

Variability and character association studies for horticultural and quality traits in garden pea (*Pisum sativum* L. var. *hortense*)

Jyoti Devil^{1*}, SK Sanwal^{1,2}, Tanmay K Koley^{1,3}, RK Dubey¹, PM Singh¹ and B Singh¹

Received: September 2018 / Accepted: January 2019

Abstract

The present study was conducted to examine the variability, heritability and correlation of important yield and quality traits and to determine the relative importance of primary and secondary traits as selection criteria to improve productivity in garden peas. Twenty-two diverse genotypes were grown in Randomized Complete Block Design with three replications during 2015-16. The data was collected on ten horticultural and four quality traits. Significant variations existed in all the traits. High value of PCV and GCV (e^{20}) were recorded for days to 50% flowering, plant height, average pod weight, number of pod per plant, 100-green seed weight, green pod yield per plant and for quality traits viz., total phenolics contents, total flavonoids contents, CUPRAC and FRAP activities. This indicates that selection can be applied on the traits to isolate more promising line. High heritability ($e^{80\%}$) and high genetic advance (e^{50}) were noticed for plant height, number of pod per plant, total phenolics contents, total flavonoids contents, CUPRAC and FRAP activities which indicated the role of additive gene action for the inheritance of these traits and are likely to respond better to selection. However, green pod yield per plant revealed moderate heritability and genetic advance. Correlation studies for green pod yield per plant showed a positive and significant correlation with days to 50% flowering, average pod weight and number of pod per plant suggesting improvement of yield by giving special focus to these traits. However, total phenolics and flavonoids contents were found negatively correlated with pod yield.

Keywords: Garden pea, heritability, genetic advance, pod yield and antioxidants activities

Introduction

Garden peas (*Pisum sativum* var. *hortense* L.) is an Old World legume first cultivated 10,000 years ago, and referred as most economically important domesticated crop till date. Being high in nutritive value and its growing acreage, it has attained a status of primary pulse (FAO 2004) and serving as a major source of protein (23-33%) and nutrients in the vegan diet (Devi et al. 2018). It is low in fat but high in fiber, protein, ascorbic acid, β -carotene, thiamine, riboflavin and iron (National Food Administration 2002). Its non-nutritive biologically active components include alkaloids, flavonoids, glycosides, isoflavones, phenols, phytosterols, phytic acid, protease inhibitors, saponins, and tannins that have been reported to contribute to its anti-carcinogenesis properties (Rungruangmaitree and Jiraungkoorskul 2017). In India, garden pea covers 0.5 m ha area with 4.81 mt of production and stands second in total green pea's production after China, sharing 24% of world production. However, insight into area and production data for last two decades showed surprising facts that although the area under green peas production has crossed double from 0.2 m ha since 1993 to 0.5 m ha in 2016, a decreasing trend in productivity has been observed from 13.3t/ha to 9.7t/ha. This might be due to multiple challenges raised by various biotic and abiotic stresses and stagnation in yield performances of newly bred cultivars. Therefore, there is an indispensable demand for varietal improvement in such situation. Yield is a complex trait, dependent on many other component traits that are further interacting with environment. Therefore, to breed the new cultivars, success of any breeding programme depends on the existing genetic variability in the base population that could lead to effective selection to obtain high yielding progenies. A comprehensive knowledge on genetic variability, heritability and genetic advance are pre requisite for improvement of any crop for selection of superior genotypes and improvement of any trait. Similarly,

¹ICAR-Indian Institute of Vegetable Research, Post Box 1, Jakhini, Varanasi-221 305

²ICAR- Central Soil Salinity Research Institute, Karnal- 132 001

³ICAR-Research Complex for Eastern Region, Patna-800014

*Corresponding author, Email: jyoti17iivr@gmail.com

information on character association in peas is important for effective and rapid selection in crop improvement. It is important to highlight that though reports on variability studies for various horticultural traits in garden peas are available, genetic information on quality traits such as total phenolics, total flavonoids and antioxidants activities is limited. In line with this, the objective of the study was to examine the existence of genetic variability, heritability, genetic advance in 22 diverse accessions of garden peas for various yield and quality traits and to determine the relative importance of primary and secondary traits as selection criteria to improve productivity.

Materials and Methods

Twenty-two diverse genotypes of green-pea that differs in maturity group, plant-height, flower-color, seed-shape and mature seed coat color comprised the basic experimental materials. These genotypes were evaluated for various horticultural and quality traits at Experimental Farm of ICAR- Indian Institute of Vegetable Research, Varanasi, located at 82°52'37" E and 25°18'21" N at an elevation of 83 m above the mean sea level (AMSL). Field evaluation of genotypes for yield and yield contributing traits was carried out in Randomized Block Design (RBD) with three replications during *Rabi*, 2015-16. Each genotype was grown in plot size of 3m² by keeping the row-to-row and plant-to-plant spacing at 30 × 10 cm. The standard agronomical practices were adopted to raise the healthy crop.

The observations were recorded on randomly taken ten plants of each genotype for yield and its contributing traits viz., days to 50% flowering, plant height (cm), pod length (cm), pod width (cm), seeds per pod, 100-green seed weight; number of pod per plant, average pod weight (g), yield per plant (g) and shelling percentage. The quality traits include total phenolics and total flavonoids contents, and their antioxidant activities through two different methods viz., Cupric Reducing Antioxidant Capacity (CUPRAC) and Ferric Reducing Antioxidant Power (FRAP). Fresh green-pea pods at the edible stage were randomly selected for total phenolic, total flavanoids and antioxidants estimation. Further, mature green-seeds were used for each biochemical trait and analysis of each sample was done in triplicates. TPC estimation was performed spectrophotometrically using Folin-Ciocalteu reagent (Singleton *et al.* 1999) whereas; total flavonoids content was evaluated using aluminium chloride method (Zhishen *et al.* 1999). CUPRAC assay was performed as described by Apak *et al.* (2005) and FRAP was estimated as described by Benzie and Strain (1996).

Mean, standard deviation, standard error, and coefficient of variation (CV) of each trait were calculated by subjecting the data on yield and related component traits to the analysis of variance (Gomez and Gomez 1983). The genotypic and phenotypic coefficient of variations (GCV and PCV) and heritability (broad sense) were estimated by following method of Burton and De Vane (1953). Genetic advance (GA) was calculated as per Burton and De Vane (1953) and Johnson *et al.* (1955). Coefficients of correlation were calculated as suggested by Al-Jibouri *et al.* (1958). Statistical analysis was performed using Windostat version 8.5 (<http://www.indostat.org>). Limits used for categorizing the magnitude of different parameters adopted from Devi *et al.* (2015) as GCV and PCV values are high (More than 20); moderate (10-20) and low (Less than 10); heritability values are high (More than 80); moderate (50-79) and low (Less than 50) and genetic advance are high (More than 50), moderate (25-49) and low (Less than 25).

Results and Discussion

Genetic variability: Crop genetic diversity treated as wealth of the breeders as adequate variability provides options from which selections are made for improvement and possible hybridization for novel recombinants. Analysis of variance revealed significant differences ($P = 0.05$) among genotypes for all the fourteen traits studied. The estimates of mean, range, genotypic and phenotypic coefficient of variations for various traits are presented in Table 1. Selection within the genotypes for a particular trait is effective when magnitude of variations in the breeding population is good enough. The genotypes showed highest diversity for the trait viz., total phenolics contents (10 folds over the minimum value) followed by plant height, green pod yield per plant, days to 50% flowering and total flavonoids contents indicating that these traits have more scope for genetic improvement. Contrary to these, least variation was observed for the traits viz., pod width, pod length, seeds per pod and average pod weight in the experimental materials used.

Furthermore, estimates of phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) ranged from 5.90 -96.88 and 8.69-97.98, respectively. High value of PCV and GCV ($e^{>20\%}$) were recorded for days to 50% flowering, plant height, average pod weight, number of pods per plant, 100-green seed weight, green pod yield per plant and for quality traits viz., total phenolics contents, total flavonoids contents, CUPRAC and FRAP activities. It indicates that selection can be applied on these traits to isolate more promising lines. High PCV and GCV values

Table 1: Estimates of variability for different horticultural and quality traits in twenty-two genotypes of garden pea

Traits	Range		Mean \pm SE(m)	GCV (%)	PCV (%)	h ² (%) (bs)	GA as % of Mean
	Minimum	Maximum					
Horticultural traits							
Days to 50% flowering	32.33	76.67	53.88 \pm 1.81	27.52	28.13	95.7	29.88
Pod length (cm)	6.31	9.97	8.11 \pm 0.31	13.37	14.94	80.1	24.65
Pod width (cm)	0.97	1.66	1.21 \pm 0.03	13.63	14.38	89.8	26.60
Plant height (cm)	46.43	170.23	84.35 \pm 4.92	31.49	33.07	90.7	61.76
Average pod weight (g)	2.49	7.87	5.43 \pm 0.46	23.67	27.84	72.4	41.51
Number of pod per plant	7.17	21.07	11.42 \pm 0.99	28.99	32.71	78.6	52.95
Seeds per pod	5.17	9.10	7.24 \pm 0.35	11.38	14.14	64.8	18.88
100-green seed weight (g)	34.7	76.2	56.91 \pm 2.30	21.36	22.49	90.3	41.8
Green pod yield per plant (g)	22.67	86.00	56.49 \pm 5.80	25.65	31.22	67.5	43.40
Shelling percentage	41.67	55.72	50.90 \pm 1.88	5.90	8.69	46.0	8.24
Quality traits							
Total phenolics content (mg GAE/100 g fw)	12.63	128.63	32.76 \pm 1.79	85.65	86.17	98.8	175.38
Total flavonoids content (mg CE/100 g fw)	4.61	45.84	13.44 \pm 1.23	73.43	75.13	95.5	147.84
Antioxidant Activities							
CUPRAC (μ mol TE/g fw)	3.20	27.79	7.47 \pm 0.61	80.92	82.17	97.0	164.15
FRAP (μ mol TE/g fw)	0.41	11.70	2.29 \pm 0.19	96.88	97.98	97.8	197.34

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation, h²: heritability; GA: genetic advance; CUPRAC: Cupric ion antioxidant reducing capacity; FRAP: ferric reducing/antioxidant power

for plant height, number of pod per plants and 100-green seed weight were also observed by Davendra et al. (2013) and for days to 50% flowering, plant height, pod weight and 100- seed weight by Selvi et al. (2014). On the other side, moderate values were observed for pod length, width and seeds per pod suggested that these traits can be improved only by applying vigorous selection. Higher phenotypic coefficient of variation than genotypic coefficient of variation indicated that most of the yield attributes were under the influence of

environment. Further, phenotypic coefficient of variation also had similar trend as genotypic coefficient of variation and there was a close correspondence between genotypic and phenotypic coefficient of variation for all the recorded traits. It showed that these characters less influenced by the environment.

Heritability and genetic advance: High heritability estimates (e²>80%) were observed for days to 50% flowering, pod length, pod width, plant height, 100-

Table 2: Phenotypic and genotypic correlation coefficients for pod yield and quality traits in garden peas

Traits		Pod length	Pod width	Plant height	Average pod weight	Number of pod per plant	Seeds per pod	Shelling percentage	100- green seed weight	Green pod yield Per Plant
Days to 50% flowering	P	0.018	-0.073	0.358**	-0.420 **	0.494 **	-0.025	-0.330 **	-0.395**	0.235
	G	0.042	-0.053	0.390**	-0.501**	0.569**	-0.082	-0.502**	-0.431**	0.318**
Pod length	P	1.000	0.509 **	-0.456 **	0.309 *	-0.250 *	0.379 **	-0.164	0.302 *	0.131
	G	1.000	0.545**	-0.523**	0.439**	-0.372**	0.512**	-0.194	0.322**	0.109
Pod width	P		1.000	-0.282 *	0.232	-0.220	-0.013	-0.468 **	0.431 **	0.131
	G		1.000	-0.310*	0.292*	-0.270*	0.065	-0.742**	0.469**	-0.016
Plant height	P			1.000	-0.643 **	0.414 **	-0.279*	-0.279 *	-0.518 **	-0.139
	G			1.000	-0.827**	0.461**	-0.302*	-0.360**	-0.568**	-0.016
Average pod weight	P				1.000	-0.489 **	0.044	0.130	0.644 **	0.402**
	G				1.000	-0.541**	0.068	0.296*	0.814**	0.336**
Number of pod per plant	P					1.000	0.021	-0.042	-0.523**	0.542**
	G					1.000	0.036	-0.153	-0.622**	0.585**
Seeds per pod	P						1.000	0.213	-0.271 *	0.026
	G						1.000	0.306*	-0.309*	0.046
Shelling percentage	P							1.000	0.030	0.008
	G							1.000	-0.020	0.017
100-green seed weight	P								1.000	0.071
	G								1.000	0.085

*Significant at 5% level of significance and **Significant at 1% level of significance

green seed weight, total phenolics contents, total flavonoids contents, CUPRAC and FRAP activities. Johanssen (1909) stressed that for estimating the actual effects of selection, heritability alone could not be the sole guideline for improvement since high heritability does not mean high expected genetic advance. Hence, prediction on the basis of both the estimates could be more useful. The characters those exhibit maximum heritability and high genetic advance as percentage of mean could be used as powerful tool in selection process such characters are controlled by the additive genes and less influenced by the environment (Panes and Sukhatme 1995). In this context, high heritability and high genetic advance ($e'' 50$) were noticed for plant height, number of pod per plant, total phenolics content, total flavonoids contents, CUPRAC and FRAP activities which indicated the role of additive gene action for the inheritance of these traits and are likely to respond better to selection. High heritability along with high genetic advance for the traits viz., days to 50 % flowering, number of pod per plant and 100 -seed weight (Barcchiya *et al.* 2018); number of pod per plant and total phenol content (Kumar *et al.* 2015); plant height and number of pod per plant (Thakur *et al.* 2016) and days to 50% flowering and 100-seed weight (Iqbal *et al.* 2015) were also reported in their respective experiments. High heritability with moderate genetic advance was observed for the traits viz., days to 50% flowering, pod width, average pod weight and 100- green seed weight. Number of seed per pod and shelling percentage exhibited moderate and low heritability, respectively along with low genetic advance. A similar observation was also made by Sharma and Sharma (2013) in garden peas however, in contrary, Thakur *et al.* (2016) reported high heritability and genetic advance for these two traits.

Correlation coefficients: Understanding the magnitude and direction of correlations can assist the breeders in selection decisions. Such studies in selection programmes are appreciable when highly heritable traits are associated with the important trait like yield (Kaswan *et al.* 2018). Estimate of the phenotypic and genotypic correlation coefficients among the ten horticultural traits of garden pea genotypes are presented in Table 2. The correlation studies indicated the greater magnitude of genotypic correlations with pod yield than the phenotypic ones in majority of cases, thus revealing the inherent relationship among these traits. However, genotypic correlation coefficient of average pod weight was less than its corresponding estimates of phenotypic correlation which indicated significant role of environment in the expression of this trait. Correlation study for pod yield showed a positive and significant

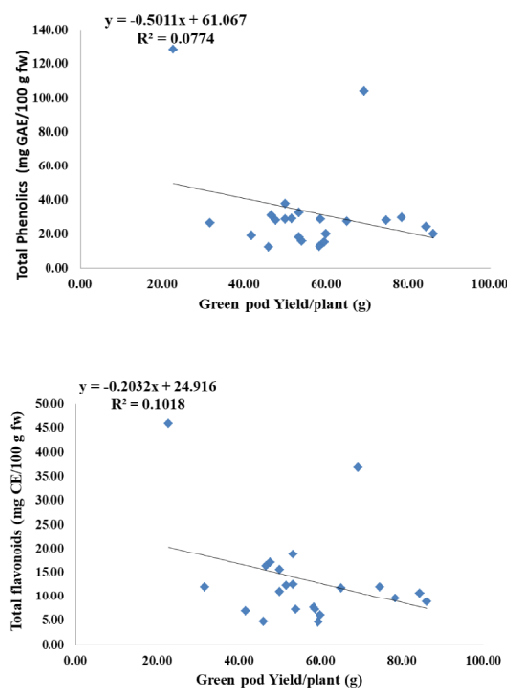


Fig 1: Linear correlation of total phenolics (a) and flavonoids contents (b) with green pod yield per plant

correlation with days to 50% flowering ($rP=0.235^{**}$ and $rG= 0.318^{**}$), average pod weight ($rP=0.402^{**}$ and $rG= 0.336^{**}$), and number of pod per plant ($rP=0.542^{**}$ and $rG= 0.585^{**}$), suggesting improvement of yield by giving special focus to these traits through indirection selection (Table 2). High positive correlation of number of pod per plant with pod yield have also been reported by Kumar *et al.* (2015) and Thakur *et al.* (2016). Figure 1(a) showed linear correlation of total phenolic with green pod yield per plant (Correlation coefficient, $r = -0.278^{*}$ and coefficient of determination, $R^2 = 0.077$, significant at the 0.05 level) whereas Figure 1(b) showed linear correlation of total flavonoids with green pod yield per plant (Correlation coefficient, $r = -0.319^{**}$ and coefficient of determination, $R^2 = 0.101$, significant at the 0.05 level). Thus, both the traits were found negatively correlated with yield. Kumar *et al.* (2015) also found a negative correlation of total phenol with pod yield in peas.

From the results of the present study, it could be concluded that direct selection can be done for traits viz., days to 50% flowering, plant height, number of pod per plant, total phenolics contents, total flavonoids contents and antioxidant activities since these traits exhibited high genetic variability, heritability and genetic advance. Correlation study revealed positive and significant correlation of green pod yield with days to 50% flowering, average pod weight and number of pod per plant. This showed that selection for these traits

would lead to indirect selection for green pod yield. Further, direct selection for a genotype with high pod yield, phenolics and flavonoids contents is difficult to achieve, due to negative association of above traits, however, genotype with high phenolics contents and high yield could be identify and utilized in crossing programme to incorporate better antioxidant potential along with higher yield traits through pedigree selection from segregating populations.

सारांश

सब्जी मटर में वर्तमान अध्ययन उपज एवं गुणवत्ता वाले लक्षणों की परिवर्तनशीलता, आनुवांशिकता और सहसंबंध की जांच करने तथा उत्पादकता में सुधार के लिए चयन मापदंड के रूप में प्राथमिक एवं माध्यमिक लक्षणों के सापेक्ष महत्व के निर्धारण हेतु किया गया। परीक्षण हेतु वर्ष 2015–16 के दौरान सब्जी मटर के 22 विविध प्रभेदों का यादृच्छिक सम्पूर्ण प्रखण्ड आकार (रैन्डमाइज्ड कम्प्लीट ब्लॉक डिजाइन) में तीन बार प्रतिकृति कर मूल्यांकन किया गया। सभी लक्षणों हेतु सार्थक भिन्नताएं पायी गयी। मटर में 50 प्रतिशत पुष्पन की अवस्था, पौधों की ऊँचाई, औसत फली वजन, प्रति पौध फलियों की संख्या, 100 हरे बीजों का वजन, प्रति पौध फली की उपज और फली गुणवत्ता वाले अन्य लक्षणों जैसे— गुल फेनोलिक्स, फ्लेवोलिक्स, क्यूप्रैक और फ्रैप के लिए बाह्यदृश्य प्रारूप विविधता गुणांक और आनुवांशिक विविधता गुणांक के लिये उच्च मापदंड पाया गया। उच्च आनुवांशिक और उच्च आनुवांशिक उन्नति, पौधों की ऊँचाई, प्रति पौध फल संख्या, कुल फ्लेवोनाइड, क्यूप्रैक और फ्रैप के लिए पाया गया जो चयन प्रक्रिया के लिए महत्वपूर्ण घटक हैं। हालांकि प्रति पौध हरी फलियों की उपज मध्यम आनुवांशिकता और आनुवांशिक उन्नति को प्रकट करती है। कुल फेनोलिक्स एवं फ्लेवोनाइड की मात्रा प्रति पौध फल उपज के साथ नकारात्मक संबंध पाया गया। प्रति पौध हरी फलियों की उपज के लिए सहसंबंध 50 प्रतिशत पुष्पन, औसत फली वजन और प्रति पौध फलियों की संख्या के साथ सकारात्मक और महत्वपूर्ण सहसंबंध पाया। उपरोक्त घटक लक्षणों को आधार मानकर सब्जी मटर के चयन प्रक्रिया सुधार लाया जा सकता है।

References

- Al-Jibouri HA, Millar PA and Robinson HF (1958) Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agron J* 50: 632-636.
- Apak R, Guclu K, Zyurek MO, Karademir SE, Altun M (2005) Total antioxidant capacity assay of human serum using copper (II)-neocuproine as chromogenic oxidant: The CUPRAC method. *Free Radical Res.* 39: 949–61.
- Barochiya J, Naidu AK, Mehta AK and Upadhyay A (2018) Genetic variability, heritability and genetic advance for yield and yield components in pea (*Pisum sativum* L.). *Inter J Chem Stud* 6: 3324-3327.
- Benzie IF and Strain JJ (1996) The ferric reducing ability of plasma (FRAP) as a measure of “antioxidant power”: the FRAP assay. *Anal Biochem* 239: 70–76.
- Burton GW and De Vane EH (1953) Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agron J* 54: 478-481.
- Davendra K, Sunil M, Singh SK, Mukesh K (2013) Genetic Variability, heritability and genetic advance for seed yield and yield components in garden pea (*Pisum sativum* L.). *Inter J Plant Res* 26(2):182.
- Devi J, Mishra GP, Sanwal SK, Dubey RK, Singh PM, Singh B (2018) Development and characterization of penta-flowering and triple flowering genotypes in garden pea (*Pisum sativum* L. var. hortense). *PLoS ONE* 13, e0201235. doi. 10.1371/journal.pone.0201235.
- Devi J, Sharma A, Singh Y, Katoch V and Sharma KC (2015) Genetic variability and character association studies in French bean (*Phaseolus vulgaris* L.) under North-Western Himalayas. *Leg Res* 38: 149-156.
- FAOSTAT (2016) <http://www.fao.org/faostat/en/#home> (Accessed on 12th April, 2018).
- Gomez AA and Gomez KA. *Statistical procedure for agriculture research*, second Ed. John Willey and Sons, Inc. New York; 1983. pp 357–427.
- Johannsen WL (1909) *Elemente der exakten Erblichkeitslehre*, Fisher, Jawa.
- Johnson HW, Robinson HF and Comstock RE (1955) Estimation of genetic and environmental variability in soybean. *Agron J* 47: 314-318.
- Kaswan V, Kaushik A, Devi J, Joshi A and Maloo SR (2018) Genetic association studies for yield and yield contributing traits in *Plantago ovata* Forsk. *Electron J Plant Breed* 9: 51-59.
- Kumar R, Kumar M, Dogra RK and Bharat NK (2015) Variability and character association studies in garden pea (*Pisum sativum* var. hortense L.) during winter season at mid hills of Himachal Pradesh. *Leg Res* 38: 164-168.
- National Food Administration (2002) *Food composition database ver. 02.2*, code 1155, Uppsala, Sweden.
- Panes VG and Sukhatme PV (1995) *Statistical methods for agricultural workers*. 3rd Edition, ICAR, New Delhi pp 58.
- Rungruangmaitree R and Jiraungkoorskul W (2017) Pea, *Pisum sativum*, and its anticancer activity. *Phcog Rev* 11:39-42.
- Selvi BS, Rajangam J and Muthuselvi R (2014) Genetic variability and heritability studies for quantitative traits in pea (*Pisum sativum* L.). *Plant Archives* 14: 955-959.
- Sharma BB and Sharma VK (2013) Genetic variability, heritability and genetic advance studies in garden peas under mid hill condition of Garhwal Himalaya. *Environ and Eco* 31: 296-301.
- Singleton VL, Orthofer R and Lamuela-Raventos RM (1999) Analysis of total phenols and other oxidation substrates and antioxidants by means of Folin-Ciocalteu reagent. *Methods Enzymol* 299:152–178.
- Thakur S, Thakur R and Mehta DK (2016) Genetic variability and association studies for green pod yield and component horticultural traits in garden pea under high hill dry temperate conditions of Tabo valley of Spiti district of Himachal Pradesh. *Inter J Sci Environ Tech* 5: 1987 -1992.
- Zhishen J, Mengcheng T and Jianming W (1999) The determination of flavonoid contents in mulberry and their scavenging effects on superoxide radicals. *Food Chem* 64: 555-559.