a positive and significant association with the number of branch per plant, number of pod per plant, number of cluster per plant. The path co-efficient analysis revealed that out of all traits studied, pod yield per plant had the maximum positive direct effect on the number of pods per plant followed by internode length, number of seeds per pod and number of branch per plant. All the genotypes were grouped into 5 clusters. The maximum number of genotypes was arranged in cluster-IV (10) and the other four clusters contained 22 genotypes each. Whereas highest inter-cluster distance was recorded between cluster V and II and lowest was observed between cluster IV and III. This result showed that it has the good thought of crossing between two different clusters which having high inter-cluster distance.

Key Words : Horticultural traits, Genotypic, Phenotypic, Genetic divergence, Path analysis

INTRODUCTION

Pea is a very common leguminous vegetable crop grown in the winter season in the plains of northern India and as an offseason grown in the hills. It is produced from hilly areas is available at a time when pea cannot be gown in plains due to high temperature and this off-season availability brings lucrative returns to the growers.

Moreover, consumers also have a special preference for pea from hilly regions because of its characteristic flavour, sweetness, freshness and good quality. Inspite of such an economic importance, production per unit area of pea is still low in the country, even when varieties are grown during the off-season and the major constraints attributed to this are lack of high yielding varieties and

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poor biotic and abiotic stress resistance. This can be mitigated by evaluating an initially large number of genotypes and to identify high yielding and superior genotypes of pea which can be released as such for commercial production or can be incorporated in the future crop improvement programmes for improvement of yield and quality contributing traits. Genetic divergence further gives an idea about the scope of improvement in a character through simple selection. However, selection for yield and quality traits can be achieved in a better way if the information with respect to the correlation between such traits is also available followed by a better understanding of the association between the relevant characters provided through path co-efficient analysis. Similarly, for improvement of those characters which didn't respond to selection, there is a need for partitioning of non-additive component of genetic variance further by hybridization which can be facilitated by genetic divergence studies.

MATERIAL AND METHODS

The experimental material comprised of a diverse set of 32 pea genotypes and along with two checks 'PB-89' and 'Solan Nirog' including all released cultivars. The investigation was carried out at the Vegetable Demonstration and Research Block, Department of Vegetable Science, College of Horticulture, Bharsar. VCSG Uttarakhand University of Horticulture and Forestry during *Kharif* 2014. The site of an experiment is located at latitude of 30.056°N and longitude 78.99°E and at an elevation of 1900-2200 meters above mean sea level. This region has fallen in a sub-humid, sub-temperate and mid-hill zone of Uttarakhand. The maximum temperature during May-June is recorded between 30°C-35°C however and nights are cool. December and January are the coldest months; the minimum temperature reaches 1°C to -4°C. Relative humidity is normally highest during the rainy season (July-August) often recorded near to saturation point (92-97%). (Bisht and Sharma, 2014). The soil textural class at the site was sandy loam. The experiment was laid out in RCBD with three replications. The net plot size was 1.22 m² with spacing 30 cm row to row and 10 cm plant to plant. The recommended package of practices was followed to raise the healthy crop. After eliminating the border plants, observations were recorded on five randomly chosen plants for 17 quantitative traits *viz.,* Days to 50 per cent germination, Days to 50 per cent

flowering, number of cluster per plant, plant height (cm), number of branch per plant, intermodal length, number of node per plant, number of pods per plant, number of seed per pod, pods length, per cent dry matter (%), days to harvesting maturity, 100-seed weight, yield per plant, yield per plots and harvest index. The statistical analysis was carried out for each observed character under the study using MS-Excel, SPSS 16.0 and SPAR 2.0 packages. The mean values of data were subjected to analysis of variance and ANOVA was set as per Gomez and Gomez (1983) for Randomized Block Design.

RESULTS AND DISCUSSION

The results obtained from the present investigation as well as relevant discussion have been summarized under following heads :

Correlation studies:

The correlation co-efficients studies among the different traits were worked out at phenotypic and genotypic levels and presented in Table 1. In general, the genotypic correlation co-efficients were higher in magnitude than phenotypic correlation co-efficients. The information on nature and magnitude of correlation co-efficients helps breeders to determine the selection criteria for the concurrent progress of various characters along with yield. The phenotypic and genotypic correlation co-efficients among different characters showed that pod yield per plant had a positive and significant association with the number of branch per plant, number of pod per plant, number of cluster per plant. Similarly, the number of pods per plant was significantly and positively correlated with the number of cluster per plant, number of branch per plant, number of node per plant, internode length and plant height. The findings get a support from studies conducted on correlation co-efficients by Dhama *et al.* (2010) and Singh *et al.* (2011).

Direct selection for complex characters like yield is not sufficiently effective as they are polygenically controlled and their expression is dependent on the performance of a number of component traits. So, for obtaining high yielding genotypes, selection should be directed through yield contributing traits which necessitate knowing the degree of their association with yield. Therefore, a correlation study for yield with its component traits has been executed to find out the major yield contributing traits.

Table 1: Phenotypic and genotypic co-efficients of correlation among different traits in pea

Traits		NCP	NNP	IL	DFG	NBP	NSP	PH	NPP	DFF	DM	PL	SP	YPP₂	SI	DMC	HI	YPP₁
NCP	P	1.000	0.514**	0.393*	0.161	0.491**	-0.092	0.458**	0.715**	0.008	0.113	-0.293	-0.126	0.425*	0.101	0.225	-0.122	0.428*
	G	1.000	0.867**	0.645**	0.300	0.728**	-0.49	0.670**	0.890**	0.057	0.181	-0.467**	-0.321	0.422*	0.115	0.379*	-0.351*	0.428*
NNP	P		1.000	0.378*	0.156	0.180	-0.272	0.483**	0.348*	0.363*	0.346*	-0.310	-0.107	0.060	-0.097	0.168	-0.276	0.065
	G		1.000	0.554**	0.270	0.328	-0.629**	0.655**	0.493**	0.511**	0.467*	-0.466**	-0.086	0.00	-0.249	0.153	-0.564**	-0.026
IL	P			1.000	0.334	0.186	0.000	0.718**	0.323	0.099	0.103	-0.119	-0.294	0.205	-0.219	0.257	-0.110	0.204
	G			1.000	0.448*	0.351*	-0.035	0.868**	0.456**	0.108	0.112	-0.172	-0.294	0.213	-0.305	0.452**	-0.228	0.217
DFG	P				1.000	0.221	-0.209	0.258	0.100	0.204	0.239	-0.270	0.054	-0.079	0.033	0.295	-0.245	-0.079
	G				1.000	0.391*	-0.272	0.344*	0.196	0.261	0.283	-0.331*	0.112	-0.171	0.123	0.709**	-0.453*	-0.178
NBP	P					1.000	-0.150	0.230	0.537**	-0.041	0.165	-0.186	0.058	0.327	0.192	0.001	-0.124	0.325
	G					1.000	-0.554**	0.471**	0.825**	-0.022	0.316	-0.432*	-0.040	0.561**	0.325	0.092	-0241	0.562**
NSP	P						1.000	-0.134	0.002	-0.224	-0.289	0.613**	0.109	0.101	-0.048	-0.045	0.319	0.111
	G						1.000	-0.196	-0.143	-0416*	0.385*	0.812**	0.152	-0.010	-0.097	-0.102	0.547**	0.008
PH	P							1.000	0.381*	0.202	0.179	-0.316	-0.242	0.111	-0.228	0.171	-0.189	0.117
	G							1.000	0.536**	0.230	0.214	-0.385*	-0.325	0.079	-0.314	0.242	-0.346*	0.087
NPP	P								1.000	-0.020	0.071	-0.241	-0.019	0.494**	0.243	0.188	-0.030	0.493**
	G								1.000	-0.011	0.104	-0.385*	0.048	0.471**	0.271	0.225	-0.206	0.479**
DFF	P									1.000	0.535**	-0.331	0.033	-0.482**	-0.293	0.121	-0.507**	-0493**
	G									1.000	0.583**	-0.380*	0.021	-0.646**	-0.343*	0.175	-0.711**	-0.659**
DM	P										1.000	-0.222	-0.003	-0.310	0.027	0.056	-0.479**	-0.319
	G										1.000	-0.230	0.033	-0.420*	0.015	0.109	-0.662**	-0.426*
PL	P											1.000	0.056	0.127	0.040	-0.224	0.300	0.131
	G											1.000	0.058	0.129	0.052	-0.303	0.411*	0.125
SP	P												1.000	0.996**	0.302	-0.026	0.512**	-0.131
	G												1.000	1.000**	0.411*	0.022	0.444**	-0.147
YPP₂	P													1.000	0.303	-0.032	0.507**	0.996**
	G													1.000	0.409*	0.011	0.451**	1.000**
SI	P														1.000	0.025	0.072	0.302
	G														1.000	-0.003	0.042	0.411*
DMC	P															1.000	-0.227	-0.026
	G															1.000	-0.472**	0.022
HI	P																1.000	0.512**
	G																1.000	0.444**
YPP₁	P																	1.000
	G																	1.000

*and ** indicate significance of values at P=0.05 and 0.01 respectively

Where, DFG=Days to 50 %germination, DFF=Days to 50 % flowering, NNP=Number of nods per plant, NCP= Number of cluster per plant, NBP= Number of branch per plant, IL= Internode length, NPP=Number of pods per plant, PL =Pod length, NSP=Number of seeds per pod, SP=Shelling percentage, PH=Plant height, DM=Days to maturity, HI= Harvesting index, DMC= Dry matter content, YPP₁= yield per plant, YPP₂=yield per plot, SI= Seed index (100 seed weight)

Path co-efficient analysis:

Although correlation studies provide helpful knowledge in determining the components of yield it does not provide a clear picture of nature and extent of contributions made by a number of independent traits. Path co-efficient analysis, however, provides a realistic basis for allocation of appropriate weightage to various attributes while designing a pragmatic programme for the improvement of crop yields. The path co-efficient analysis (results obtained have been presented in Table 2) revealed that out of all the characters studied, number of pods per plant had the maximum positive direct effect on pod yield per plant followed by the number of seeds per pod, number of branch per plant, internode length and dry matter content. While, number of clusters per plant, harvest index, shelling percentage, plant height, pod length, days to 50 per cent germination, number of node per plant, days to 50 per cent flowering were observed to have a negative direct effect on pod yield per plant. These findings showed that selection should be made since the number of pods per plant, number of seeds per pod, number of branch per plant, internode length and dry matter content while making improvement in yield of pea. Further, number of branch per plant, number of pods per plant, harvest index, number of cluster per plant, number of node per plant, shelling percentage and internode length recorded maximum positive indirect effect via pod yield per plant (g/plant). Earlier workers like Chaudhary and Sharma (2003) also reported the similar effects of component traits on yield.

Genetic divergence:

Pea is a self-pollinated crop, the focus of breeding in recent times was to develop high yielding variety which led to narrow genetic diversity among pea varieties. To produce transgressive segregants, genetically different parents must be selected for recombination breeding in self-pollinated crops. The characterization of genetic diversity in crop species has long been based on morphological attributes, however, morphological variation is often found to be of limited use because the expression of morphological attributes may be affected by environmental conditions, thereby constraining the analysis of genetic variation (Nisar *et al.*, 2008). Knowledge of genetic diversity is a useful tool in gene bank management and in planning experiments, as it facilitates efficient sampling and utilization of germplasm by identifying and/or eliminating duplicates in the gene

Table 2 : Genotypic path estimates of direct and indirect effects of different traits on pod yield per plant in pea

Traits	NCP	NNP	IL	DFG	NBP	NSP	PH	NPP	DFF	DHM	PL	SI	DMC	HI	SP	GCCYP
NCP	-0.051	-0.012	0.021	-0.006	0.007	-0.005	-0.017	0.051	-0.002	-0.001	0.011	-0.001	0.002	0.012	0.011	0.430**
NNP	-0.045	-0.014	0.014	-0.006	0.003	-0.007	-0.016	0.028	-0.002	-0.001	0.011	-0.001	0.002	0.012	0.011	0.399*
IL	-0.033	-0.008	0.033	-0.009	0.003	0.000	-0.022	0.026	-0.005	0.000	0.004	0.032	0.002	0.008	0.010	0.217
DFG	-0.015	-0.004	0.015	-0.021	0.004	-0.003	-0.009	0.011	-0.011	-0.001	0.008	-0.01	0.003	0.016	-0.004	-0.178
NBP	-0.037	-0.005	0.011	-0.008	0.009	-0.006	-0.012	0.047	0.001	-0.001	0.010	-0.002	0.000	0.008	0.001	0.560**
NSP	0.025	0.009	-0.001	0.006	-0.005	0.011	0.005	-0.008	0.018	0.001	-0.019	0.031	0.000	-0.019	-0.005	0.009
PH	0.034	0.009	0.028	0.007	0.004	-0.002	-0.025	0.031	0.010	-0.001	0.009	0.032	0.001	0.012	0.011	0.087
NPP	-0.046	-0.007	0.015	-0.004	0.007	-0.002	-0.013	0.057	0.000	0.000	0.009	-0.002	0.001	0.007	-0.002	0.477**
DFF	-0.003	-0.007	0.004	-0.005	0.000	-0.005	-0.006	-0.001	-0.043	-0.002	0.009	0.032	0.001	0.024	-0.001	-0.639**
DM	-0.009	-0.007	0.004	-0.006	0.003	-0.004	-0.005	0.006	-0.025	-0.003	0.005	0.000	0.001	0.023	-0.001	-0.425*
PL	0.024	0.007	-0.006	0.007	-0.004	0.009	0.010	-0.022	0.016	0.001	-0.023	0.000	-0.001	-0.014	-0.002	0.127
SI	-0.006	0.004	-0.010	-0.003	0.003	-0.001	0.008	0.016	0.015	0.000	-0.001	-0.007	0.000	-0.001	-0.002	0.412*
DMC	-0.019	-0.002	0.015	-0.015	0.001	-0.001	-0.006	0.013	-0.008	0.000	0.007	0.000	0.005	0.016	0.006	0.009
HI	0.018	0.008	-0.007	0.009	-0.002	0.006	0.009	-0.012	0.031	0.002	-0.010	0.000	-0.002	-0.034	-0.008	0.445**
SP	0.017	0.001	-0.010	-0.002	0.000	0.002	0.008	0.003	-0.001	0.000	-0.001	0.000	-0.001	-0.008	-0.034	-0.145

Residual effect= -0.001:1

Where, DFG= Days to 50 % germination, DFF=Days to 50 % flowering, NNP=Number of nods per plant, NCP= Number of cluster per plant, NBP= Number of branch per plant, IL= Internode length, NPP=Number of pods per plant, PL=Pod length, NSP=Number of seeds per pod, SP=Shelling percentage, PH=Plant height, DHM=Days to maturity, HI= Harvesting index, DMC= Dry matter content, SI= Seed index (100 seed weight), GCCYP=Genotypic correlation co-efficient yield per plant

stock and helps in the establishment of core collections (Ghafoor *et al.,* 2005). Grouping of genotypes based on non-hierarchical Euclidean cluster analysis will be more useful in choosing reliable parents for obtaining superior segregants. The value of D^2 statistics (Mahalanobis, 1936) has been demonstrated effective in choosing the parental stocks for cross-breeding (Malhotra and Singh, 1971; Bhatt, 1970 and Dasgupta and Das, 1984). However, the D^2 statistics groups a set of potential parents based on genetic divergence with the assumptions

that the best parent may be those revealing the maximum genetic diversity (Bhatt, 1970). Based on the performance of various traits, the clustering pattern of 32 diverse genotypes of pea has been presented in Table 3. All the genotypes were grouped into 5 clusters. The maximum number of genotypes was arranged in cluster-IV (10) and the other four clusters contained 22 genotypes each. Averages inter and intra cluster divergence (D^2) values are presented in the (Table 4). The diagonal figures in the table represent the intra cluster

Table 3: Clustering pattern of 32 genotypes of pea based on genetic divergence

Cluster	Number of genotypes	Genotypes along with their sources
I	7	Arka Ajit, AP-1, AP-3, BP-801, VL-7, PSM-5 and Arkel
II	4	PP-74, PP-13, PP-14 and PP-96
III	6	Arka Sampurna, CHP-2, Palam Sumul, Palam Priya, PPC-66 and DPP-1526P
IV	10	Arka Karthika, Solan Nirog, AP-4, VL-12, PP-86, PP-25, PP-155, Pant Uphar, DPP-3 and DPPM-65
V	5	PC-531, PB-89, Kashi Shakti, Kashi Udai and Palam Triloki

Table 4: Average intra and inter cluster distance (D^2)

Cluster	I	II	III	IV	V
I	2.975				
II	4.404	3.008			
III	4.737	5.488	2.428		
IV	3.895	3.330	3.637	2.860	
V	3.957	6.550	4.256	5.195	3.095

Table 5: Cluster means for different characters among 32 genotypes of pea

Sr. No.	Characters	Clusters				
		I	II	III	IV	V
1.	Days to 50% flowering (number)	45.44	58.08	63.77	60.13	47.39
2.	Number of pods per plant	18.97	25.88	12.57	18.41	12.24
3.	Shelling percentage (%)	49.15	42.69	51.34	20.26	41.07
4.	Dry matter content (%)	47.29	61.85	45.14	44.63	49.27
5.	100 seed weight(g)	23.71	23.98	20.32	19.57	20.81
6.	Harvest index	48.77	39.80	40.28	40.40	54.19
7.	Plant height (cm)	102.69	142.76	72.05	197.15	87.77
8.	Number of branch per plant	2.75	2.91	2.25	2.22	1.88
9.	Pod yield per plant (g/plant)	86.68	64.82	37.14	53.47	58.49
10.	Pod yield (kg/plot)	3.46	2.5	1.5	2.27	2.33
11.	Number of seeds per pod	7.35	7.13	7.04	6.94	8.6
12.	Pods length (cm)	8.86	7.67	8.54	7.81	9.8
13.	Number of cluster per plant	15.20	18.50	9.52	15.50	8.82
14.	50% germination	15.56	22.57	15.77	15.49	14.66
15.	Number of node per plant	17.74	19.97	17.48	20.56	14.54
16.	Internode length (cm)	8.47	10.51	7.07	9.67	8.6
17.	Days to marketable maturity (number)	136.95	162.82	158.49	158.42	137.67

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distances. The intra cluster distance was highest in cluster V (3.095) and lowest in cluster III (2.428). Whereas, highest (6.55) inter-cluster distance was recorded between cluster V and II and lowest (3.330) was observed between cluster IV and III. The inter-cluster distance was maximum between cluster V and II indicating that hybridization between genotypes from cluster V and III can be utilized for getting the superior recombinants/transgressive segregants in segregating generations in pea. The cluster means for various horticultural traits are presented in the (Table 5). The lowest mean was recorded in cluster I (45.44) for days to 50 per cent flowering followed by cluster V, cluster II, cluster IV and cluster III. The maximum mean of a number of pods per plant was observed in cluster II (25.88) followed by cluster I cluster IV, cluster III and V. Maximum Shelling percentage was recorded in cluster III (51.34) followed by cluster I, cluster II, cluster V and cluster III. The maximum dry matter content estimated in cluster II (61.85) followed by cluster V, cluster I, cluster III and cluster IV. Maximum 100 seed weight was recorded in cluster II (23.98) followed by cluster I, cluster V, cluster III and cluster IV. Maximum per plant yield was recorded in cluster I (86.68) followed by cluster II, cluster V, cluster IV and cluster III and Minimum days required for maturity was recorded in cluster I (136.95) followed by cluster V, cluster IV cluster III and cluster II. Hence, hybridization between parents from cluster V and cluster II for these characters can produce better segregants in segregating populations. The studies on genetic divergence in pea corroborated with the findings of Parihar *et al.* (2014).

Conclusion:

The investigation was concluded that yield in pea can be improved by selecting genotypes having a greater number of pods per plant, the number of seeds per pod, 100-seed weight and pod length which are major yield contributing traits. Cluster analysis of the genotypes indicates that hybridization between genotypes of cluster V and cluster II, based on their mean cluster performance can be effectively utilized for getting desirable recombinants.

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