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Genetic variability, heritability and genetic advance for seed yield and related traits in diverse genotypes of pea (*Pisum sativum* L.)

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Abstract

An investigation was carried out with 64 genotypes of pea were tested using a randomized block experimental design with three replication in the Agriculture Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (U.P.). The result showed highly significant difference for all the characters under study among sixty four germplasm lines. The variability, heritability and genetic advance as percent mean were studied for all the characters. A wide range of variation was found for all the characters. The seed yield per plant, the ultimate trait of improvement ranged from 4.06 gm in EC 322745 to 12.99 gm in HFP-14. Estimates of phenotypic variance (σ^2_p) were higher than genotypic variance (σ^2_g). The PCV and GCV was maximum for seed yield per plant (31.94 and 31.60) and minimum value for days to maturity (4.04 and 3.90). The broad sense heritability ranged from 87.62 (days to flowering) to 95.76 percent (plant height) and similarly, high genetic advance as percent of mean was found highest for seed yield per plant (64.42 %) and lowest value for days to maturity (7.75). Significant difference among genotypes for all characters performance out of 64 genotypes, ten genotypes (IPF-9981, KPMR-557, HFP-14, EC324108II, EC324112, HUP-5, EC328747, EC31363II, Rachana and JP-4) were found to be best genotypes for multiple traits, so these can be used as parent for future breeding programme.

Keywords: Genetic variability, heritability, genetic advance, diverse genotypes, seed yield

Introduction

Pulses are one of the most important crops worldwide, having major impact on agriculture, environment, animal and human nutrition and health (Graham and Vance, 2003) [9]. Pulses are mostly cultivated under rainfed conditions and do not require intensive irrigation facility and this is the reason why pulses are grown in areas left after satisfying the demand for cereals/cash crops. Even in such conditions, pulses give better returns. They are rich in proteins, energy, minerals and certain vitamins. The total world acreage under pulses as recorded during 2014 is about 851.91 lakh ha with production at 774.73 lakh tones and productivity 909 kg/ha. It reveals that the India ranked first in area and production with 35% and 25% respectively of world area and production. However, in case of productively Bahrain stood first with 18485 kg/ha. Thus it is also evident that the country's productivity at 660 kg/ha is far below the world average productivity of 909 kg/ha (Annual Report DPD, 2016-17) [1]. In India, during 2015-16, pulses were grown an area of 24.91 million ha with a production of 16.35 million tone and average productivity was 656 kg/ha. Despite its potential attributes, the per capita availability of pulses in India has declined sharply from 61 g per day during 1951 to 43 g per day during 2016 (Annual Report DPD, 2016-17) [1] as against the per capita requirement of 55-60 g per day. This puts country's current requirement of pulses at the level of 25 MT annually.

Field pea (*Pisum sativum* L.) belongs to the family leguminoceae ($2n = 2 \times = 14$) and a valuable cool-season pulse 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. 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 rich in lysine and other essential amino acids, but low in sulfur containing amino acids, cysteine and methionine (Ceyhan and Avci, 2005) [7].

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Canada rank first in area (21%) and production (35%) at Global level while India occupy fourth position in area (10.53 %) and 5th position in production (5.36 %). Highest productivity is recorded in Ireland (5000 kg/ha) while, India's productivity is only 822 kg/ha (Annual Report DPD, 2016-17) [1]. In India, during 2015-16, pea was grown over an area of 0.90 million ha with a production of about 0.74 million tone and average productivity was 821 kg/ha (Annual Report DPD, 2016-17) [1], which is highest among Rabi pulses grown in India. However, this present level of productivity of pea is still far below than those attained in other countries in the world.

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) [18]. 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) [19].

Materials and Methods

The present experiment was carried out at the Agriculture Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, and Varanasi during the Rabi season of 2009-10. For the present experiment 64 germplasm lines of pea (*Pisum sativum* L.) were undertaken (Table 1) which were provided by the All India Coordinated Research Project on Improvement of MuLLaRP in the Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The experiment was laid out in randomized block design with three replications. Each variety representing one treatment was grown in a three row plot with row to row and plant to plant spacing were 45 cm and 10 cm, respectively.

The technique of random sampling was adopted for recording the observations of various quantitative characters of pea. Five plants of each treatment from each replication were selected at random at the time of recording the data on various characters. Data of five plants were averaged replication wise and mean data was used for statistical analysis. Recommended package of practices were applied to raise a healthy crop and some observations were recorded *viz.*, days to flowering (50 %), days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-grain weight (g) and seed yield per plant (g)

Mean is the average value of the character in a sample *i.e.*, it is the average of all the observations on a character in sample. Range was taken as the difference between the highest and lowest mean value for each character. It is the simple measure

of variability and gives an idea of the dispersion or spread of the observations in sample. Components of variance are defined as the average of the square deviation from the mean or it is the square of the standard deviation. It is an effective measure of variability which permits partitioning of various components. Analysis of variance was done for partitioning the total variation into variation due to treatment and replication according to procedure given Panse and Sukhatame (1967) [26]. This also facilitates in dividing the total variance into phenotypic, genotypic and environmental variance. The genotypic variance (V_G or σ^2_g) is variance due to the genotype present in the population. This was calculated by the formula suggested by Burton (1952) [6]. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated by the formula given by Burton (1952) [6]. Heritability in broad sense was calculated using the formula suggested by Burton and Devane (1953) [5]. Improvement in the mean genotype value of selected plants over the parental population is known as genetic advance. The genetic advance *i.e.*, the expected genetic seed was worked out by using the formula suggested by Johnson *et al.* (1955) [11].

$$\text{Genetic Advance as Percentage of Mean} = \left(\frac{GA}{\bar{X}} \right) \times 100$$

GA = Genetic advance

\bar{X} = Mean of character

Results and Discussion

The present experiment was designed to compute the different genetic parameters for nine quantitative traits in sixty four germplasm lines of pea. The estimates of mean sum of square due to genotypes were highly significant for all the characters under study (Table 2), indicating the presence of sufficient genetic variability in the existing material. The results are similar with the findings of Singh and Singh (2006) [31], Sharma *et al.* (2007) [28], Kumari *et al.* (2008) [18], Singh *et al.* (2011) [30], Tiwari and Lavanya (2012) [33], Jaiswal *et al.* (2013) [10], Kumar *et al.* (2013) [14], Katiyar *et al.* (2014) [12], Katoch *et al.* (2016) [13], Kumar *et al.* (2017) [15], Barcchiya *et al.* (2018) [3] and Kumawat *et al.* (2018) [20] in pea.

The development of an effective plant breeding programme is dependent upon the existence of genetic variability. The efficiency of selection largely depends upon the magnitude of genetic variability present in plant population. Thus, the success of genetic improvement in any character depends on nature of genetic variability present in gene pool for that character. Hence, insight into the magnitude of variability present in the gene pool of a crop species is of at most importance to a plant breeder for initiation a judicious breeding programme.

A wide range of variation was found for all the characters (Table 3). Range for days to flowering varied from 54.33 days (JP-BB-5) to 75.00 days (HFP-12). In case of days to maturity it varied from 101.66 days (Local Kashmiri) to 121.66 days (HUP-11). The plant height showed a markedly a higher range of variation from 45.76 cm (Local Kashmiri) to 152.06 cm (KPMR 642). The minimum number of primary branches was observed for EC 313635I (2.20) where as it was highest (5.50) for Rachna. Pods per plant varied from 9.20 (IPF-9981) to 23.63 (EC31363II). The maximum pod length of 7.09 cm was recorded for HFP-14 while the minimum of 4.12 cm for JP-861. Maximum number of seeds per pods was found 5.40

for JP-4 whereas minimum number of seeds per pods was found 2.56 in EC313629I. The range for seed weight was 10.37 gm for JP-BB 4 to 21.30 gm for KPMR 642. The seed yield per plant ranged from 4.06 gm in EC 322745 to 12.99 gm in HFP-14.

Estimates of phenotypic (σ^2_p) variance were obtained for different traits (Table 3). Estimates of (σ^2_p) were higher than (σ^2_g). An insight into the extent of genotypic and phenotypic variances existing in the germplasm would be of immense value. The characters like plant height, days to maturity, days to flowering and number of pods per plant exhibited higher value of phenotypic variance while other traits showed a narrow range (Table 3). Genotypic variance also followed almost similar trend. This suggests that there is a good scope of selection for these factors. This is supported by finding of Sureja *et al.* (2000) [32], Singh *et al.* (2006) [31] and Kumar (2008) [16].

Phenotypic coefficient of variance (PCV) was higher than genotypic coefficient of variance (GCV), which indicated the effect of environment on the expression of characters for all the characters under study indicating environmental influence on the traits (Table 2). Same trends were also reported by Bashir *et al.* (2017) [4], Meena *et al.* (2017) [23], Barcchiya *et al.* (2018) [3] and Lal *et al.* (2018) [21] [22]. The seed yield per plant, plant height and number of pods per plant showed maximum phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). These variations were minimum for days to maturity. Thus, the characters showing maximum phenotypic coefficient of variation would be considered while making selection in spite of influence of environment to a certain extent. These results are similar to those reported by highest estimate of GCV and PCV for these characters by Ramesh *et al.* (2002) [27], Kumar *et al.* (2003) [17], Mehta *et al.* (2005) [24], Singh and Singh (2006) [31], Dhama *et al.* (2007) [8], Sharma *et al.* (2007) [28], Singh *et al.* (2011) [30], Kumar *et al.* (2013) [14], Jaiswal *et al.* (2015) [10], Katoch *et al.* (2016) [13], Barcchiya *et al.* (2018) [3] and Lal *et al.* (2018) [21, 22].

The most essential aspect of breeding programmes is selection within a base population of genetically variable individual (families). The genetic advance under selection of the selected lines over the base population from which selection was practiced would depend on the amount of genetic variability in the base population the magnitude of environment effect and the intensity of selection. So study of heritability and genetic advance under selection was undertaken in the present investigation. The effectiveness of selection for a trait depends in the expression of phenotypic differences among the genotypes in a population, a concept referred to as heritability. The heritability of a character has major impact on the method chosen for population improvement. Since heritability and genetic advance are the direct selection parameters, one should emphasize the attention on characters having high heritability.

All the characters showed high heritability in broad sense. Among the characters studied, highest heritability estimates was recorded for plant height followed by 100-seed weight, seed yield per plant, number of pods per plant, number of primary branches per plant, pod length, number of seeds per pod, days to maturity and days to flowering. Similar findings were reported in pea by Sureja *et al.* (2000) [32], and Kumar (2008) [16] and Singh *et al.* (2011) [30], Sharma and Bora (2013) [22] for plant height; Kumari *et al.* (2008) [18] for 100 seed weight (g) and no. of pods per plant; Jaiswal *et al.* (2015) [10] for days to flowering; Barcchiya *et al.* (2018) [3] for most

of characters studied. 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.

High genetic advance as percent of mean was maximum for seed yield per plant followed by plant height and number of pods per plant. These results are also agree with the findings of Singh *et al.* (2011) [30] and Katoch *et al.* (2016) [13] for plant height; Kumari *et al.* (2012) [19] and Jaiswal *et al.* (2015) [10] for plant height and no. of pods per plant, Kumar *et al.* (2013) [14] and Barcchiya *et al.* (2018) [3] for plant height, no. of pods per plant and seed yield per plant. The characters which showed moderate genetic advance as per cent mean were 100-seed weight, number of seeds per pod and number of primary branches per plant. Similar results obtained by Kumari *et al.* (2012) [19], Pandey *et al.* (2015) [25] and Barcchiya *et al.* (2018) [3]. Whereas, pod length, days to flowering and days to maturity showed low genetic advance as per cent of mean. These findings are in tune with those of Kumari *et al.* (2012) [19].

High heritability coupled with high genetic advance as percent of mean has been reported for seed yield per plant, number of pods per plant and plant height. It would offer better scope of selection for plant height. 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 Kumari *et al.* (2012) [19] and Barcchiya *et al.* (2018) [3].

High heritability coupled with moderate genetic advance as percent was observed for 100-seed weight, number of seeds per pod and number of primary branches per plant. 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.* (2012) [19], Pandey *et al.* (2015) [25] and Barcchiya *et al.* (2018) [3]. Whereas, high heritability and low genetic advance reported for pod length, days to flowering and days to maturity. High heritability with moderate genetic advance indicated the presence of both additive and non-additive gene effects; while high heritability with low genetic advance 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 as percent like seed yield per plant, number of pods per plant and plant height could be used for selection will be effective for these traits. Characters which having high heritability and moderate genetic advance viz., 100-seed weight, number of seeds per pod and number of primary branches per plant could be used for a limited extent for Mass selection or pureline selection. These finding indicates that number of pods per plant, 100-seed weight, pod length, number of primary branches per plant, number of seeds per pod and plant height may be considered as key characters during selection programme i.e. varietal improvement.

In short, the present set of experimental material, i.e., the sixty four genotypes studied, represents considerable and diverse variability for different traits evaluated which could be utilized in breeding programme for varietal improvement in pea crop. The variance measures the variation within a particular trait, but it does not provide a real measure for comparison of variances between different traits. The term

coefficient of variation truly provides a relative measure of variance among the different traits.

On the basis of *per se* performance the line *viz.*, IPF-9981, KPMR-557, HFP-14, EC324108II, EC324112, HUP-5,

EC328747, EC31363II, Rachana and JP-4 were found to be best genotypes for multiple traits, so these can be used as parent for future for breeding programme.

Table 1: Germplasm lines of pea evaluated in the study.

S. No.	Germplasm line	Sources	S. No.	Germplasm line	Sources
1	EC324107	NBPGR, New Delhi	33	EC324742II	NBPGR, New Delhi
2	EC313629I	NBPGR, New Delhi	34	IARI 3138	IARI, New Delhi
3	EC313629II	NBPGR, New Delhi	35	PRS 8III	IARI, New Delhi
4	EC374160	NBPGR, New Delhi	36	PRS 8I	IARI, New Delhi
5	EC341753II	NBPGR, New Delhi	37	3-9-I	BHU, Varanasi
6	EC313635I	NBPGR, New Delhi	38	PANT P-9	GBPUA&T, Pantnagar
7	EC341793	NBPGR, New Delhi	39	JP-BB-5	JNKVV, Jabalpur
8	EC322745	NBPGR, New Delhi	40	JP-BB-3	JNKVV, Jabalpur
9	EC322748II	NBPGR, New Delhi	41	JP-BB-4	JNKVV, Jabalpur
10	EC313639	NBPGR, New Delhi	42	JP-4	JNKVV, Jabalpur
11	EC31363II	NBPGR, New Delhi	43	JP-625	JNKVV, Jabalpur
12	EC324118	NBPGR, New Delhi	44	JP-861	JNKVV, Jabalpur
13	EC324121II	NBPGR, New Delhi	45	JP-1193	JNKVV, Jabalpur
14	EC324705	NBPGR, New Delhi	46	LOCAL KASHMIRI	LOCAL Collection
15	EC324108II	NBPGR, New Delhi	47	RACHANA	CSAUAT, Kanpur
16	EC324108I	NBPGR, New Delhi	48	VL-40	VPVV, Almora
17	EC304135	NBPGR, New Delhi	49	VL-6	VPVV, Almora
18	EC324112	NBPGR, New Delhi	50	HUP-14	BHU, Varanasi
19	EC3624113	NBPGR, New Delhi	51	HUP-11	BHU, Varanasi
20	EC328768I	NBPGR, New Delhi	52	HUP-5	BHU, Varanasi
21	EC328773	NBPGR, New Delhi	53	KPMR-45I	CSAUAT, Kanpur
22	EC318760II	NBPGR, New Delhi	54	KPMR 619	CSAUAT, Kanpur
23	EC318761	NBPGR, New Delhi	55	KPMR 497	CSAUAT, Kanpur
24	EC328758	NBPGR, New Delhi	56	KPMR 557	CSAUAT, Kanpur
25	EC328742	NBPGR, New Delhi	57	KPMR 642	CSAUAT, Kanpur
26	EC328752	NBPGR, New Delhi	58	HFP-14	HAU, Hisar
27	EC328752II	NBPGR, New Delhi	59	HFP-12	HAU, Hisar
28	EC318762	NBPGR, New Delhi	61	IPF-9981	IIPR, Kanpur
29	EC328747	NBPGR, New Delhi	62	IPF-400	IIPR, Kanpur
30	EC388773I	NBPGR, New Delhi	63	IPF-22	IIPR, Kanpur
31	EC328753	NBPGR, New Delhi	64	IPF-9728	IIPR, Kanpur
32	EC328773II	NBPGR, New Delhi	61	IPF-9981	IIPR, Kanpur

Table 2: Analysis of variance (ANOVA) for various characters of sixty four genotypes of Pea

Mean Sum of square (MSS)									
Source	Days to Flowering	Days to maturity	Plant height	No. of primary branches/plant	No. of pods per plant	No. of seeds/pod	Pod length	100-seed weight	Seed yield per plant
Replication	6.02	5.27	1.65	0.003	1.26	0.07	0.07	0.18	0.05
Treatment	52.64*	64.75*	2599.08**	1.05**	49.48**	0.85**	1.44**	19.40*	11.89**
Error	3.88	4.44	6.33	0.05	1.59	0.05	0.07	0.14	0.25

*, ** Significant at 5 percent and 1 percent level, respectively

Table 3: Range, mean, PCV and GCV, heritability and genetic advance as percent of mean for nine characters of Pea

Source	Days to Flowering	Days to maturity	Plant height	No. of primary branches/plant	No. of pods per plant	No. of seeds per pod	Pod length	100-seed weight	Seed yield per plant
Range	54.33-75.00	101.66-121.66	45.76-152.06	2.20-5.50	9.20-23.63	2.56-5.40	4.12-7.09	10.37-21.30	4.06-12.99
Grand mean	66.13 ±1.13	114.94 ±1.20	112.66 ±1.44	3.02 ±0.13	16.02 ±0.722	4.01 ±0.136	5.75 ±0.153	15.02 ±0.214	6.23 ±0.286
Phenotypic variance	17.54	21.58	866.36	0.35	16.49	0.28	0.48	6.46	3.96
Genotypic variance	16.25	20.1	864.25	0.33	15.96	0.26	0.45	6.42	3.88
PCV (%)	6.33	4.04	26.12	19.57	25.34	13.32	12.07	16.92	31.94
GCV (%)	6.09	3.90	26.09	19.08	24.93	12.88	11.76	16.86	31.60
GA	2.97	1.83	2.23	7.48	7.86	5.92	4.66	2.49	8.02
Heritability (%)	87.62	88.14	95.76	91.12	92.79	89.42	90.03	94.28	93.90
Genetic advance as percent mean	12.08	7.75	53.68	38.35	50.52	25.664	23.63	34.60	64.42

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