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Genetic variability, heritability and genetic advance for yield and yield components in pea (*Pisum sativum* L.)

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Abstract

Twelve pea genotypes 7 lines and 5 testers crossed in a Line x Tester mating design were evaluated with their 35 F₁'s along with parents in a randomized block design in three replications at Department of Horticulture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) during *rabi* season of 2015-16 and 2016-17. The variability, heritability and genetic advance as percent mean were studied for all the characters under investigation. The estimates of heritability varied from 32.3 % (harvest index) to 99 % (plant height). The heritability estimates were moderate for harvest index. For remaining characters, estimates of heritability were high. Genetic advance as percent mean was highest for weight of hundred seed, days to 50 % flowering, green pod yield per plant, number of pods per plant, seed yield per plant, days to maturity and shelling percent while characters viz. protein content in seed, no. of seeds per pod, biological yield per plant, pod length, no. of effective nodes per plant no. of branches per plant, showed moderate genetic advance, while harvest index showed lowest genetic advance. The consequences of heritability coupled with high genetic advance showed for characters viz. days to 50 % flowering, days to maturity, plant height at maturity, no. of pods per plant, green pod yield per plant, shelling %, weight of hundred seed, seed yield per plant thus, these characters may be improved through selection method.

Keywords: genetic variability, heritability, genetic advance, pea

Introduction

Pea (*Pisum sativum* L.) is an important vegetable crop grown throughout India for its tender and immature seeds which is used as vegetable. It is grown as winter vegetable in the plains of north India. Large proportion of peas is processed (canned, frozen or dehydrated) for consumption in off season. Pea is an excellent source of protein (27.8%), carbohydrates (42.65%), vitamin, minerals, dietary fibers 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) [2]. Pea protein is low in sulfur containing amino acids, cysteine and methionine but rich in lysine and other essential amino acids. (Ceyhan and Avci, 2005) [4]. Crop improvement depends upon the magnitude of genetic variability and extent of which the desirable characters are heritable for a successful breeding programme. Genetic variability, heritability and genetic advance are pre requisite for improvement of any crop for selection of superior genotypes and improvement of any traits.

Yield is a complex character influenced by several genetic factors interacting with environment. Therefore success of any breeding programme for its improvement depends on the existing genetic variability in the base population and on the efficiency of selection (Kumari *et al.*, 2008) [12]. Heritability indicates the proportion of phenotypic variance that is due to genotypes which is heritable. It serve as a useful guide to breeders as the selection for trait having high heritability will be effective and improvement will be brought through selection. The genetic advance is an improvement in the genetic value new population as compared to original one. It will be possible to decide various breeding programmes for improvement of different characters based on the study of heritability and genetic advance (Kumari *et al.*, 2012) [11].

Materials and Methods: The investigation was conducted at Horticulture complex, Department of Horticulture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.) during *rabi* season of 2015-16 and 2016-17. The geographical situation is 23.9° North latitude

and 79.58° East longitudes with an altitude of 411.8 metres above mean sea level. The experimental material consisted of twelve genotypes of pea namely viz., were Arkel, Kashi Shakti, Kashi Samarth, Kashi Uday, Azad Pea 3, Matar Ageta-6, Pant Sabji Matar 3 used as a female parents (line), Arka Karthik, Kashi Nandini, Kashi Mukti, Arka Ajit, and Pusa Pragati used as a male parent (tester) were crossed in line x tester fashion design and obtained 35 F₁ crosses. All the 35 F₁'s along with parents were grown in Randomized Complete Block Design with three replications. Observations were recorded on five randomly selected plants from each treatment on Sixteen characters viz. days to 50 % flowering, days to maturity, plant height at maturity (cm), branches per plant, effective node per plant, pods per plant, pod length (cm), seeds per pod, green pod yield per plant (g), weight of hundred seed (g), seed yield per plant (g), biological yield per plant (g), harvest index (%), shelling percent (%) and protein (%), TSS (°brix) and their mean obtained. The data were statistically analyzed for computation of genetic coefficient of variation using appropriate statistical analysis. Analysis of variance was carried out as per the procedure given by Panse and Sukhtame (1967) [15], phenotypic and genotypic coefficients of variation were estimated by given by Burton (1952) [3], and heritability in broad sense was estimated as per formula given by Allard (1960) [1]. The expected genetic advance was calculated by using formula as suggested by Johnson *et al.* (1955) [5].

Results and discussion

The analysis of variance revealed significant differences between genotype indicating sufficient variability in all characters studied. The results are similar with the findings of Singh and Singh (2006) [20], Sharma *et al.* (2007) [17], Kumari *et al.* (2008) [12], Singh *et al.* (2011) [19], Tiwari and Lavanya (2012) [16], Kumar *et al.* (2013) [10], Katiyar *et al.* (2014) [7], Jaiswal *et al.* (2015) [6], Katoch *et al.* (2016) [8], Kumar *et al.* (2017) [9]. The results of analysis of variance for fifteen characters viz. days to 50 % flowering, days to maturity, plant height at maturity, branches per plant, effective node per plant, pods per plant, pod length, seeds per pod, green pod yield per plant, weight of hundred seed, seed yield per plant, biological yield per plant, harvest index, shelling percent and protein (%), TSS (°brix) characters are manifested in table 1. The extent of variability was measured in terms of range, phenotypic and genotypic coefficient of variation. Wide range of variability was observed for days to 50 % flowering, days to maturity, plant height at maturity, branches per plant, effective node per plant, pods per plant, pod length, seeds per pod, green pod yield per plant, weight of hundred seed, seed yield per plant, biological yield per plant, harvest index, shelling percent and protein, TSS (°brix) indicating the scope for selection of suitable initial breeding material for improvement of crop.

The estimates of variability, heritability and genetic advances for 16 attributes are presented in Table 2. The estimates of genotype coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed. Both phenotypic coefficient of variation and genotypic coefficient of variation were almost similar for all the characters under study. However, the phenotype coefficient of variation was higher in magnitude than genotypic coefficient of variation. The highest estimates of genotype coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for traits viz., plant height at maturity (cm), weight of 100 seed (g), days to 50 % flowering indicating greatest

diversity for these characters. These results are similar to those reported by highest estimate of GCV and PCV for plant height by Singh *et al.* (2011) [18], Kumar *et al.* (2013) [10], Jaiswal *et al.* (2015) [6], Singh and Singh (2006) [20], Sharma *et al.* (2007) [17], Katoch *et al.* (2016) [8]; weight of 100 seed by Kumar *et al.* (2013) [10] and no. of branches per plant by Singh and Singh (2006) [20]. High genetic variability for different quantitative trait has been reported by Singh and Singh (2006) [20], Kumar *et al.* (2013) [10].

Moderate genotypic and phenotypic coefficient of variations were recorded for green pod yield per plant (g), number of pods per plant, seed yield per plant (g), days to maturity, biological yield per plant (g), seeds per pod, shelling percentage indicating that the characters studied were more influenced by environment. Kumari *et al.* (2008) [12] and Sharma *et al.* (2007) [17] reported for pod yield per plant and pods per plant and Kumari *et al.* (2008) [12] by shelling percent similar result in garden pea whereas, low genotypic and phenotypic coefficient of variations were observed for effective nodes per plant, pod length, harvest index and protein and TSS.

Most the characters showed high heritability in broad sense. Among the characters studied, highest heritability estimate was recorded for, days to maturity plant height at maturity (cm), days to 50% flowering, pod yield per plant (g), weight 100 seed (g), seed yield per plant (g), shelling percentage, percent protein content in dry seeds, pods per plant, pod length (cm), branches per plant, effective node per plant, TSS, seeds per pods, biological yield per plant (g). Similar findings were reported in pea by Singh *et al.* (2011) [19], for plant height, Kumari *et al.* (2008) [12] for shelling percentage, hundred seed weight (g), no. of pods per plant, Sharma and Bora (2013) [18] for plant height (cm), by Jaiswal *et al.* (2015) [6] for days to 50 % flowering, pod yield per plant (g), TSS by Pandey *et al.* (2015) [13] whereas, medium heritability estimate was recorded only for harvest index. The high value of heritability suggests that these characters are under the genotypic control and expected to give constant results under simple selection. Thus, the heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative traits.

The plant height at maturity (cm) showed highest genetic advance as percent of mean followed by weight of 100 seed (g), days to 50 % flowering, green pod yield per plant (g), number of pods per plant, seed yield per plant (g), days to maturity and shelling percent. These results are in agreement with the findings of Singh *et al.* (2011) [19] for plant height ; Kumari *et al.* (2012) [11] for plant height and days to 50 % flowering, no. of pods per plant, pod yield per plant ; Kumar *et al.* (2013) [10] plant height, no. of pods per plant and seed yield per plant; Jaiswal *et al.* (2015) [6] for plant height, weight of hundred seed, no. of pod per plant and days to maturity, Katoch *et al.* (2016) [8] for plant height and pod yield per plant.

The characters which showed moderate genetic advance as per cent mean were protein content in seed, number of effective nodes per plant, number of branches per plant, whereas, harvest index showed low genetic advance as per cent of mean. These findings are in tune with those of Kumari *et al.* (2012) [11].

High heritability coupled with high GA as percent has been reported for the characters for days to 50 % flowering, days to maturity, plant height at maturity (cm), pods per plant, green pod yield per plant (g), shelling percent, weight of hundred

seed (g) and seed yield per plant (g). This is indicating the importance of additive gene action controlling these characters. Simple selection therefore could be effective for improvement of these traits. In pea, high heritability coupled with high genetic advance for these characters was reported by Sharma *et al.* (2007) [17], Kumari *et al.* (2012) [11], Singh and Singh (2006) [20], Pallavi *et al.* (2013) [14], Sharma and Bora (2013) [18].

High heritability coupled with moderate GA as percent has been observed for the characters for no. of branches per plant, no. of effective node per plant, pod length (cm), biological yield per plant (g), Protein, TSS. These results indicated that an effective selection for this trait could be done which might be attributed to additive gene action conditioning their expression and phenotype selection for their amenability can bring about. Similar results obtained by Kumari *et al.* (2008) [12], Katiyar *et al.* (2014) [7], Kumari *et al.* (2012) [11], Singh *et al.* (2011) [19], Pandey *et al.* (2015) [13]. Whereas high heritability and low genetic advance reported for only one character i.e. harvest index. High heritability with moderate genetic advance indicated the presence of both additive and non-additive gene effects; while high/low heritability with low genetic advance for harvest index indicated the importance of non-additive gene action.

Hence, based on the discussion, it may be concluded that characters obtained high heritability and high genetic advance days to 50 % flowering, days to maturity, plant height at maturity (cm), green pods per plant, green pod yield per plant (g), shelling percent, weight of hundred seed (g) and seed

yield per plant (g) could be used for selection will be effective for these traits. Mass selection or pureline selection would be effective for a limited extent for characters which having high heritability and moderate genetic advance viz., no. of branches per plant, no. of effective nod per plant, pod length (cm), biological yield per plant (g) and Protein (%), TSS.

Table 1: ANOVA for yield and its components in pea for characters

S.N.	Characters	Degree of freedom		
		2	46	92
		Replication	Treatment	Error
1	Days to 50% Flowering	4.750	443.046***	5.4944
2	Days to Maturity	4.581	415.610***	2.7128
3	Plant Height At Maturity	0.973	1029.900***	3.7499
4	Branches Per Plant	0.404	3.205***	0.2442
5	Effective Node Per Plant	0.113	1.713***	0.1834
6	Pods Per Plant	1.486	26.179***	1.2398
7	Pod Length(cm)	0.096	1.588***	0.1163
8	Seeds/ Pod	0.050	1.799***	0.2331
9	Pod Yield Per Plant(green)	10.903	522.770***	6.4965
10	Weight of 100 Seed(green)	1.267	460.373***	2.8082
11	Seed Yield Per Plant(green)	2.348	166.772***	1.3255
12	Biological Yield Per Plant	0.080	0.582***	0.0901
13	Harvest Index	0.296	26.244***	10.8041
14	Shelling %	4.075	84.132***	1.4137
15	Protein	0.016	11.758***	0.2495
16	TSS	1.505	8.291***	0.889

* - Significant at 5%

** - Significant at 1 %

Table 2: Heritability, genetic advance & genetic advance in percent over mean for 16 characters in Line x Tester fashion in pea

Characters	Range		General mean	Coefficient of Variation (%)		h ² (%)	Genetic advance as per cent of mean
	Min	Max		PCV (%)	GCV (%)		
Days to 50% flowering	33.29	75.67	55.81	21.64	22.04	96.37	43.76
Days to maturity	78.22	118.82	97.16	12.19	12.07	98.07	24.63
Plant height at maturity	34.32	94.03	59.57	31.22	31.05	99	63.61
Branches per plant	11.17	15.33	13.17	8.43	7.55	80.16	13.91
Effective node per plant	7.12	9.58	8.34	9.98	8.56	73.55	15.12
Pods per plant	10.56	22.44	16.73	18.47	17.23	87.02	33.12
Pod length(cm)	6.93	10.20	8.24	9.46	8.50	80.84	15.75
Seeds per pod	5.64	9.44	7.44	11.68	9.71	69.13	16.64
Pod yield per plant(green)	39.81	93.82	68.34	19.56	19.20	96.36	38.82
Weight of 100 seed(green)	31.93	94.53	53.733	23.19	22.98	98.19	46.92
Seed yield per plant(green)	38.10	74.20	53.13	14.15	13.98	97.65	28.46
Biological yield per plant	3.14	5.19	4.203	11.99	9.63	64.51	15.93
Harvest index	35.78	51.49	42.95	9.30	5.28	32.27	61.81
Shelling (%)	41.24	61.73	48.40	11.12	10.85	95.12	21.79
Protein (%)	19.30	26.84	23.10	8.75	8.48	93.89	16.92
TSS (%brix)	14.99	21.68	18.19	10.07	8.63	74.10	19.54

GCV = Genotypic Coefficient of variation, PCV=Phenotypic coefficient of variation and h²=heritability in broad sense

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