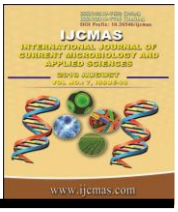

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Estimation of Genetic Architecture in Agro-Morphological Traits of Garden Pea in Mid Hill Region of Uttarakhand, India

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ABSTRACT

Keywords

Genetic variability, Heritability, Genotype, Diversity and Genetic gain

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In order to appraise genetic parameters and variability in the crop, the information on the nature and degree of diversity in the genotypes is crucial. Thirty two genotypes along with two commercial varieties (PB-89 and SolanNirog) as check were evaluated for assessing genetic variability and heritability for seventeen different agro-morphological characters. The mean sums of squares due to genotype were highly significant for all of the characters. The estimates of GCV and PCV is highest values were shown by plant height, pod yield per plant & pod yield per plots whereas moderate for dry matter content, No. of node per plant and 100 seed weight. High heritability estimates associated with high genetic gain for plant height, pod yield per plant and pod yield per plot reflecting the involvement of additive gene action suggesting more scope of selection of these traits.

Introduction

Pea (*Pisum sativum* L.) 2n = 2x = 14 is one the most important legume crop of India, Based on genetic diversity, Central Asia, the Near East, Abyssinia and the Mediterranean have been recognized as centres of origin for pea (Gritton, 1980). Pea is rich source of different phyto-nutrients, minerals, vitamins and anti-oxidants benefiting for human health. Greens pods are excellent source of Folic acid, Ascorbic acid (Vitamin C) & Vitamin K. It is grown at higher altitudes in tropics with temperatures from 7 to 30 °C (Duke, 1981). The overall yield of pea is low in India as compared to the world average yield due to the narrow genetic base and limited variability used in the development of local varieties (Kumar *et al.*, 2004). Genetic variability plays an important role in a crop in selecting the best genotypes for making rapid improvement in yield and quality characters as well as to select the potential parent for hybridization programmes.

Heritability is an index for calculating the relative influence of environment on expression of genotypes. The selection for highly heritable characters is effective. Therefore, heritability along with other parameters of variability can be used in predicting the gain for a given selection intensity, Genetic divergence further gives an idea about the scope of improvement in a character through simple selection. But a considerable level of genetic variance among peas of diverse origin has also been reported by some breeders (Nisar *et al.,* 2011). Therefore, continuous efforts are required to increase the production and productivity of pea using diverse and exotic sources. Crop improvement depends immensely on the availability of diverse materials and their judicial utilization. Therefore, present investigation was carried out to assess the genetic components and trait associations in diverse set of pea genotypes for their utilization in crop improvement programs.

Materials and Methods

The present investigation was carried out at the 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 experiment is located at latitude of 30.056^0 N and longitude 78.99^0 E and at an elevation of 1900-2200 meters above mean sea level. This region has falls in sub-humid, sub-temperate and mid-hill zone of Uttarakhand. The maximum temperature during May-June is recorded between 30^0C - 35^0C however, and nights are cool. December and January are the coldest months, the minimum temperature reaches to 1^0C to -4 ^{0}C. Relative humidity is normally highest during rainy season (July-August) often recorded near to saturation point (92-97%). The soil textural class at the site was sandy loam. The experimental material comprised of a 32 promising genotypes including with two checks 'PB-89' and 'SolanNirog' in RCBD with three replications. The net plot size was 1.22 m^2 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 *et al.,* (1983) for Randomized Block Design.

Results and Discussion

The mean sum square shows the highly significant differences among the genotypes for all the traits under study, which revealed the existence of good amount of variability in the germplasms and suggested that the experimental materials were genetically divergent (Table 1). This indicates that there is plentiful scope for selection of promising lines from the present gene pool for yield and yield contributing traits. Table 2 exist the mean performance of 32 genotypes along with two commercial checks for 17 agro-morphological traits along with coefficient of variation and critical difference. The assessment of genotypic coefficient of variation and phenotypic coefficient of variation is gave a clear cut picture of variations present in the available germplasms. Table 3 revealed that all the characters studied, phenotypic coefficients of variation were higher in magnitude than genotypic coefficients of variation, though difference was very less in most of the characters. This indicates that these traits are less influenced by environmental factors. Generally coefficients of variation were of higher to medium magnitude which further suggests that genetic diversity was present in the germplasms. These results get a support from the findings of Mehta *et al.*, (2005) and Rai *et al.*, (2006). The phenotypic coefficients of variation (PCV) were found high gain for plant height, pod yield per plant, pod yield per plot, number of pods per plant, number of cluster per plant, number of branch per plant, 50% germination, internode length and harvest index.

This shows greater genetic variability among all the genotypes for these characters. Moderate phenotypic coefficients of variation (PCV) were found for dry matter content, number of node per plant, 100 seed weight, days to 50 % flowering, shelling percentage, number of seed per pod, pod length and days to maturity. These results also supported with the findings of Saxesena *et al.*, (2014) Similarly, the genotypic coefficients of variation (GCV) were high for plant height, pod yield per plant, pod yield per plot, number of pods per plant, number of cluster per plant, number of branch per plant, 50% germination and internode length whereas, moderate genotypic coefficients of variation (GCV) were recorded for, harvest index number of branch per plant, 100 seed weight, days to 50 % flowering, number of node per plant, dry matter content, pod length, days to maturity shelling percentage and 100 seed weight. Similar results for different characters have also been reported by Kosev *et al.*, (2015).

Heritability is good index for transmission of character from parent to their offspring. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations. It determines the amount of genetic variance to total phenotypic variance.

Table.1 Analysis of variance for different agro-morphological traits in garden pea

Character	Treatment (d. f=31)	CV%
Days to 50% germination (number)	40.548**	12.424
Days to 50% flowering (number)	226.46**	5.290
Number of pods per plant	106.360**	27.109
Pod length (cm)	2.965**	4.319
Number of seeds per pod	1.881**	7.952
Number of cluster per plant	52.576**	27.925
Number of branch per plant	0.845**	23.841
Number of node per plant	23.619**	12.545
Inter node length	11.190**	13.830
Plant height (cm)	6,338.353**	20.215
Yield per plant (g)	1,524.402**	25.633
Yield per plots (kg)	2.369**	25.548
100 seed weight	38.689**	9.136
Dry matter content (%)	178.702**	14.994
Shelling per cent	76.781**	9.673
Harvest index	218.808**	14.818
Days to harvesting maturity	842.863**	1.942

**Significant at 1

Table.2 Mean performance for different agro-morphological characters in garden pea

Genotype	DG	DF	NPP	PL (cm)	NSP	NCP	NBP	NNP	IL	PH (cm)	YP_1 (g)	YP_2 (kg)	100SW (g)	DMC (%)	SP	HI	DHM
ArkaAjit	14.333	41.000	27.400	8.173	7.000	17.867	3.267	17.733	6.553	102.367	70.005	2.797	28.867	46.500	50.090	39.067	151.000
ArkaKarthika	11.333	57.333	23.467	10.060	8.267	16.867	2.400	21.133	9.733	114.500	69.311	2.767	25.033	43.877	32.530	34.623	177.667
ArkaSampurna	14.333	59.000	9.467	8.780	6.733	7.667	3.000	14.467	6.053	67.733	48.873	1.950	23.967	36.723	40.517	47.833	182.000
PC-531	14.667	58.333	10.000	10.187	8.533	9.333	1.867	15.267	9.473	105.160	47.622	1.900	20.327	49.027	42.717	44.763	162.333
PB-89*	16.667	41.667	11.133	10.307	9.000	7.667	1.867	15.467	8.187	72.953	61.923	2.472	16.267	40.327	47.750	69.363	134.333
SolanNirog*	16.667	55.000	17.600	6.743	6.533	16.400	2.600	20.600	11.020	205.767	48.683	1.946	21.967	41.703	35.777	43.570	161.667
CHP-2	19.333	65.667	11.467	8.407	6.333	9.600	2.683	19.067	7.987	90.300	38.842	1.790	20.167	46.417	48.580	38.240	177.667
Kashi Shakti	17.333	50.667	15.400	10.453	8.867	12.067	2.417	16.667	11.280	116.467	67.854	2.710	20.233	61.677	35.593	41.637	147.667
KashiUdai	13.667	38.333	12.100	9.467	7.733	11.000	1.800	15.000	8.187	96.800	78.139	3.122	22.633	48.313	33.630	54.870	122.000
AP-1	16.000	44.000	14.533	9.330	7.667	15.933	2.800	16.333	7.220	94.333	66.547	2.661	20.533	53.837	33.783	46.787	133.333
AP-3	11.667	46.667	16.667	9.047	7.467	14.600	2.467	19.067	8.570	118.433	73.023	2.921	18.900	43.823	45.287	44.220	150.000
AP-4	18.000	60.000	17.533	7.558	6.267	11.667	2.550	17.100	7.193	98.393	70.366	2.814	24.567	50.707	34.927	37.613	172.333
Arkel	11.667	40.667	20.733	9.120	7.600	12.667	2.367	17.250	7.513	87.673	119.475	4.778	25.567	44.687	40.383	55.937	120.000
BP-801	22.667	55.000	17.267	9.038	7.867	15.867	2.867	17.667	9.527	102.000	76.780	3.071	24.600	55.553	44.473	43.720	132.333
VL-7	20.333	47.667	12.200	8.537	6.600	10.200	2.800	17.333	10.080	103.167	73.100	2.924	24.633	41.537	40.603	44.943	137.667
VL-12	17.333	65.667	14.067	7.360	6.667	14.333	2.133	19.333	11.627	162.667	38.930	1.556	15.033	59.330	39.180	32.517	147.667
Pant Pea -74	18.667	60.000	34.600	7.289	6.600	21.933	3.756	19.667	9.853	124.200	86.869	3.474	23.233	55.120	42.783	43.760	147.667
PSM-5	12.333	46.667	24.067	8.923	7.533	19.133	2.867	18.867	9.967	110.870	128.330	5.133	22.933	45.143	45.160	64.693	134.333
Pant Pea-13	23.333	55.667	21.133	7.247	7.067	19.350	2.400	21.267	9.093	99.420	54.833	2.193	27.267	55.067	40.817	39.897	162.667
Pant Pea-14	23.667	60.000	19.333	8.207	7.267	12.933	2.533	20.333	8.920	122.456	54.080	2.163	26.233	72.577	50.023	37.763	177.667
Pant Pea-86	18.667	58.333	17.267	7.640	6.667	14.200	2.533	22.400	11.567	212.275	57.909	2.316	15.133	50.537	40.640	39.573	147.667
Pant Pea-96	24.667	55.667	28.467	8.133	7.667	19.800	2.933	18.667	14.327	225.000	63.513	2.540	19.200	59.670	36.943	37.820	163.333
Pant Pea-25	14.000	55.000	20.333	6.993	7.533	15.333	2.600	19.333	8.860	99.400	58.173	2.327	14.900	54.507	44.493	46.103	163.667
Pant Pea-155	15.000	56.667	20.000	7.439	6.533	16.133	3.333	19.400	9.748	118.400	71.385	2.855	21.000	53.350	34.187	43.110	149.000
Pant Uphar	12.667	56.667	13.067	7.947	6.267	16.400	1.600	22.067	9.753	115.067	59.547	2.381	20.880	60.473	34.580	43.987	151.000
PalamSumul	16.333	65.000	12.600	7.713	7.133	8.389	1.889	14.333	6.573	67.444	46.408	1.856	20.967	56.600	39.817	38.880	137.667
PalamPriya	15.000	60.000	12.267	8.260	7.667	8.267	1.900	16.217	5.880	56.359	25.150	1.005	17.633	45.033	44.030	36.027	144.000
PalamTriloki	11.000	48.000	12.600	8.975	9.000	4.133	1.467	10.333	6.031	47.523	36.949	1.477	24.633	47.033	45.680	60.350	122.000
DPP- 3	14.000	70.000	25.933	8.387	8.200	16.800	2.867	22.133	10.507	225.230	60.260	2.410	18.500	43.977	40.980	43.397	153.000
DPPM- 65	17.333	66.667	14.933	8.220	6.733	16.924	2.200	22.133	6.820	119.787	39.173	1.567	18.870	48.420	38.467	39.587	160.667
PPC- 66	14.000	65.000	14.200	9.660	7.400	11.083	2.200	18.933	7.433	63.441	26.927	1.077	19.360	42.163	46.000	34.870	158.667
DPP- 1526 P	15.667	68.000	15.467	8.573	7.067	12.133	1.733	21.933	8.600	87.067	36.700	1.668	19.867	43.930	45.103	45.883	151.000
SE(m)±	**1.171**	**1.693**	**3.855**	**0.212**	**0.338**	**2.200**	**0.339**	**1.330**	**0.709**	**13.249**	**9.044**	**0.362**	**1.127**	**4.322**	**2.296**	**3.784**	**1.693**
SE(d)±	**1.656**	**2.394**	**2.726**	**0.300**	**0.478**	**3.111**	**0.479**	**1.881**	**1.003**	**18.737**	**12.791**	**0.512**	**1.594**	**6.112**	**3.247**	**5.351**	**2.395**
C.D.0.05%	**3.318**	**4.798**	**7.724**	**0.601**	**0.957**	**6.235**	**0.959**	**3.768**	**2.009**	**37.546**	**25.630**	**1.027**	**3.194**	**12.248**	**6.506**	**10.723**	**4.799**

*Check cultivar

Where, DG=Days to 50 % germination, DF=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, YP_1= yield per plant, YP_2=yield per plot, SI= Seed index (100 seed weight)

Table.3 Range, mean, PCV, GCV, heritability and genetic gain for different traits in garden pea

Sr. No.	Characters	Range	Mean ± SE(m)	Coefficients of Variation (%)		Heritability (%)	Genetic Gain (%)	Genetic Advance
				Phenotypic	Genotypic			
1.	**Days to 50% flowering**	38.33-70.0	55.43±1.693	16.26	15.37	89.4	0.29	16.60
2.	**Number of pods per plant**	9.47-34.60	17.41±2.726	40.73	30.40	55.7	46.75	8.14
3.	**Shelling percentage (%)**	32.53-50.09	41.11±2.296	14.62	10.97	56.2	16.93	6.96
4.	**Dry matter content (%)**	36.72-72.58	49.92±4.322	19.72	12.81	42.2	17.14	8.56
5.	**100 seed weight(g)**	14.90-28.87	21.37±1.127	18.38	15.95	75.3	28.54	6.10
6.	**Harvest index (%)**	32.52-69.36	44.23±3.784	22.79	17.31	57.7	27.08	11.98
7.	**Plant height (cm)**	47.52-225.23	113.52±13.249	43.73	38.77	78.6	70.82	80.40
8.	**Number of branch per plant**	1.47-3.76	2.45±0.339	29.07	16.63	32.7	19.59	0.48
9.	**Pod yield per plant (g)**	25.15-128.33	61.11±9.044	42.41	33.79	63.5	55.45	33.89
10.	**Pod yield (kg)**	1.01-5.13	2.45±0.362	41.75	33.02	62.6	53.38	1.32
11.	**Number of seeds per pod**	6.67-9.00	7.07±0.338	12.57	9.73	60.0	16.12	1.14
12.	**Pods length (cm)**	6.74-10.45	8.50±0.212	12.21	11.42	87.5	22.0	1.87
13.	**Number of cluster per plant**	4.13-21.93	13.64±2.200	38.22	26.10	46.6	36.73	5.01
14.	**50%germination**	11.0-24.67	16.32±1.171	24.70	21.35	74.7	37.99	6.20
15	**Number of node per plant**	10.33-22.40	18.35±1.330	18.40	13.46	53.5	20.27	3.72
16	**Internode length(cm)**	5.88-14.33	8.87±0.709	24.51	20.23	68.2	34.49	3.06
17	**Days to harvesting maturity**	120.0-182.0	151.0±1.693	11.21	11.42	97.0	22.39	33.83

In the present investigation, the estimates of heritability (broad sense) were and varied from 32.7% to 97.00% for different characters under studies found high for the characters for days to maturity, days to 50% flowering, pod length, plant height, 100 seed weight, days to 50% germination, internode length, pod yield per plant, pod yield per plot and number of seed per pod whereas for and harvest index, number of node per plant, number of cluster per plant, dry matter content and number of branch per plant moderate heritability was recorded.

Similar results for different characters have also been reported by Kosev *et al.*, (2015). Genetic advance a measure of genetic gain under selection as per cent of population mean was low to high for various characters studied in the present experiment. The range was from 0.029% to 70.82%. It was found high for the characters *viz.* plant height, pod yield per plant, pod yield per plot, number of pods per plant, days to 50 % germination, number of cluster per plant, internode length, 100 seed weight, harvest index, days to maturity and number of node per plant whereas, moderate genetic gain was recorded for number of branch per plant, dry matter content and shelling percentage. Results corroborated with the findings of Sureja and Sharma (2000). In the present investigation, High heritability coupled with high genetic advance as percent of mean were observed for plant height, pod yield per plant and pod yield per plot. Estimate of GCV was also high for these traits indicating presence of additive gene effects suggesting more scope of selection for these traits. Number of seed per pod, pod length, internode length and 50% germination showed higher heritability along with moderate genetic advance as percent of mean, which indicated that these characters are under the control of additive genes and are more reliable for effective selection similar result were reported by Kumar *et al.*, (2004)

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