RESEARCH PAPER

Association pattern among yield and its related attributes for early peas (*Pisum sativum* L.)

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Abstract

A study was conducted in Vegetable Research Institute, Faisalabad, Pakistan during 2017-18 and 2018-19 to estimate the genetic variability and correlation among eight different genotypes of pea (Meteor, 9800-5, Pea-2009, 2001-20, Samrina zard, Olympia, 9200-10 and 2001-40). These accessions were sown in RCBD triplicate. Data was collected on morphological parameters i.e. days to 50% flowering, 100-seed weight, yield per plot, plant height, pods per plant, pod length, seed per pod and pod width. The analysis of genetic variability showed high values in genotypic coefficient of variation (GCV 22.42 & 17.81) for pods per plant in bi-annual study of yield related attributes. Maximum genetic advance (36.76% & 20.87%) was also found for pods per plant among all traits in early pea lines. Positive and highly significant correlation (0.8393 and 0.8846) was found with 100 seed weight and pod width during consecutive years (2017-2019). Maximum heritability was found for Pod length (97.95) and days to 50% flowering (96.64) during sequential years. It is concluded that these attributes could be used as selection criteria for the development of early bearing and high yielding varieties.

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Introduction

Pea (*Pisum sativum* L.) contributes to development of low-input farming systems by serving as a break crop which minimizes the need for external inputs. Pea seed contains 23-25% protein, 50% slowly digestible starch, 5% soluble sugars in addition to fiber, minerals and vitamins (Bastianelli *et al.*, 1998). As a legume pea has the capacity for symbiotic nitrogen fixation (Phillips, 1980). Pea has been used as a model system in plant biology since the work of Mendel (Reid *et al.*, 2011) due to its simple nature.

Utilization of landraces and wild relatives of plants to establish adaptation to climate change will be necessary. Pea, through its physiological properties, may partially offset growth reduction associated with higher temperature and shorter growing season (Coyne *et al*, 2011). Normally three categories of pea genotypes are exit around the globe; one for short duration called early pea lines second normal duration called normal pea lines and last long duration called late pea lines. Early pea varieties leave field in 60-70 days while normal lines takes 80-90 days whereas late lines take more 100 days. All types of pea are being cultivated in different regions according to topography and cropping pattern of that particular area. Raising pressure on agriculture and multiple cropping systems urge the farmers to grow early picking and high yielder lines. There is a need to develop early lines with good yield potential so that farmer can raise multiple crops from same field in a year. Plant breeders depend upon variability present in crops for improvement of quantitative and qualitative characters and their mutual association with seed yield. The investigation was undertaken to predict appropriate morphological attributes that could lead for selection criteria to achieve the prescribed goal.

Materials and methods

The study was conducted at the research farm of the Vegetable Research Institute, Faisalabad, Pakistan, during October to February of 2017-18 and 2018-19. In both years eight pea genotypes (Meteor, 9800-5, Pea-2009, 2001-20, Samrina zard, Olympia, 9200-10, 2001-40) were sown in second week of October in a randomized complete block design with 3 replications. All agronomic practices are performed to raise better crop. Data were recorded on days to 50% flowering, 100-seed weight, yield per plot, pod width, pod length, plant height, pods per plant, seed per pod. Data for years were pooled and analyzed to estimate the extent of variability, heritability, and genetic advance as percent of mean, among genotypes. Second order statistics were employed using estimates of variances and co-variances. All quantitative traits were analyzed using analysis of variance (Steel *et al.*, 1997) with MSTATC (Ver.1.5 Michigan state University, East Lansing Mich.). The expected genetic advance resulting from selection of 5% superior individuals were determined. Correlation analysis on genotypic and phenotypic factors was performed as per Burton (1952).

Results and discussion

High magnitude of coefficient of variability in 2017-18 occurred for days to 50% flowering, pods/plant, seed/pod, yield/plot and 100-seed weight (Table 1).

Table 1. Estimates of genetic parameters for traits in pea during crop season 2017-18.

Trait	Coefficient of variation		Heritability Broad sense	Genetic advance
	GCV [a]	PCV	$h^2_{B.S}$	(%)
Days to 50% flowering	23.04	29.71	60.12	31.26
100-Seed weight (g)	13.74	15.13	82.52	21.84
Yield/plot (kg)	12.09	18.09	44.65	14.14
Plant height (cm)	10.57	11.13	90.30	17.58
Pods/plant	22.42	23.94	87.75	36.76
Pod length (cm)	13.80	13.95	97.95	23.91
Seed/pod	17.71	18.26	94.04	30.05
Pod width (cm)	08.43	08.87	90.36	14.02

Similar array was found during 2018-19, the highest value for the coefficient of variation occurred for pods/plant, 100-seed weight and yield/plot (Table 2). Maximum coefficient of variation for yield/plot, pods per plant and 100 seed weight was also reported in pea (Iqbal *et al.*, 2015). The both years study on same lines emphasized that these attributes lead to right direction for breeding early pea varieties.

Table 2. Estimates of genetic parameters for traits in PEA during crop season 2018-19.

Trait	Coefficient of variation		Heritability	Genetic advance
	GCV	PCV	$h^2_{B.S}$	(%)
Days to 50% flowering	05.66	05.76	96.64	09.74
100-Seed weight (g)	12.87	14.90	74.65	19.40
Yield/plot (kg)	15.13	20.61	53.88	19.43
Plant height (cm)	12.52	17.95	48.68	15.29
Pods/plant	17.81	26.59	44.85	20.87
Pod length (cm)	09.34	10.24	83.23	14.91
Seed/pod	05.83	11.17	27.19	05.32
Pod width (cm)	05.54	06.81	66.09	07.88

[a] GCV = Genotypic coefficient of variation   ; PCV = Phenotypic coefficient of variation.

Table 3. Genotypic coefficient correlations for traits in peas during the crop season 2017-18.

Trait	DF	100-SW	Y/P	PH	P/P	PL	S/P
100-SW	0.4903						
Y/P	-0.0585	0.1106					
PH	0.0214	0.4224	0.4995				
P/P	0.5881	0.7335*	-0.0274	0.6345			
PL	0.5543	0.6692	-0.1090	-0.1086	0.4484		
S/P	-0.3732	-0.1127	0.2031	-0.2885	-0.4469	0.3921	
PW	0.4072	0.8393**	0.0092	0.4004	0.7419*	0.6696	-0.0283

All characters with maximum coefficient of variation are economically important in breeding and there is an opportunity for improvement of these characters through selection. Heritable variation can be determined with a greater degree of accuracy if genetic advance is studied along with heritability. The high heritability in broad sense is helpful in selection if coupled with phenotypic performance. The high heritability during 2017-18 occurred for most traits (Table 1). High heritability for pod length, seed/pod, pod width, plant height, pods/plant, 100-seed weight, days to 50% flowering, and minimum heritability occurred for yield/plot. During 2018-19, the highest values for heritability occurred for days to 50% flowering, pod length, 100-seed weight, and there were low values for seed/pod, pods/plant and plant height (Table 2). Data for heritability in this study agreed with Nawab *et al.* (2008) and Fikreselassie (2012). The traits 100 seed weight and pods per plant revealed high genetic advance escorted with high values of heritability could be used in selection of early and high yielding pea lines.

The association between yield and its components and the interrelationship among them, can be useful for effective and successful breeding. In general, genotypic correlation coefficients were higher than their corresponding phenotypic values (Table 3, 4). High genotypic correlation coefficients indicate that there was an inherent relationship between the studied traits and environment but did not reduce their actual association. In 2017-18 pods/plant were

positively, and significantly, correlated with 100-seed weight (Table 3). Pod width was positively, and significantly, correlated with 100-seed weight and significantly correlated with pods/plant (Table 3).

During 2018-19, days to 50% flowering was positively, and significantly, correlated with 100-seed weight and pod width (Table 4).

Table 4. Genotypic coefficient correlations for traits in peas during the crop season 2018-19.

Trait	DF	100-SW	Y/P	PH	P/P	PL	S/P
100-SW	0.7433*						
Y/P	0.4456	0.0096					
PH	0.3771	0.1348	0.0400				
P/P	0.5518	0.6667*	0.3032	0.5376			
PL	0.6268	0.1347	0.3514	-0.4260	0.1889		
S/P	0.5369	0.4277	0.3800	-0.2312	-0.3066	0.4967	
PW	0.7487*	0.8846**	0.2063	0.3553	0.1113	0.4929	0.4404

*= Significant, **= highly significant

[a]DF = Days to 50% flowering, 100-SW = 100-seed weight, Y/P = Yield/plot, PH = Plant height, P/P = Pods/plant, PL = Pod length, S/P = Seed/pod, PW = Pod width.

The 100-seed weight was positively, and significantly, correlated with pod width which was positively correlated with yield/plants (Table 4).

Positive association of 100 seed weight and pod width was also reported by Tiwari and Lavanya, 2012 and Singh and Singh, 2005. So the traits showing positive correlation with yield and its contributing attributes could be helpful for breeding early pea varieties to meet the present challenges.

Conclusion

It is concluded that traits like days to 50%flowering, pods/plant, 100 seed weight and pod width should keep in mind while setting a selection criteria in early pea breeding.

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