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Assessment of genetic variability, heritability and genetic advance in pea (*Pisum sativum*)

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Abstract

Studies on genetic variability, heritability and genetic advance were carried out among twenty genotypes of pea for character to identify genotypes to be used in breeding programme. The result showed high phenotypic and genotypic co-efficient of variation for traits like plant height (GCV = 27.62; PCV = 27.65). High heritability values were obtained all the characters. In high heritability coupled with high genetic advance as per cent of mean was observed plant height (56.84%), number of pods per plant (43.73 %), length of first fruiting node (43.44 %), pod yield per plant (38.62 %), pod yield q/ha (38.61 %), days to 50% flowering (33.25 %) and number of seeds per pod (24.28 %). This indicated substantial of additive genetic variance in expression of these characters and can be useful in hybridization and selection for higher pod yield.

Keywords: Assessment, genetic variability, heritability, genetic advance, pea (*Pisum sativum*)

Introduction

Pea belongs to the family Leguminosae (Fabaceae) and having chromosome number $2n = 14$. Pea occupy a position of considerable value because of its importance in agriculture economy of the country. This considered the cheapest source of protein in diet. Pea is an important plant in human and animal nutrition because of its high protein level (23- 33%) (Cousin *et al.*, 1985) [2]. Besides, it contain a higher proportion of mineral matter.

Presence of high variability in this crop offers much scope for its improvement. A wide range of variability present in any crop always provides the better chances of selecting desired types (Vavilov, 1951) [11]. Heritability is the portion of phenotypic variation which is transmitted from parent to progeny. The higher the heritable variation, the greater will be the possibility of fixing the character by selection methods (Sharma and Bora, 2013) [8]. Lack of sufficient genetic variability for economically important character is one of the reasons attributed for in significant progress in crop improvement. The natural selection over years operated towards increasing the potentiality for survival and wider adoption at the cost of yield traits. Further the ones contributing for higher yield seem to be scattered in the natural population. Hence, an attempt was made to estimate genetic variability, heritability and genetic advance of some traits in the available germplasm of pea which may help to select suitable genotypes for future breeding programs.

Method and materials

The present investigation was carried out in 2016-17 at Research farm of HRC, SVPUA&T, Meerut. The experiment was laid out in Randomization Block Design, comprising twenty genotypes and replicate trice. The crop was successfully raised by following recommended agronomic practices during period of crop growth. Five plants selected at random per variety per replication avoiding border plants were tagged, which constituted the sample for observations. Observations were recorded on ten different traits. Phenotypic and genotypic co-efficient of variation, heritability and genetic advance were estimated.

Result and discussion

The extent of genetic variability, phenotypic and genotypic co-efficient of variation, heritability and genetic advance for different traits (Table 1) showed wide range of variability for all the traits days to 50% flowering, plant height, number of first fruiting node, length of first fruiting node, number of pods per plant, length of pod, width of pod, number of seeds per pod, pod yield per plant, pod yield q/ha. The GCV was found to be less than PCV for all traits studied which indicated that these characters were having interaction with environment to some extent (Ram and Singh, 1993) [7]. Results from the present study in this context indicated that PCV and GCV were high (more than 25%) observed for plant height, while moderate

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(10-25%) for number of pods per plant, length of first fruiting node, length of first fruiting node, pod yield per plant, pod yield q/ha, days to 50% flowering, number of seeds per plant and number of first fruiting node and low (<10%) for length of pod and width of pod. Further, the present finding showed that estimates of PCV were generally higher than their corresponding GCV for all the character studied. These finding are similar in agreement with earlier reported by Sirohi *et al.*, (2006)^[10], Singh *et al.*, (2012)^[9], Jaiswal *et al.*, (2013)^[5], The difference among the genotypic coefficient of variance and phenotypic coefficient of variance value for different characters indicated that the influence of environment in expressing the variability with traits. If the difference least, mean the environment is much affecting in the variable performance of the characters. But if the difference is more means there is much influence of environment in the expression of the traits.

High heritability values were obtained for all the characters. Highest heritability value were obtained were noticed for plant height (99.80) and pod yield per plant (99.57). The high heritability denotes high proportion of genetic effects in the determination of these characters and can be adopted for improving pod yield. The characters showing high heritability, could be owing to greater contribution of additive

genetic components in the inheritance of these attributes. Similar results were also reported by earlier finding of Katiyar, *et al.* (2014)^[6] and Georgieva *et al.*, (2016)^[3].

For an effective selection, the knowledge alone on the estimates of heritability is not sufficient and genetic advance if studied along with heritability is more useful. The high genetic advance as percent of mean along with high heritability was obtained for plant height (56.84%), number of pods per plant (43.73 %), length of first fruiting node (43.44 %), pod yield q/ha (38.61 %), pod yield per plant (38.62 %), days to 50 % flowering (33.25 %), number of seeds per pod (24.28 %). High heritability along with high genetic advance indicated substantial of additive genetic variance in expression of these characters and can be useful in hybridization and selection for higher grain yield. Some of these characters have also been reported earlier by Gupta *et al.*, (2006)^[4], Chadha *et al.*, (2008)^[11].

Conclusion

From the present study, it could be conclude that PCV and GCV were high for plant height which indicated that high degree of variability in this character and suggested that possibility of yield improvement through selection of this trait.

Table 1: Heritability, genetic advance, GCV and PCV for different characters in pea

Characters	Heritability (%)	GA	GA as %	GCV (%)	PCV (%)
Days to 50% flowering	98.00	16.41	33.25	16.31	16.47
Plant height(cm)	99.80	36.51	56.84	27.62	27.65
Number of first fruiting node	79.61	2.36	18.60	10.12	11.35
Length of first fruiting node(cm)	99.61	16.20	43.44	21.13	21.17
Number of pods per plant	99.57	13.91	43.73	21.27	21.32
Length of pod (cm)	75.85	1.35	15.55	8.67	9.95
Width of pod (cm)	69.00	0.10	7.49	4.38	5.27
Number of seeds per pod	81.78	1.94	24.28	13.04	14.42
Pod yield q/ha	99.56	53.71	38.61	18.78	18.83
Pod yield per plant(g)	99.57	21.48	38.62	18.79	18.83

References

- Chadha S, Sharma R, Chaudhary DR, Sagar V. Genetic variability studies in summer pea under cold desert areas of North-Western Himalayas. *Agricultural Science Digest*. 2008; 28(1):10-13
- Cousin JR, Massager A, Vingere A. Breeding for yield in common peas. The peas Crops. P.H. Hebblethwaite, M.C. Heath and T.C.K. Dawkins (Eds.). *Butterworths*, 1985, 115-129.
- Georgieva N, Nikolova I, Kosev V. Evaluation of genetic divergence and heritability in pea (*Pisum sativum* L.) *J Bio. Sci. Biotechnol*. 2016; 5(1):61-67.
- Gupta AJ, Singh YV, Verma TS. Genetic variability and heritability in garden pea (*Pisum sativum* L.). *Indian Journal of Horticulture*. 2006; 63(3):332-334
- Jaiswal NK, Gupta AK, Dewangan H, Lavanya GR, Roopa. Genetic variability analysis in Field Pea (*Pisum sativum* L.). *International Journal of Science and Research (IJSR)*. 2013, 4.
- Katiyar SKR, Singh HC, Gangwar RS, Verma MC, Singh RK. Genetic variability and selection parameters in table pea (*Pisum sativum* L.) *Trends in Biosciences*. 2014; 7(9):720-723.
- Ram T, Singh S. Genetic analysis of yield and its components in urdbean (*Vigna mungo* L.). *Indian J Pulses Res*. 1993; 6:194-196.
- Sharma VK, Bora L. Studies on genetic variability and heterosis in vegetable pea (*Pisum sativum* L.) under high hills condition of Uttarakhand, India *African Journal of Agricultural Research*. 2013; 8(18):1891-1895.
- Singh M, Malik S, Kumar M, Singh KV, Kumar S, Dev P *et al.* Studies of variability, heritability and genetic advance in field pea (*Pisum sativum* L.). *Progressive Agriculture*. 2012; 12(1):219-222.
- Sirohi SPS, Ramashray Y, Malik S. Genetic variability, correlations and path coefficient analysis for seed yield and its component characters in pea (*Pisum sativum* L.). *Plant Archives*. 2006; 6(2):737-740.
- Vavilov NI. The origin, variation, immunity and breeding of cultivated plants. Translated form Russian by K.S. Chester, New York, The Ronald Press Co, 1951.