Research Article

Variability, Correlation and Path Analysis in Pea (*Pisum Sativum L.*) Genotypes Under Western Himalayan Conditions

Shilpa Devi[1]*, Manish Kumar[2], Kuldeep Thakur[3], N K Bharat[2], R K Dogra[4], and Arvind Nagar[1]

[1]Division of Vegetable Science, ICAR-IARI, Pusa -110012 New Delhi, India
[2]Department of Seed Science & Technology, Dr YSP UHF, Nauni, Solan- 173230, HP, India
[3]Department of Vegetable Science, Dr YSP UHF, Nauni, Solan- 173230, HP, India
[4]Department of Fruit Science, Dr YSP UHF, Nauni, Solan- 173230, HP, India

Abstract

Forty three diverse pea genotypes were evaluated for their genetic variability attributes under mid hills of western Himalayas during *Rabi* 2014-15. Mean performance of five genotypes, *viz.*, 14/PEVAR-6, 14/PMVAR-3, 14/PEVAR-2, 14/PMVAR-1 and EC-598628 was observed to be better over other genotypes. 14/PEVAR-6 was recorded as earliest maturing cultivar taking 32.67 days to reach marketable maturity stage. High PCV, GCV (>30%) estimates for days to fifty per cent flowering, days to marketable maturity and total soluble solids revealed that sufficient variability is present among the genotypes. High heritability (>80%) coupled with high to moderate genetic gain was observed for days to fifty per cent flowering, days to marketable maturity and 100-pod weight indicating prominent role of additive gene effects. Pod length (2.047cm) had shown maximum positive direct effect on pod yield per plot followed by number of pods per plant (1.717), number of seeds per pod (1.618), harvest duration, 100-pod weight, TSS and pod width.

Keywords: Diverse, Genotype, Heritability, Variability

*Correspondence
Author: Shilpa Devi
Email: shilpa04911@gmail.com

Introduction

Pea is a member of Fabaceae family, placed under genus *Pisum* (2n=2x=14) and comprises both the wild (*P. fulvum* and *P. elatius*) and cultivated species (*P. abyssinicum*, *P. sativum*). It is predominantly a self pollinated, annual herb having climbing or bush type growth habit. It is an important cash crop in the hilly regions of western Himalayas especially for the growers of Himachal Pradesh having acreage of 23.67 thousand hectares with annual production of 280.23 thousand metric tonnes [1]. Peas from hilly areas are available at a time when it can't be grown in plains of adjoining states due to higher temperature; have high consumer preference because of their characteristic flavour, sweetness, freshness and good quality. Beside its high economic importance productivity per unit area is still low which is more prevalent and common in offseason production. Amongst major constraints, lack of varieties with high and stable productivity, losses from several biotic factors are common. Hence, there is a need to explore genetic variability which is considered as an important factor for crop improvement program for obtaining high yielding progenies [2].

An insight into the magnitude of variability present in a crop is provided through coefficients of variation, heritability and genetic gain. Selection for yield and quality traits can be achieved to best possible extent if information about correlation between such traits is available followed by better understanding of the association between the relevant characters provided by path coefficient analysis. Information about association of various component traits with yield and among each other is of immense importance as unfavourable association between the desirable attributes under selection may result in genetic slippage and limit the genetic advance. Yield being the end product of many correlated characters, the selection of such characters which are highly heritable and positively correlated is more desirable. Being a offseason crop for growers in western Himalayan region there is a dire need to plan research work for identification of genotypes which can adapt well and can mature earlier to catch early market. Keeping in view this study aimed at studying genetic variability and character association of some traits in pea (*Pisum sativum* L.) genotypes which may help to select suitable genotypes for future breeding programs.

Materials and methods

The present investigation was carried out involving forty three pea genotypes at the experimental farm of the department of Vegetable Science, Dr Y.S. Parmar University of Horticulture and Forestry, Nauni, Solan (HP) during *Rabi* 2014-15.The genotypes along with their source of availability have been presented in **Table 1**. Seeds were directly sown at a spacing of 45×10 cm in plots of 2.25×2 m² size having five rows each in the month of October, 2014. 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 [3] were followed to ensure a healthy crop stand. Observations were recorded on ten randomly selected plants in each replication on days to fifty per cent flowering, node at which first flower appear (No.), number of pods per plant, pod length (cm), pod width (cm), days to marketable maturity, harvest duration (days), number of seeds or grains per pod, pod yield (kg/plot), TSS (%), total phenols (%). For shelling (%) and 100-pod weight (g) data was recorded on 25 and 100 randomly selected pods from each genotype in each replication at the time of 2nd harvest. Total phenol content of each genotype in each replication was recorded by Folin-ciocalteu procedure given by AOAC and average values were expressed in per cent. The mean values of data were subjected to analysis of variance and ANOVA was set [4] for Randomized Complete Block Design using MS Excel-2007 worksheet. The genotypic and phenotypic coefficients of variability were calculated according to the formulae [5]. Broad sense heritability was calculated by formula [6]. Genetic advance as percent of mean (genetic gain) was calculated by the method suggested by Johanson *et al.* [7]. The genotypic and phenotypic correlations were calculated as per Al-Jibouri *et al.* [8]. The direct and indirect paths were worked out as per Dewey and Lu [9].

Table 1 List of studied pea genotypes along with their sources of availability

Genotype	Source
EC-598655, EC-598615, EC-598628, EC-598677	NBPGR, Regional Research Station, Phagli
14/PEVAR-2, 14/PEVAR-3, 14/PEVAR-4, 14/PEVAR-5, 14/PEVAR-6, 14/PEVAR-7, 12/PEVAR-1, 12/PEVAR-2, 12/PEVAR-3, 12/PEVAR-4, 12/PEVAR-5, 14/PMVAR-1, 14/PMVAR-2, 14/PMVAR-3, 14/PMVAR-4, 14/PMVAR-5, 12/PMVAR-1, 12/PMVAR-2, 12/PMVAR-3, 12/PMVAR-4, 12/PMVAR-5, 12/PMPMVAR-1, 12/PMPMVAR-2, 12/PMPMVAR-3, 12/PMPMVAR-4, 12/PMPMVAR-5, Arka Ajit, VP-233, IP-3, AP-3, VRP-7, VRP-6*	IIVR, Varanasi
Solan Nirog, Pb 89*	UHF, Solan
AP-2, AP-4	CSAUAT, Kanpur
Pusa Pragati, KTP-101, KTP-102	IARI Regional Research Station, Katrain
*Check cultivars	

Results and discussion

The analysis of variance indicated existence of significant differences among the genotypes for all traits under study. The genetic parameter of variability, heritability and expected genetic advance over mean for pod yield related characters is shown in **Table 2**. The differences among PCV and GCV for most of the traits are small indicating the greater role of genetic factors in their expression with less influence of environmental factors offering great scope for improvement. The phenotypic (PCV) and genotypic coefficient of variation (GCV) ranged from 10.21 to 43.23 and 8.59 to 41.56 per cent respectively. The maximum PCV and GCV were observed for days to fifty per cent flowering (No.) followed by days to marketable maturity, TSS (%) reflecting presence of high genetic variability among all the genotypes for these traits.

Burton [5] suggested that GCV along with heritability estimates would provide better understanding of the extent of advance to be expected by selection. Heritability estimates were also found higher for the characters, *viz.* days to fifty per cent flowering (No.), days to marketable maturity and total phenols (%) while, for pod yield (kg/plot), TSS (%) and pod length (cm) heritability estimates were moderate. High to moderate heritability coupled with high to low genetic gain were observed for days to fifty per cent flowering, days to marketable maturity, total phenols, TSS and pod yield indicating the prevalence of additive gene effect which in turn offers good scope for effective selection. The

results were corroborated with findings of Kumar et al. [10], Rai et al. [11], Sardana et al. [12], Sharma and Bora [13], Tiwari and Lavanya [2], Selvi et al. [14] and Kumar et al. [15]. Kumar et al. [15] observed that phenotypic coefficients of variation (PCV) were invariably higher than their corresponding genotypic coefficient of variation (GCV).

Table 2 Range, Mean, PCV, GCV, Heritability and Genetic gain for different traits in pea

Trait	Range	Mean ± SE (m)	Coefficients of variation (%)		Heritability (%)	Genetic gain (%)
			Phenotypic	Genotypic		
Days to 50 per cent flowering	32.67-128.00	89.79±2.55	40.55	40.25	98.53	82.31
Node at which first flower appear (No.)	7.10-15.13	11.69±1.08	29.34	24.55	70.04	42.33
No. of pods per plant	13.67-31.80	21.05±1.85	25.01	19.86	63.04	32.48
Pod length (cm)	5.87-9.23	8.03±0.26	10.21	8.59	70.80	14.89
Pod width (cm)	0.97-1.62	1.21±0.07	14.07	10.48	55.51	16.09
No. of seeds per pod	5.40-8.93	7.43±0.26	10.98	9.14	69.36	15.69
Shelling (%)	38.10-66.18	53.11±2.58	12.56	9.33	55.13	14.27
Days to marketable maturity	49.67-156.67	120.03±2.58	36.94	36.75	98.99	75.32
Harvest duration (days)	16.67-29.00	24.01±1.52	14.64	9.67	43.69	13.17
100-pod weight (g)	210.67-480.00	311.28±17.78	24.39	22.29	83.54	41.96
Total phenols (%)	0.32-0.92	0.65±0.01	25.54	25.17	97.11	51.10
TSS (%)	6.40-18.50	11.20±0.13	31.74	28.25	79.19	51.78
Pod yield (kg/plot)	1.36-5.77	3.29±0.32	36.90	32.88	79.41	60.36

In order to understand correlation of various traits under study with yield and with one another the genotypic and phenotypic correlations were calculated. Generally, genotypic correlation coefficients were higher in magnitude than corresponding phenotypic correlation coefficients as presented in **Table 3**. The phenotypic and genotypic correlation coefficients among different characters showed that pod yield per plot had positive association with number of pods per plant, pod length, number of seeds per pod, shelling (%), days to marketable maturity and TSS. Hence selection for number of pods per plant, pod length, number of seeds per pod and shelling (%) would be much effective for yield improvement. A significantly negative correlation was recorded between total phenols and total soluble solids. These results are corroborated with the findings of Kumar and Sharma [16], Patel et al. [17], Rai et al. [11], Guleria et al. [18], Pal and Singh [19], Tyagi et al. [20] and Kumar et al. [15]. Pal and Singh [19] observed positive correlation among green pod yield per plant and days for fifty per cent flowering, number of seeds per pod, number of pods per plant both at phenotypic and genotypic level. Similarly, Kumar et al. [15] also reported positive correlation between pod yield and number of pods per plant, pod length, number of seeds per pod, shelling (%) and TSS suggesting that these are major yield contributing characters. Beside it significantly negative correlation was reported among total phenols and TSS.

The path coefficient analysis in the present studies indicated that pod length (cm) had maximum positive direct effect on pod yield per plot followed by number of pods per plant, number of seeds per pod, 100-pod weight, TSS and pod width as shown in **Table 4**. While, for days to marketable maturity maximum negative direct effect was recorded. It indicates that characters, *viz.* pod length, number of pods per plant, number of seeds per pod, 100-pod weight can act as important selection criteria for yield improvement in pea. The characters under study contributed 99.99 per cent variability of pod yield per acre. These findings are in line with those of Rai et al. [11], Kaur et al. [21], Yadav et al. [22], Kumar et al. [15]. Kaur et al. [21] in their studies also revealed high direct effects for number of pods per plant, number of seeds per pod and pod length which can serve as reliable variables of selection for improvement in yield. Similarly, Kumar et al. [15] in their studies revealed that direct effects were higher for number of pods per plant and number of seeds per pod.

Table 3 Phenotypic and genotypic coefficients of correlation among different traits of pea

Trait		NFF	NPP	PL	PW	NSP	SP	DMM	HD	WHP	TP	TSS	PYPP
DFPF	P	0.827*	0.463*	-0.066	0.253	-0.095	-0.120	0.987*	0.291	0.256	0.318*	0.333*	0.366*
	G	0.956*	0.588*	-0.076	0.342*	-0.113	-0.156	0.996*	0.449*	0.286	0.318*	0.382*	0.410*
NFF	P		0.424*	-0.013	0.227	-0.048	-0.013	0.812*	0.256	0.371*	0.206	0.324*	0.354*
	G		0.659*	-0.018	0.388*	-0.078	-0.037	0.972*	0.530*	0.483*	0.237	0.416*	0.488*
NPP	P			0.394*	0.093	0.347*	0.369*	0.506*	0.051	0.345*	-0.050	0.403*	0.524*
	G			0.641*	0.119	0.583*	0.660*	0.632*	0.148	0.475*	-0.063	0.567*	0.764*
PL	P				-0.148	0.953*	0.876*	-0.030	0.028	0.371*	-0.217	0.211	0.397*
	G				-0.164	0.976*	0.989*	-0.040	-0.094	0.452*	-0.250	0.236	0.493*
PW	P					-0.166	-0.173	0.259	0.169	0.019	0.076	0.052	0.019
	G					-0.176	-0.185	0.361*	0.182	0.017	0.078	0.078	0.086
NSP	P						0.860*	-0.062	-0.061	0.364*	-0.287	0.224	0.400*
	G						0.965*	-0.078	-0.215	0.444*	-0.334*	0.261	0.496*
SP	P							-0.080	-0.081	0.363*	-0.300	0.243	0.412*
	G							-0.119	-0.148	0.525*	-0.407*	0.319*	0.572*
DMM	P								0.275	0.258	0.306*	0.342*	0.377*
	G								0.428*	0.282	0.313*	0.385*	0.419*
HD	P									0.040	0.423*	-0.099	0.027
	G									0.033	0.671*	-0.174	0.088
WHP	P										-0.093	0.297	0.428*
	G										-0.102	0.357*	0.487*
TP	P											-0.403*	-0.237
	G											-0.468*	-0.261
TSS	P												0.542*
	G												0.717*

Where, DFPF = Days to fifty per cent flowering, NFF = Node at which the first flower appear, NPP = Number of pods per plant, PL = Pod length, PW = Pod width, NSP = Number of seeds per pod, SP= Shelling percentage, DMM = Days to marketable maturity, HD = Harvest duration, WHP = Weight of hundred pods, TP = Total phenols, TSS = Total soluble solids, PYPP = Pod yield per plot; *Significant at 5% level

Table 4 Estimates of direct and indirect effects of different traits on pod yield per plot in pea

Trait	DFPF	NFF	NPP	PL	PW	NSP	SP	DMM	HD	WHP	TP	TSS	GCCYP
DFPF	**0.287**	-0.504	1.010	0.155	0.049	-0.183	0.028	-3.724	0.220	0.071	-0.047	0.062	0.410*
NFF	3.144	**-0.526**	1.132	0.037	0.055	-0.126	0.007	-3.633	0.260	0.119	-0.035	0.066	0.488*
NPP	1.934	-0.347	**1.717**	-1.312	0.017	0.943	-0.119	-2.363	0.072	0.118	0.009	0.091	0.764*
PL	-0.248	0.009	1.101	**2.047**	-0.023	1.579	-0.181	0.150	-0.046	0.112	0.035	0.038	0.493*
PW	1.125	-0.204	0.203	0.335	**0.142**	-0.285	0.033	-1.349	0.089	0.004	-0.011	0.013	0.086
NSP	-0.371	0.041	1.001	-1.998	-0.025	**1.618**	-0.174	0.293	-0.106	0.110	0.049	0.042	0.496*
SP	-0.514	0.019	1.135	-2.057	-0.026	1.561	**-0.181**	0.446	-0.073	0.130	0.060	0.051	0.572*
DMM	3.274	-0.512	1.086	0.082	0.051	-0.127	0.022	**-3.739**	0.210	0.070	-0.046	0.062	0.419*
HD	1.474	-0.279	0.254	0.193	0.026	-0.348	0.027	-1.602	**0.490**	0.008	-0.099	-0.028	0.088
WHP	0.941	-0.255	0.817	-0.926	0.002	0.719	-0.095	-1.056	0.016	**0.247**	0.016	0.057	0.487*
TP	1.047	-0.125	-0.108	0.512	0.011	-0.540	0.074	-1.170	0.329	-0.025	**-0.147**	-0.075	-0.261
TSS	1.257	-0.219	0.974	-0.482	0.011	0.423	-0.058	-1.440	-0.085	0.088	0.069	**0.161**	0.717*

Residual effect: 0.129; Diagonal figures represent the direct effect

Where, DFPF = Days to fifty per cent flowering, NFF = Node at which the first flower appear, NPP = Number of pods per plant, PL = Pod length, PW = Pod width, NSP = Number of seeds per pod, SP= Shelling percentage, DMM = Days to marketable maturity, HD = Harvest duration, WHP = Weight of hundred pods, TP = Total phenols, TSS = Total soluble solids, GCCYP = Genotypic correlation coefficient of yield per plot; *Significant at 5% level

Conclusion

From this present investigation it can be concluded that five genotypes 14/PMVAR-3, 14/PEVAR-6, 14/PEVAR-2, 14/PMVAR-1 and EC-598628 showed better performance while 14/PMVAR-3 outperformed among them with respect to traits like number of pods per plant, pod length (cm), pod width (cm), number of seeds per pod, shelling percentage (per cent), weight of 100 pods (g), pod yield (kg/plot, q/ha) yield and total soluble solids (per cent). 14/PEVAR-6 is an early maturing genotype with good attractive dark green pods. Significantly positive, phenotypic and genotypic correlation of pod yield per plot was observed with days to fifty per cent flowering, node at which first flower appear, number of pods per plant, pod length, number of seeds per pod, shelling percentage, weight of 100 pods and total soluble solids indicating that simple selection for these traits can be helpful in identifying superior genotypes. Maximum positive direct effect toward pod yield per plot was contributed by days to fifty per cent flowering followed by pod length, number of pods per pant, number of seeds per pod, harvest duration, weight of 100 pods and total soluble solids. Maximum positive indirect effect toward yield was recorded by pod length followed by shelling percentage through number of seeds per pod whereas, node at which first flower appear, total soluble solids also contributed positive indirect effect toward pod yield per plot through number of pods per plant indicating the path through which traits influence the pod yield which is the trait of interest. Thus these genotypes can be recommended for cultivation after multi-location testing in the different regions of state and can also be exploited in future breeding programmes.

Refrences

[1] National Horticulture Database. 2014. Indian Horticulture Database - 2014, Ministry of Agriculture, Govt. of India., 169-176.

[2] Tiwari G and Lavanya G. Genetic variability, character association and component analysis in F4 generation of field pea (Pisum sativum var. arvense L.). Karnataka J. Agric. Sci. 2012, 25: 173-75.

[3] Anonymous. Package of Practices for Vegetable Crops, Directorate of Extension Education, Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan. 2013, 77p.

[4] Gomez K A and Gomez A A. Statistical procedures for Agricultural Research, John Wiley and Sons, New York. 1983, 680p.

[5] Burton G W and DeVane E H.. Estimating heritability in tall fescue (Festuca arundiancea) from replicated clonal material. Agronomy Journal. 1953, 45: 478-481.

[6] Allard R W. Principles of Plant Breeding, John Wiley and Sons, New York. 1960, 485p.

[7] Johanson H W, Robinson H F and Comstock R E. Estimates of genetic and environment variability in soybean. Agronomy Journal. 1955, 47: 314-318.

[8] Al-Jibouri H A, Miller P A and Robinson H P. Genotypic and environmental variance and covariance in an upland cotton cross of interspecific origin. Agronomy Journal. 1958, 50: 633-636.

[9] Dewey D R and Lu K H. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal. 1959, 51: 515-518.

[10] Kumar P, Partap P S and Rana M K. Correlation studies in garden pea (Pisum sativum L.). Haryana Journal of Horticultural Sciences. 2004, 33: 243-245.

[11] Rai M, Verma A, Kumar R and Vishwanath. Multivariate genetic analysis of pea (Pisum sativum L.). Vegetable Science. 2006, 33: 149-154.

[12] Sardana S, Mahajan R K, Gautam N K and Ram B. Genetic variability in pea (Pisum sativum L.) germplasm for utilization. SABRAO Journal of Breeding and Genetics. 2007, 39: 31-41.

[13] Sharma V K and Bora L. Studies on genetic variability and heterosis in vegetable pea (Pisum sativum L.) under high hills condition of Uttarakhand, India. African Journal of Agricultural Research. 2011, 8: 1891-195.

[14] Selvi B S, Rajangam J and Muthuselvi R. Genetic variability and heritability studies for quantitative traits in pea (Pisum sativum L.). Plant Arch. 2014, 14: 955-959.

[15] Kumar R, Kumar M, Dogra R K and Bharat N K. Variability and character association studies in garden pea (Pisum sativum var. hortense L.) during winter season at mid hills of Himachal Pradesh. Legume Research. 2015, 38: 164-168.

[16] Kumar V R A and Sharma R R. Character association studies in garden pea. Indian Journal of Horticulture. 2006, 63: 185-187.

[17]   Patel P J, Patel N H, Prajapati B H, Tikka S B S and Patel P T. Correlation and path analysis in fieldpea. Indian Journal of Pulses Research. 2006, 19: 109-110.
[18]   Guleria S, Chongtham N and Dua S. Genetic variability, correlation and path analysis studies in pea (Pisum sativum L.). Crop Research. 2009, 38: 179-183.
[19]   Pal A K and Singh S. Correlation and path analysis in garden pea (Pisum sativum L. var. hortense). Asian Journal of Horticulture. 2012, 7: 569-573.
[20]   Tyagi N, Singh A K, Rai V P, Kumar S and Srivastava C P. Genetic variability studies for lodging resistance and yield attributes in pea (Pisum sativum L.). Journal of Food Legumes. 2012, 25: 179-182.
[21]   Kaur H, Singh M and Brar P S. Correlation and path analysis in garden pea (Pisum sativum L.). Crop Improvement. 2007, 34 : 186-191.
[22]   Yadav R, Srivastava R K, Kant R and Singh R. Studies on genetic divergence in fieldpea (Pisum sativum L.). Legume Research. 2009, 32: 121-124.