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GENETIC VARIABILITY AND HERITABILITY ANALYSIS FOR SOME QUANTITATIVE TRAITS IN FIELD PEA (*PISUM SATIVUM* L.)

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ABSTRACT

To best exploit the available genetic wealth in the crop, the information on the nature and degree of diversity in the genotypes is crucial. Twenty one advanced breeding lines along with two commercial varieties (HUDP 15 and IPFD 1-10) as check were evaluated for assessing genetic variability and heritability for eleven different quantitative characters. The mean sums of squares due to advanced breeding lines were highly significant for all of the characters. The estimates of GCV and PCV were high for plant height (24.58, 25.17), whereas moderate for yield per plant (18.40, 19.58), number of clusters per plant (17.61, 20.31) and number of pods per plant (15.12, 19.24). High heritability coupled with high genetic advance was recorded for plant height (95.00, 33.72), moderate for days to 50% flowering (95.00, 14.85) and high heritability coupled with low genetic advance was observed for yield per plant (88.00, 3.81) and 100 seed weight (70.00, 2.95). Based on *Per se* performance for seed yield per plant and other characters taken in to consideration advanced breeding line FP8-242 was found best performer.

INTRODUCTION

Field pea is high yielding cool season legume crop that is grown on worldwide, believed to be the native of Mediterranean region of Southern Europe and Western Asia. It is the third most important grain legume globally after beans and chickpea .As suggested by Santalla *et al.* (2001) and Tyagi *et al.* (2012), since the crop has high protein content (23-33%) people raised their interest on it for animal feed as well as human nutrition.

The genetic improvement of field pea is essential for delivering superior new varieties to growers that can improve crop production, management, profitability and grain marketing. Unfortunately, the yield of pea is low in India as compared to the world average yield owing to the narrow genetic base and limited variability used in the development of local varieties (Kumar *et al.,* 2004). The production has been constrained by several yield limiting factors such as powdery mildew, poor soil fertility and unimproved cultural practices. Therefore, in order to best exploit the available genetic wealth, unravelling the information on the extent and nature of genetic diversity of the population and the interrelationship among the character that would help in formulating efficient scheme of selection based on multiples of traits is of utmost importance (Million Fikreselassie, 2012). The objective of the study was to examine the existence of genetic variability, to establish such fundamental genetic facts as heritability and to determine the relative importance of primary and secondary traits as selection criteria to improve productivity.

MATERIALS AND METHODS

Experimental location

The experimental materials were grown at Genetics and Plant Breeding Research Farm of Allahabad Agricultural Institute, Deemed University, Naini, Allahabad (U.P.). The site of experiment is located at 25.5°N latitude, 81.5°E longitude and 98 meter above the sea level. This region has subtropical climate with extreme of summer and winter. The temperature falls down to as low as 1°C-2°C during winter season especially in the months of December and January. The mercury rises up to 46°C-48°C during summer. The average rainfall in this area is around 1013.4 mm annually with maximum concentration during July to September with few showers and drizzles in winter also.

Experimental material and design

The experimental materials consisted of 21 advance breeding lines of field pea along with two local checks namely HUDP 15, IPFD 1-10. These advance breeding lines were received from Indian Institute of Pulses Research (IIPR), Kanpur under All India Co-ordinated Research Project on Improvement of MULLaRP crops during 2008-09. The experimental materials were grown under randomized block design (RBD) with three replications. The experimental field was divided into 3 blocks of equal size and each block possesses 23 plots. Each advanced breeding line was accommodated in a six rows of 4 m length, spaced at 30 cm with an approximate plant to plant distance of 10 cm. Fertilizers and manures were applied as per recommended dose. Necessary weeding was done to keep the crops free from weeds. Flood irrigation was given to the plants at particular growth stages.

Data collection and analysis

Data were recorded for eleven quantitative characters viz., Day to emergence, Number of primary branches per plant, Days to 50% flowering, Plant height (cm), Number of pods per plant, Number of clusters per plant, Pod length (cm), Number of seeds per pod, Days to maturity, Hundred seed weight (g) and Seed yield per plant (g). The observations were recorded on five randomly selected competitive plants in each entry of each replication for all the characters except days to emergence, days to 50% flowering and days to maturity which was recorded on plot basis (Saxesena *et al.*, 2013). Analysis of variance was carried out as suggested by Panse and Sukhatme (1964). The per cent contribution of characters towards genetic divergence was calculated according to Singh and Chaudhary (1997).

Table 1: Analysis of variance for different quantitative traits in field pea

Characters	Treatments (df = 22)	CV%
Days to emergence (days)	1.391*	10.63
Number of primary branches per plant	0.195**	12.69
Days to 50% flowering (days)	167.528**	2.59
Plant height (cm)	856.546**	5.41
Number of pods per plant	21.385**	11.89
Number of clusters per plant	3.223**	10.11
Pod length (cm)	1.144**	5.19
Number of seeds per pod	1.821**	9.08
Days to maturity (days)	54.119**	1.54
100 seed weight (g)	10.106**	7.14
Yield per plant (g)	12.156**	6.70

** Significant at 0.01 level of significance;* Significant at 0.05 level of significance

RESULTS AND DISCUSSION

The mean sum of squares due to advanced breeding lines of field pea showed significant differences for all the characters under study, suggested that the experimental materials were genetically divergent (Table 1). This indicates that there is ample scope for selection of promising lines from the present gene pool for yield and its components. Table 2 depicts the mean performance of 21 advanced breeding lines along with two local checks for 11 quantitative characters along with co-efficient of variation and critical difference. An estimate of genotypic coefficient of variation and phenotypic coefficient of variation (Table 3) revealed that phenotypic coefficient of variation was higher than genotypic coefficient of variation, which indicates less effect of environment on the expression of characters studied. Higher estimates of GCV and PCV were depicted by plant height (24.58, 25.17) followed by seed yield per plant (18.40, 19.58), number of clusters per plant (17.61,

Table 2: Mean performance for different quantitative characters in field pea

S. No.	Character	Days to Emergence	N0. 0f Primary Branches/ Plant	Days to 50% Flowering	Plant Height (cm)	No. of Pods/ Plant	N0. 0f Clusters/ Plant	Pod Length (cm)	No. of Seeds/ Pod (g)	Days to Maturity	100 Seed Weight (g)	Yield/ Plant (g)
1	FP8-211	7.67	1.60	77.67	54.53	13.33	5.50	6.88	4.47	111.33	14.47	8.35
2	FP8-214	7.00	1.33	66.33	64.93	10.47	4.23	7.50	5.53	108.00	14.93	8.39
3	FP8-215	7.00	1.53	62.33	60.57	17.10	5.87	6.71	4.97	103.67	15.47	9.46
4	FP8-216	7.33	2.00	72.33	61.87	21.73	7.40	7.03	4.50	110.33	16.43	12.69
5	FP8-217	8.33	2.27	65.67	56.50	19.67	5.87	6.72	4.60	109.33	15.50	11.30
6	FP8-219	6.67	1.67	71.33	70.07	16.20	5.27	6.94	6.00	110.67	17.24	11.61
7	FP8-220	6.67	1.53	66.33	80.47	16.33	5.73	6.48	5.33	109.67	16.95	12.34
8	FP8-223	6.67	1.47	68.00	64.00	13.53	4.00	7.17	6.20	111.67	19.22	11.77
9	FP8-225	6.00	1.73	56.33	139.33	19.20	6.80	6.10	4.60	106.67	14.61	12.21
10	FP8-226	7.00	1.60	61.00	60.80	18.87	5.93	6.05	5.27	105.00	14.29	10.21
11	FP8-227	7.67	1.33	73.00	67.00	16.47	5.60	6.22	4.77	109.00	14.34	8.65
12	FP8-228	7.67	1.47	75.33	61.87	17.67	5.27	6.69	3.87	110.33	16.44	8.65
13	FP8-229	6.33	1.60	72.33	63.33	16.73	5.50	7.53	6.73	110.67	13.82	10.64
14	FP8-232	7.67	1.60	59.67	61.33	15.27	4.43	6.73	5.03	105.33	16.87	9.41
15	FP8-233	7.00	1.40	53.67	61.13	13.27	4.13	8.49	6.87	105.67	14.95	10.79
16	FP8-236	6.33	1.87	70.00	68.53	13.53	4.60	6.76	4.63	110.00	14.34	7.79
17	FP8-237	8.33	1.47	65.00	65.00	14.67	4.40	8.03	6.27	109.67	20.31	12.20
18	FP8-239	8.33	1.53	77.00	70.80	14.33	5.80	7.17	5.63	109.67	14.36	7.62
19	FP8-240	7.67	1.47	65.67	81.90	15.60	7.17	7.40	6.33	106.00	13.93	9.41
20	FP8-241	7.33	1.47	55.33	69.53	13.73	5.07	7.73	5.50	105.67	16.57	11.34
21	FP8-242	8.33	1.93	56.67	58.47	14.40	5.57	7.39	5.70	92.67	19.63	15.09
22	HUDP 15	7.33	2.20	75.33	58.27	19.60	7.60	6.83	5.40	110.33	15.08	14.10
23	IPFD 1-10	7.67	1.53	77.00	68.27	18.00	6.73	6.20	5.33	114.33	15.47	12.16
	Grand Mean	7.30	1.63	67.10	68.19	16.07	5.56	6.99	5.37	108.07	15.88	10.70
Range	Maximum	8.33	2.27	77.67	139.33	21.73	7.60	8.49	6.87	114.33	20.31	15.09
	Minimum	6.00	1.33	53.67	54.53	10.47	4.00	6.05	3.87	92.67	13.82	7.62
	C.V.	10.63	12.69	2.59	5.41	11.89	10.11	5.19	9.08	1.54	7.14	6.70
	C.D. 5%	1.27	0.34	2.86	6.07	3.15	0.93	0.59	0.80	2.74	1.86	1.18

Table 3: Estimation of component of variance and genetic parameters for 11 quantitative characters in field pea

Characters	VG	VP	GCV	PCV	h^2(bs)	GA	GA as % of mean
Days to emergence (days)	0.26	0.87	7.02	12.74	30.00	0.58	7.97
Number of primary branches per plant	0.05	0.09	13.77	18.72	54.00	0.34	20.85
Days to 50% flowering(days)	54.83	57.86	11.04	11.34	95.00	14.85	22.13
Plant height (cm)	280.98	294.60	24.58	25.17	95.00	33.72	49.45
Number of pods per plant	5.91	9.57	15.12	19.24	62.00	3.94	24.49
Number of clusters per plant	0.97	1.29	17.61	20.31	75.00	1.76	31.47
Pod length (cm)	0.34	0.47	8.31	9.80	72.00	1.01	14.52
Number of seeds per pod	0.53	0.77	13.53	16.29	69.00	1.24	23.13
Days to maturity (days)	17.11	19.89	3.83	4.13	86.00	7.91	7.31
100 seed weight (g)	2.94	4.23	10.80	12.95	70.00	2.95	18.56
Yield per plant (g)	3.88	4.39	18.40	19.58	88.00	3.81	35.62

VG =Genotypic variance. VP =Phenotypic variance; GCV = Genotypic coefficient of variation, GA = Genetic advance; PCV = Phenotypic coefficient of variation, h^2 (bs) = Heritability (broad sense)

Table 4: Percent contribution of different quantitative characters to genetic diversity

Source	Times Ranked1st	Contribution %
Days to emergence (days)	0.00	0.00
Number of primary branches per plant	3.00	1.19
Days to 50% flowering (days)	100.00	39.53
Plant height (cm)	41.00	16.21
Number of pods per plant	4.00	1.58
Number of clusters per plant	10.00	3.95
Pod length (cm)	15.00	5.93
Number of seeds per pod	5.00	1.98
Days to maturity (days)	23.00	9.09
100 seed weight (g)	8.00	3.16
Yield per plant(g)	44.00	17.39

20.31) and number of pods per plant (15.12, 19.24), respectively. Similar findings were reported by Tyagi and Srivastava (2002), Nawab *et al.* (2008) and Kumar *et al.* (2013).

Heritability for the considered traits were estimated and results revealed high estimates of heritability (above 60%) in broad sense were observed for plant height (95.00), days to 50% flowering (95.00), yield per plant (88.00) days to maturity (86.00), number of clusters per plant (75.00), pod length (72.00), 100 seed weight (70.00), number of seeds per pod (69.00) and number of pods per plant (62.00). Sable *et al.*, (2002), and Singh and Singh (2006) also recorded high heritability estimates for plant height, yield per plant and 100 seed weight, yield per plant and pod length. High values indicate that heritability may be due to higher contribution of genotypic component thus heritability estimates of various traits help

researchers to determine a suitable strategy for crop improvement and are frequently used by breeders to produce response to selection. Heritability alone provides no indication of amount of genetic improvement that would result from selection of individual genotype; hence knowledge about genetic advance coupled with heritability is most useful. Characters exhibiting high heritability may not be necessarily give high genetic advance (Kumar *et al.*, 2012). Johnson *et al.* (1955), showed that high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. The breeder should be cautious in making selection based on heritability alone as it includes both additive and non-additive gene effect.

A perusal of genetic advance (Table 3) revealed that it was high for plant height (33.72) and moderate for days to 50% flowering (14.85), The heritability estimates coupled with expected genetic advance indicate the mode of gene action in the expression of traits which helps in choosing an appropriate breeding methodology. High heritability coupled with high genetic advance was observed for plant height (95.00, 33.72), suggesting predominance of additive gene action in the expression of these traits (Kumar *et al.,* 2013). High heritability along with moderate genetic advance was obtained for days to 50% flowering (95.00, 14.85) suggesting predominance of additive and non-additive gene action in the expression of these traits (Ranjan *et al.,* 2006). Therefore, these characters can be improved by mass selection and other breeding methods based on progeny testing, similar results were reported in pea by Mahanta *et al.* (2001). However, characters like days to maturity (86.00, 7.91), number of pods per plant (62.00, 3.94), yield per plant (88.00, 3.81), 100 seed weight (70.00, 2.95), number of cluster per plant (75.00, 1.76), number of seeds per pod (69.00, 1.24), and pod length (72.00, 1.01) possessed high heritability with low genetic advance, suggesting non-additive gene action. The high heritability of these traits was due to favourable influence of

Environment rather than genotype and selection for these traits may not be rewarding. The highest contribution in the manifestation of genetic divergence (Table 4) was exhibited by days to 50% flowering (39.53%) followed by yield per plant (17.39%), plant height (16.21%), days to maturity (9.09%) and pod length (5.93%) suggesting that selection for these characters may be rewarding. Whereas, characters like plant height exhibited high GCV, PCV, heritability and genetic advance. Albeit, seed yield per plant showed moderate GCV, PCV and high heritability should be given top priority during selection. Based on *Per se* performance for seed yield per plant and other characters taken in to consideration advance breeding line FP8-242 was found promising.

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