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Genetic Variability in Advanced Generations of Vegetable Pea (*Pisum sativum* L.)

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ABSTRACT

An experiment was undertaken to study genetic variability and character association in 26 advanced lines of vegetable pea (*Pisum sativum* L.) based on eight characters. Among twenty six advanced lines twelve obtained from the cross between Edible Podded Pea and IPSA Motorsuty-1, nine obtained from the cross between Local White and IPSA Motorsuty-3 and five parental lines were included to measure genetic variability. The field experiment was conducted at the research farm, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh. Analysis of variance showed significant differences among the genotypes for all characters. Phenotypic coefficients of variation (PCV) was close to genotypic coefficients of variation (GCV) for all the characters except branches per plant, seeds per pod, pods per plant, 100-seed weight and seed yield per plant. High heritability associated with high genetic advance was observed for plant height, pod length and seed yield per plot. Significant positive genotypic and phenotypic correlation between seed yield per plant and days to 50% harvest, pod length, pod breadth and seeds per pod were observed. Path coefficient analysis revealed that days to 50% flowering, days to 50% harvest, number of branches per plant, pods per plant, seeds per plant and 100-seed weight had positive direct effect on seed yield per plant.

Keywords: vegetable pea, heritability, genetic advance, character association

INTRODUCTION

Pea (*Pisum sativum* L., 2n=2x=14) is one of the earliest food crops. It thrives well in places with cool climate and hence is grown in almost all the temperate regions of the world (Vavilov 1926; Blixt 1970). Pea has a wide range of agricultural and horticultural uses. The green seeds are used as fresh, frozen or canned vegetables and the mature dry seeds are used as dhal. It is a high protein (27%) crop for human consumption. In recent years the value of peas for fodder purposes has increased (its green matter contains 14 to 24% proteins, average 16%) as well as its value as a vegetable crop (green peas are the high protein-containing vegetable with a protein content of 6-7% on the fresh weight basis). The protein of peas contains all the essential amino acids important for the normal activity of living organisms (Smirnova-Ikonnikova 1960). As part of a nutritious diet, especially for children and the elderly, green peas are very valuable when consumed in fresh, canned or frozen form. The green pea seeds and immature pods of peas have the best balance of vitamins. Garden peas and immature pods of peas, unlike other vegetables, are typified by a high level of active lipotropic antisclerotic substances-choline deficiency may lead to the development and growth of malignant tumors (Petrovskii 1968).

The inclusion of peas in crop rotation is agronomically very significant. The pea is a good predecessor to other crops as it enriches the soil with the nodule bacteria which live in its roots and it fixes nitrogen which live in its roots and it fixes nitrogen which becomes available to other plants (Rudnicki and Wenda 2002). Moreover, peas have a higher capacity to utilize minerals (inorganic compounds) which are difficult to assimilate and therefore practically not available for cereals (Adgo and Schulze 2002). The root system of peas penetrates to a depth of 1-1.5 m and as a result peas can extract nutrients from the deeper soil layers unlike grain crops (Tricot *et al.* 1997; Vocanson *et al.* 2006). There is a shortage of off-season vegetable in our country, green pea can be considered as vegetable crop as it need smaller area of land and can also be grown without competition with cereal crops (Hasan Mitu *et al.* 2004). In recent years, due to the need for intensive land utilization aiming at obtaining two to three crops a year from the same piece of land (Vinning 2004), new trends of breeding have to developed in our country for higher number of functional nodules on the pea roots, the activity of which makes this once of the nitrogen fixing crop (Sattar *et al.* 1998).

Genetic variability has been considered as an important factor which is also essential prerequisite for crop improvement program for obtaining high yielding progenies (Tiwari Lavanya 2012). The evaluation of genetic variability is important to know the source of genes for a particular trait within the available germplasm (Chakraborty and Haque 2000; Bhardwaj and Kohli 1999). There was no common criterion for selection of genotypes on the basis of specific objectives among the plant materials. The most important tasks for a pea breeding are development of high yielding varieties with stable productivity with a high output of seeds from the total biological yield (relatively high seed production-the harvest index), with sufficiently good resistance to diseases and unfavorable environmental conditions (drought, heat, high salt content in the soil), with different maturing types with a high rate of organic matter accumulation during the initial phases of growth, sufficiently high intensity of photosynthesis, increases in protein content, essential amino acids and favorable rations among them (Gritton 1986; Abdou *et al.* 1999; Tiwari *et al.* 2001). For all of these, genetic variability is very important to select suitable types among the segregating populations. It is necessary to partition the observed variability into its heritable and non-heritable components with the help of suitable genetic parameter such as genotypic coefficient of

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Table 1 Analysis of variance for yield and yield related characters in vegetable pea.

Sources of variation	df	DFPF	DFPH	PH	PPP	PL	PB	HGSW	SYPP
Replication	2	3.32	1.19	10.87**	1.70	1.48*	0.01	5.77*	1.05*
Genotype	25	231.85**	320.53**	1557.27**	4.90**	245.96**	9.60**	190.69**	9.51**
Error	50	3.21	2.66	27.98	0.74	8.31	0.18	16.79	1.56
CV%		3.55	2.10	6.90	13.99	4.18	3.41	18.88	24.38

** &* Significant at 1% and 5% level of probability, respectively

DFPF = days to 50% flowering, DFPH = days to 50% harvesting, PH = plant height (cm), PPP = pods per plant (no), PL = pod length (cm), PB = pod breadth (mm), HGSW = 100 green seed Weight (g), SYPP = seed yield per plant (g)

Table 2 Genetic component of variation for yield and yield related characters in vegetable pea.

Components	DFPF	DFPH	PH	PPP	PL	PB	HGSW	SYPP
Mean	50.59	77.63	75.74	6.13	69	12.49	21.89	166.08
Range	29-59	52-98	22.5-126.6	3.1-11.5	48.49-90.94	9.51-16.87	12.5-68	2.49-10.49
σ^2g	79.29	110.62	509.27	1.44	82.51	3.16	59.51	2.76
σ^2p	82.62	112.62	537.27	2.2	91.07	3.35	76.9	4.37
GCV	17.6	13.55	29.8	19.59	13.16	14.23	35.25	32.41
PCV	17.97	13.67	30.6	24.22	13.83	14.63	40.07	40.81
h^2b (%)	95.97	98.22	94.79	65.48	90.6	94.54	77.38	63.08
GA	17.97	21.47	45.26	2	17.81	3.56	13.98	2.72
GA(%mean)	35.52	27.52	59.76	32.66	25.81	28.5	63.87	53.03

DFPF = days to 50% flowering, DFPH = days to 50% harvesting, PH = plant height (cm), PPP = pods per plant (no), PL = pod length (cm), PB = pod breadth (mm), HGSW = 100 green seed Weight (g), SYPP = seed yield per plant (g)

variation (GCV), heritability estimates and genetic advance etc. (Johnson *et al.* 1955; Hanson *et al.* 1956). It is also beneficial to make comparative study of a few characters to select the desirable ones in different strains. Study of association of characters is to identify the role of each individual character towards yield (Dewey and Lu 1959). The research work in this study aims at studying genetic variability available in advanced generations of pea which may help to select suitable types for commercial cultivation.

MATERIALS AND METHODS

The experiment was conducted at the field laboratory, Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Bangladesh during the winter season (November to March). The experimental materials were included five varieties (IPSA-1, IPSA-2, IPSA-3, BARI-1 and Local white), 12 advanced lines obtained from cross Edible Podded Pea × IPSA Motorsuty-1 (L-19, L-95, L-128, L-227, L-145, L-195, L-252, L-20, L-92,L-160, L-141 and L-72) and nine advanced lines obtained from cross Local white × IPSA Motorsuty-3 {L-120, L-20, L-105, L-247, L-26, L-244, L-142 (tall) and L-142 short)}. The seeds were sown in the field and seedlings were emerged five to twelve days after seed sowing. The experiment was conducted using the Randomized Complete Block Design (RCBD) with three replications. The unit plot size was 50 m × 4 m with a row-to-row distance of 50 cm and a plant-to-plant distance of 20 cm. Each plot consisted of 78 rows and plot to plot distance was 0.5 meter. The unit plots were fertilized with cow dung, urea, TSP and MP at 10 t, 45 kg, 62.5 kg, 50 kg per ha, respectively. The entire cow dung, TSP, MP and half of the urea were applied at the time of final land preparation. The remaining half of urea was applied as top dressing in two installments. First top dressing was done at 21 days after and second at 42 days after sowing.

Data were noted on individual plant basis from eight randomly selected competitive plants. Days to 50% flowering (DFPF), days to 50% harvesting (DFPH), plant height (PH), pod length (PL), pod breadth (PB), pods per plant (PPP), 100-green seed weight (HGSW), and seed yield per plant (SYPP). The mean, range and standard deviation (σ_x) for each character have been calculated and analysis of variance for each of the character was performed. The mean square (MS) at error and phenotypic variances were estimated as per Johnson *et al.* (1995). Genotypic and phenotypic co-efficient of variation was calculated by the formula suggested by Burton (1952). Broad sense heritability was estimated (defined by Lush 1949) by the following formula, suggested by Hanson *et al.* (1956) and Johnson *et al.* (1955). The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1949) and Johnson *et al.* (1955). Genotypic and phenotypic correlation coefficients were measured with the formula suggested by Johnson *et al.* (1955) and later on adopted Hanson *et al.* (1956). Correlation coefficient was further partitioned into components of direct and indirect effects by path coefficient analysis originally developed by Wright (1921) and later described by Dewey and Lu (1959) and Singh and Choudhary (2006).

RESULTS AND DISCUSSION

Genetic variability, heritability and genetic advance

The analysis of variance (**Table 1**) indicated the existence of significant variability for all the characters studied except branch per plant and seeds per pod. The mean, range, genotypic, phenotypic and environmental variance; genotypic, phenotypic and environmental coefficients of variation, heritability estimates, genetic advance and genetic advance in percent mean are presented in **Table 2**. The minimum and maximum duration for DFPF were required by the genotypes IPSA-1 (29 days) and L-160 (59 days). The minimum days required for DFPH was recorded in IPSA-1 and maximum days for this trait was noted in Local White. The genotype IPSA-1 was found to be shortest (24.72) and genotype L-145 was found to be tallest (L-126). The highest and the lowest number of PPP were produced by the genotypes L-141 (9.2) and IPSA-2 (4.17) respectively. Plant height ranged from 48.49 cm in L-105 (brown seed) to 90.94 cm in L-72. The maximum and minimum PB was observed in L-95 (16.87 mm) and L-142 (short) (9.51 mm). The lowest number of SPP was found in L-20 and the highest in L-26. The highest seed yield per plant was observed in genotype L-72 (10.49 g) followed by Local White. Genotype L-252 produced the highest SYPP (10.49 g) and genotype L-20 produced lowest yield (2.49 g) per plant. Other studies have also indicated the existence of variation among the genotypes for most of the traits studied (Devendra *et al.* 1998; Devendra *et al.* 2001; Tiwari and Lavanya 2012).

The phenotypic variance was higher than genotypic variance in all the characters studied. The phenotypic coefficients of variation were higher than genotypic coefficients of variation in all the characters studied indicating the importance of environmental influence on their expression (**Table 2**). Similar results were also reported by Sardana *et al.* (2007) and Fikreselassie (2012). Phenotypic coefficients of variation were close to genotypic coefficients of variation except plant height, seeds per pod, 100 seed weight and seed yield per plant. High heritability (>50%) was observed for all characters. Nawab *et al.* (2008) also reported high heritability DFPF (90.62), PL (92.46) and HGSW (90.86). The high heritability coupled with high genetic advance in

Table 3 Genotypic (r_g) and phenotypic (r_p) correlation coefficient of eight different characters in vegetable pea.

Characters		DFPH	PH	PPP	PL	PB	HSW	SYPP
DFPF	r_g	0.841**	0.296	0.133	0.694**	0.280	-0.026	-0.327
	r_p	0.818**	0.283	0.132	0.634**	0.268	-0.016	-0.254
DFPH	r_g		0.321	0.191	0.714**	0.385	0.122	0.586**
	r_p		0.308	0.154	0.676**	0.367	0.112	0.462*
PH	r_g			0.008	0.167	0.048	-0.290	-0.102
	r_p			0.004	0.161	0.046	-0.246	-0.067
PPP	r_g				0.347	0.262	-0.235	0.197
	r_p				0.269	0.212	-0.151	0.217
PL	r_g					0.725**	0.485*	0.701**
	r_p					0.670**	0.416	0.551*
PB	r_g						0.611**	0.656**
	r_p						0.544*	0.512*
HSW	r_g							0.166
	r_p							0.193

** and * Significant at 1% and 5% level of probability, respectively

DFPF = days to 50% flowering, DFPH = days to 50% harvesting, PH = plant height (cm), PPP = pods per plant (no), PL = pod length (cm), PB = pod breadth (mm), HGSW = 100-green seed weight (g), SYPP = seed yield per plant (g)

percent mean observed in DFPF, DFPH, PH, HGSW and SYPP suggested that effective selection may be done for these characters (**Table 2**). Singh and Singh (2006) reported high heritability for PH (95.70%), PPP (90.80%), HSW (89.90%) and SYPP (93.20%) coupled with high expected genetic advance in pea.

Association in yield-contributing characters

Yield is a complex character and associated with several yield contributing characters. Selection for yield may not be effective unless other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercise for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection. Genotypic and phenotypic correlations between pairs of characters are presented in **Table 3**. The genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the cases indicating the association is largely due to genetic reason.

Days to 50% flowering showed highly significant positive correlation with days to 50% harvesting (r_g= 0.841, r_p= 0.818) and pod length (r_g= 0.694, r_p= 0.634) and non-significant positive correlation both at genotypic and phenotypic levels with the rest of characters (**Table 4**). Tiwari and Lavanya (2012) found days to 50% flowering was positively associated with days to maturity (r_g= 0.97, r_p= 0.18). Days to 50% harvest (r_g= 0.586, r_p= 0.462), pod length (r_g= 0.701, r_p= 0.551) and pod breadth (r_g= 0.656, r_p= 0.512) showed significant positive genotypic and phenotypic correlation with seed yield per plant. Days to 50% harvesting also showed non-significant positive correlation (r_g= 0.166, r_p= 0.193) with days to 50% flowering (**Table 3**). According to Mahak *et al.* (2004) days to maturity is a major yield-contributing character in field pea. Kumar *et al.* (2003) reported number of days to flowering showed a positive association with number of days to maturity and number of seeds per pod.

Plant height showed positive and non-significant correlation found in pods per plant, pod length, pod breadth at both genotypic and phenotypic level. Vivek *et al.* (1999) reported that plant height showed a negative correlation (-0.233) with seed yield per plant in chickpea genotypes. Pods per plant showed positive correlation with pod length (r_g= 0.347, r_p= 0.269), pod breadth (r_g= 0.262, r_p= 0.212) and seed yield per plant (r_g= 0.197, r_p= 0.217) both at genotypic and phenotypic level (**Table 3**). Seed yield significantly and positively correlated (r_g= 0.68, r_p= 0.38) with pods per plant (Tiwari and Lavanya 2012). Correlations among the characters indicated that pods per plant are an important character in selection for improved seed yield. Natarajan and Rathinasamy (1999) and Devendra *et al.* (1998) assessed pods per plant exerted positive direct effect on yield. Grain yield had significant genotypic (0.760) and phenotypic (0.780) correlation with pods per plant (Muhammad *et al.* 2009).

Pod length showed significant positive genotypic and phenotypic correlation with pod breadth and significant positive genotypic correlation with 100 green seed weight (**Table 3**). Significant positive genotypic and phenotypic correlation was observed by 100 green seed weight. Pod length and pod breadth showed highly significant positive correlation with 100 green seed weight and seed yield per plant at genotypic level (**Table 3**). Islam *et al.* (1999); Sharma (2003); Singh and Singh (2006); Sardana *et al.* (2007) assessed pod length exerted the highest positive direct effect on yield. The character 100 green seed weight showed positive and non significant correlation with seed yield per plant (r_g= 0.166, r_p= 0.193) both at genotypic and phenotypic level (**Table 3**). Vikas and Singh (1999) evaluated positive correlation (r_g= 0.211, r_p= 0.236) between seed yield per plant and 100-seed weight.

Path coefficient analysis

Association of character determined by correlation coefficient may not provide an exact picture of the relative importance of direct and indirect influence of each yield components on yield. As a fact, in order to find out a clear picture of the interrelationship between yield per plant and other yield attributes, direct effects were worked out using path analysis at genotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable and 50% flowering, days to 50% harvest, plant height, pods per plant, pod length, pod breadth, 100 green seed weight causal (independent) variables. The cause and effect relationship of seed yield per plant and yield related characters have been presented in **Table 4**.

Days to 50% harvesting showed the positive but low direct effect on SYPP (0.288) and had indirect influence via PPP (0.025) followed by HGSW (0.053) (**Table 4**). Hassan *et al.* (1995) reported positive direct effect of days to maturity direct on seed yield. Tyagi *et al.* (2000) recorded days to 50% flowering as a negative (-0.129) direct effect on seed yield per plant. They also found negative direct effect of plant height on seed yield per plant and showed negative indirect effect via seeds per pod (-0.327), pod length (-0.046) and pod breadth (-0.009). Plant height showed positive indirect effect via days to 50% harvest (0.090), 50% flowering (0.085) and pods per plant (0.001). Manoj *et al.* (2003) in pea found plant height had the greatest negative direct effect (-0.279) on pod yield per plant.

Pods per plant showed the positive direct effect on seed

Table 4 Partitioning of genotypic correlation (r_g) into its direct and indirect effects for seed yield components in vegetable pea.

Characters	DFPF	DFPH	PH	PPP	PL	PB	HSW	SYPP
DFPF	**0.289**	0.243	-0.003	0.018	-0.193	-0.054	0.026	0.327
DFPH	0.244	**0.289**	-0.003	0.025	-0.198	-0.074	0.053	0.586**
PH	0.086	0.093	**-0.009**	0.001	-0.046	-0.009	0.091	-0.102
PPP	0.039	0.055	-0.001	**0.133**	-0.096	-0.050	-0.026	0.197
PL	0.201	0.206	-0.002	0.046	**-0.278**	-0.139	0.006	0.701**
PB	0.081	0.111	-0.001	0.035	-0.201	**-0.191**	-0.007	0.656**
HSW	0.059	0.120	-0.006	-0.026	-0.013	0.011	**0.128**	0.166

** and * Significant at 1% and 5% level of probability, respectively; residual effect= 0.141

DFPF = days to 50% flowering, DFPH = days to 50% harvesting, PH = plant height (cm), PPP = pods per plant (no), PL = pod length (cm), PB = pod breadth (mm), HGSW = 100-green seed weight (g), SYPP = seed yield per plant (g)

yield per plant (0.197). Pods per plant showed maximum positive indirect effect through DFPF (0.039) followed by DFPH (0.055). Pods per plant however showed the negative indirect effect via PH (-0.001), PL (-0.096), PB (-0.050), HGSW (-0.026) resulted ultimately the total positive genotypic correlation with yield per plant (**Table 4**). In path coefficient analysis of Kumar (2003) revealed that the number of pods per plant had the greatest direct effect on yield per plant in pea. The direct effect of HGSW on seed yield per plant was positive but low in magnitude (0.128). This character also contributed low positive value in indirect effect via DFPH (0.120) followed by DFPF (0.050) and PB (0.011). Hundred green seed weight however showed the negative indirect effect via PPP (-0.026), PH (-0.006) and PL (-0.013). Ghobary (2010) found 100-grain weight had the lowest positive direct effect (0.043) on grain yield. Pods per plant showed the highest positive direct effect (1.133) with seed yield per plant (**Table 4**). Path analysis of days to 50% flowering (1.48), pods per plant (2.99) and 100-green seed weight (3.16) showed positive direct effect on green pod yield in pea (Nawab *et al.* 2008). The highest indirect effect (0.111) of pod breadth observed with DFPH (**Table 4**). The character showed high direct effect on yield indicated that direct selection for this trait might be effective and there is a possibility of improving seed yield per plant through selection based on those characters (Dewey and Lu 1959). The residual effect (0.141) indicated that the character under study contributed 86.9% of the yield. It is suggested that there are some other characters those contributed 14.1% to the yield per plant (**Table 4**).

CONCLUSION

Based on the results of the study, the following conclusions may be drawn:

1) High heritability coupled with high genetic advance and high genetic advance in percent mean were observed in plant height, 100 seed weight, seed yield per plant and yield per plot. Hence, yield improvement in pea would be achieved through selection of these characters.

2) The characters days to 50% harvest, pod length, pod breadth, seeds per pod showed positive and significant correlation with seed yield per plant. This result suggested that seed yield per plant can be increased by improving this characters.

3) 50% flowering, days to 50% harvest, branches per plant, pods per plant, seeds per pod and 100-seed weight showed positive direct effect on yield. So yield improvement is associated with these characters.

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