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Estimation of genetic variability, heritability and genetic advance for yield and its components in Pea (*Pisum sativum* L.)

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Abstract

Genetic variability, heritability and genetic advance as percent over mean for nineteen quantitative traits of pea germplasms were assessed during rabi season 2017-2018 under Pea Improvement Project at Seed Breeding Farm, Department of Plant Breeding and Genetics, J.N.K.V.V., Jabalpur, (M.P.). High value of PCV and GCV was recorded high for number of pods per plant followed by number of effective nodes per plant, number of seeds per plant, number of nodes per plant. High heritability coupled with high genetic advance as percentage of mean would offer better scope of selection for number of pod per plant followed by number of effective nodes per plant, number of seeds per plant, number of effective pod per plant, number of nodes per plant, seed yield per plant, number of primary branches per plant, number of secondary branches per plant.

Keywords: Pea (*Pisum sativum* L.), variability, PCV, GCV, heritability, genetic advance

Introduction

Pea (*Pisum sativum* L.) is the third most important pulse crop at global level, after dry bean and chickpea and third most popular rabi pulse of India after chick pea and lentil. The crop belongs to the family Fabaceae, genus 'Pisum', with genetic composition of ca. 4800 Mbp spread across $2n=2x=14$ chromosomes. It is a member of family Fabaceae, subfamily Papilionaceae, and tribe Viciae. Pea is an excellent source of protein (27.8%), carbohydrates (42.65%), vitamin, minerals, dietary fibres and antioxidant compounds. Peas can supply the required nutrients to various age groups owing to their high protein content and favourable composition of amino acids and low trypsin inhibitor levels (Aysh *et al.*, 2014). In the states of India, Uttar Pradesh ranked first both in area and production (45.80% and 48.72%) followed by Madhya Pradesh (25.57% and 23.64%) and Jharkhand (2.70 % and 4.46%). Madhya Pradesh is the second largest producing state of field pea with area, production and productivity are 450 thousand hectare, 267.30 thousand tonnes and 594 kg/ha respectively (Anonymous, 2016) [2]. Though field pea is the third most important rabi pulse crop in India, but it has quite low productivity as comparison to other growing countries. This may be due to lack of improved high yielding varieties, narrow genetic base of released varieties, and use of poor quality seeds and non-availability of irrigation. Knowledge of genetic variability, heritability and genetic advance of characters under improvement is essential and pre-requisite for launching any breeding programme to achieve the goal (Janaki *et al.* (2015) [9]. The success of crop improvement programme depends on the considerable amount of variability present in the concern crop. So, the present investigation was carried out to estimate the extent of genetic variability, heritability and genetic advance of pea germplasms for yield and its components.

Materials and methods

The experiments were laid out in Randomized Complete Block Design (RCBD) with three replications. The germplasms were sown in single row pattern having 30 cm row to row and 10 cm plant to plant distance. Sowing was done in rabi season 2017-18. Experimental materials were received from Pea Improvement Project, Department of Plant Breeding & Genetics, JNKVV, Jabalpur and AICRP on MULLaRP, IIPR Kanpur and twenty-two local collections.

Observations were recorded on five randomly selected plants from each treatment on nineteen quantitative traits. The coefficient of variation at genotypic and phenotypic levels was calculated as per the formula proposed by Burton, (1952) [5]. The phenotypic and genotypic variances were also estimated according to the method suggested by Burton and De Vane (1953) [4]. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are categorized as low (< 10 %), Moderate (10-20 %) and high (> 20 %) as suggested by Sivasubramanian and Madhavamenon (1973) [16] in rice. In the present study the heritability was calculated in broad sense by the formula as suggested by Hanson *et al.* (1956) [8]. The broad sense heritability estimates were categorized as low, moderate and high by Robinson (1966). Expected genetic advance (GA) was calculated by the method suggested by Johnson *et al.* (1955) [11].

Results and discussion- It was observed that estimated variances due to various genotypes for yield contributing traits were significant that indicates the existence of considerable variability for all the characters (table 1). The mean performance of various germplasms also showed good range of variability for various characters like number of primary branches per plant, number of secondary branches per plant, number of nodes per plant, number of effective nodes per plant, pod cluster per plant, number of pods per

plant, number of effective pods per plant, pod length, number of seeds per pod which were studied in present investigation (table 1). Results are in favour with the findings of Guleria *et al.* (2009) [7], Singh *et al.* (2011) [15], and Pallavi *et al.* (2013) [14] in pea. The characters under investigation were analysed for genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as percent of mean (table 2). The coefficient of variation was recorded high for number of pods per plant followed by number of effective nodes per plant, number of seeds per plant, number of nodes per plant, number of effective pods per plant, seed yield per plant, number of primary branches per plant, number of secondary branches per plant. Based on above findings the characters were noted on the basis of high PCV and GCV suggesting for substantial improvement on field pea through selection for these traits in later generations. Hundred seed weight, Harvest index, pod cluster per plant, Number of seeds per pod were found moderate phenotypic and genotypic coefficient of variation. Similarly, the moderate PCV and GCV were observed is suggesting existence of considerable extent of variability in the population. Tiwari and Lavanya (2012) [17], and Jeberson *et al.* (2016) [10] also reported similar result of moderate GCV and PCV for the above traits in field pea.

Table 1: Analysis of variance yield and its component traits

Source of variations	d.f.	Mean sum of squares									
		DFFO	DFF	DM	NPBPP	NSBPP	PH	NNPP	NENPP	PBL	PCPP
Replications	2	1.088297	0.643768	1.101161	0.004612	0.022003	65.87695	26.27516	0.106596	0.566029	0.001449
Treatments	91	134.023**	189.3604**	265.9066**	1.191872**	5.171004**	2877.731**	1865.273**	148.825**	735.2641**	0.213744*
Error	182	0.729707	0.84989	0.819666	0.004226	0.012161	71.47583	30.41987	0.155937	0.768914	0.002518
Source of variations	d.f.	Mean sum of squares									
		NPPP	NEPPP	PL	NSPP	NSPPIt	100 SW	BYPP	HI	SYPP	
Replications	2	0.996149	0.213398	0.006419	0.002546	0.120144	0.013744	1.320659	1.682944	0.000021	
Treatments	91	312.4954**	190.8324**	0.945095*	0.961038*	3029.493**	24.22747**	189.3925**	109.145**	48.45058**	
Error	182	0.810463	0.22574	0.003613	0.00281	0.731994	0.041386	0.489934	0.339414	0.016477	

* Significant at 5%,

** Significant at 1%

Table 2: Genetic parameters of nineteen characters in field pea

Traits	Mean	Range				h ² (bs)	GA% of mean
		Min.	Max.	GCV (%)	PCV (%)		
DFFO	58.50	31.47	75.08	11.39	11.49	98.400	23.28
DFF	65.71	41.50	81.20	12.06	12.15	98.700	24.69
DM	96.91	74.27	114.97	9.70	9.75	99.100	19.89
NPBPP	1.75	1.02	3.20	35.88	36.07	98.900	73.53
NSBPP	3.80	1.48	8.52	34.54	34.66	99.300	70.91
PH	93.31	39.78	164.45	32.78	34.01	92.900	65.08
NNPP	60.48	24.50	158.05	40.89	41.90	95.300	82.22
NENPP	16.03	7.25	43.25	43.93	44.00	99.700	90.35
PBL	48.48	23.22	104.83	32.28	32.33	99.700	66.39
PCPP	1.48	1.02	2.19	17.93	18.25	96.500	36.30
NPPP	23.11	10.42	60.77	44.11	44.28	99.200	90.50
NEPPP	19.12	9.39	50.47	41.69	41.76	99.600	85.72
PL	5.27	3.80	6.72	10.63	10.69	98.900	21.78
NSPP	4.57	3.45	6.10	12.37	12.43	99.100	25.37
NSPPIt	74.94	38.22	217.47	42.40	42.42	99.900	87.31
100 SW	14.73	6.76	25.26	19.27	19.32	99.500	39.60
BYPP	31.01	20.22	75.23	25.59	25.69	99.200	52.51
HI	32.81	21.48	47.27	18.35	18.44	99.100	37.63
SYPP	10.32	6.01	29.21	38.92	38.94	99.900	80.14

(DFFO = Days to first flower opening, DFF= Days to 50% flowering, DM= Days to maturity, NPBPP = Number of primary branches per plant, NSBPP =Number of secondary branches per plant, PH= Plant height(cm), NNPP = Number of nodes per plant, NENPP = Number of effective nodes per plant, PBL= Pod bearing length(cm),PCPP=Pod cluster per plant NPPP = Number of pods per plant, NEPPP= Number of effective pods per plant, PL= Pod length (cm), NSPP =Number of seeds per pod, NSPPIt =Number of seeds per plant, 100 SW=100-seed weight (g), BYPP =Biological yield per plant (g), HI= Harvest index (%), SYPP =Seed yield per plant)

Rest of only one trait viz., days to maturity exhibited low coefficient of variation suggesting existence of low variability for this trait. Thus, selection for this trait may not be worthwhile in early generations. An attempt was made to estimate the broad sense heritability and genetic advance as percentage of mean. High heritability was recorded for the characters viz., number of seeds per plant (99.90%), seed yield per plant (99.90%), number of effective nodes per plant (99.70%), pod bearing length (99.70%), number of effective pods per plant (99.60%), 100 seed weight (99.50%), number of secondary branching per plant (99.30%), number of pod per plant (99.20%), biological yield per plant (99.20%). These findings are in general agreement with the findings of workers Katiyar *et al.* (2014)^[12], Georgieva *et al.* (2016)^[6] and Meena *et al.* (2017)^[13] who also reported high heritability for these yield attributing trait. The genetic advance as percentage of mean were highest for number of pods per plant (99.50%) followed by number of effective nodes per plant (99.35%), number of seeds per plant (87.31%), number of effective pods per plant (85.72%), number of nodes per plant (82.20%), seed yield per plant (80.14%). This result corroborated with the findings of Sharma *et al.* (2007), Ahmad *et al.* (2014)^[1], and Katiyar *et al.* (2014)^[12]. High heritability coupled with high genetic advance as percentage of mean would offer better scope of selection for number of pods per plant followed by number of effective nodes per plant, number of seeds per plant, number of effective pods per plant, number of nodes per plant, seed yield per plant.

Conclusion

Based on above findings the characters could be noted with high PCV and GCV for substantial improvement on pea through selection for these traits. High heritability coupled with high genetic advance as percentage of mean would offer better scope of selection for all traits except one viz., days to maturity. Days to maturity showed high heritability along with moderate genetic advance, which indicated that this character is under the control of additive genes and are more reliable for effective selection.

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