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Studies on genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* L. var. hortense)

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Abstract

The present experiment was carried out to find out the diversity among the different genotypes with the using 42 diverse genotypes including two checks for quantitative traits and qualitative traits. The study was conducted with the field evaluation of 44 genotypes during 2019-20. The wide range of variation variability among the traits during 2019-20. The observation was recorded Days to 50 per cent flowering, primary branches per plant, node to first flower appears, node to first pod appears, length of pod (cm), pod diameter (cm), number of seeds per pod, number of pods per plant, number of pods per 250g, number of seeds per 250g, shelling (%), T.S.S.(⁰B) and pod yield per plant (g). Genotypes involved in this study were genetically diverse and have good breeding value, which confirmed the predictions of analysis of variance. Out of 44 genotypes among eighteen genotypes were produced significantly higher yield than best check PC-521.

Keywords: Garden pea, heritability, variability, PCV, GCV and genetic advance

Introduction

Garden Pea (Pisum sativum L. var. hortense) belongs to family Leguminaceae sub family Fabaceae and is an important legume vegetable grown throughout world during cool season. It is a self-pollinated crop having diploid chromosome number 2n = 14. It is most extensively cultivated in the temperate regions and restricted to cooler altitudes in the tropics and winter season in the sub tropics. It is highly nutritious and capable of using atmospheric nitrogen. Pea has low nitrogen requirement and does not show any marked response to application of nitrogenous fertilizer. Phosphorus is however essential for growth of nitrogen-fixing organism. On poor soil as well as on soil where the crop is newly grown inoculation of the soil with bacterial culture and adequate manuring with complete fertilizer are essential to increase the yield and to improve the quality of pod. India ranks third in area after China and USSR under pea (vegetable and pulse pea) cultivation. The total area covered by peas is 563 million hectares with the production of 5703 metric tonnes whereas, productivity is 10.12 metric tonnes per hectare (Anonymous, 2019-20 II Estimate). The main objectives in breeding pea crop are yield, regional adaptability, suitable plant type, lodging and shattering resistance disease and insect resistance, environmental stress resistance, quality and effective nitrogen fixation. At present, the yield potential of pea for green pod as well as for the grain is very low and there exists a scope for its improvement. The environmental factor limiting the yield should be considered, while developing genotypes for yield. Pod and grains characteristics, which directly influence the yield and its quality, should be given due consideration. The information usually needed for developing high yielding varieties in a particular species pertains to the extent of genetic variability for desirable traits in the available germplasm. Evaluation of germplasm is the basic tool for identification of important genotypes. The great extent of natural variation available for various characters among the genotypes suggests good scope for improvement in economic traits. Large variability ensures better chance of producing new forms. Variability parameters like genotypic and phenotypic coefficient of variations, heritability and genetic advance, and degree of association between the various characters and direct effect of yield contributing characters on total yield, is of paramount significance in formulating an appropriate breeding strategy aimed at exploiting the inherent variability of the original population. Phenotypic variability changes under different environmental conditions, while genetic variability remains unchanged and more useful to a plant breeder for exploitation in selection or hybridization. Yield is a complex trait controlled by several yield contributing components.

Material and Methods

The present research work entitled "Studies on genetic variability, heritability and genetic advance in garden pea (Pisum sativum L. var. hortense)" was carried out during Rabi season 2019-20, at the Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.). The experimental materials for the present investigation was comprised of 44 different genotypes (42 genotype + 2 check) of garden pea selected on the basis of genetic variability from the germplasm stock maintained in the Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya (U.P.) India. These forty-four genotypes were evaluated for the study of evaluation genotypes. The experiment laid out in Randomized Block Design with three replications forty-four treatment including two check. The observation was recorded days to 50 per cent flowering, primary branches per plant, node to first flower appears, node to first pod appears, length of pod (cm), pod diameter (cm), number of seeds per pod, number of pods per plant, number of pods per 250g, number of seeds per 250g, weight of seed per 250g, shelling (%), T.S.S. (⁰B), pod yield per plant.

Result and Discussion

The estimate of genotypic coefficient of variation is of prime importance to breeder because genetic variance alone, does not allow a decision as to which characters were showing the highest degree of variability. Therefore, accurate relative comparison can be made with the help of phenotypic and genotypic coefficient of variation. In general, the phenotypic coefficients of variability were higher than the genotypic coefficient of variability for all the characters under study which indicated that environment played very important role in the expression of the traits.

The estimates of genotypic and phenotypic coefficients of variation for fourteen characters of garden pea germplasm had been presented in table. The estimates of phenotypic coefficients of variations (PCV) were higher than genotypic coefficients of variations (GCV) for all the characters. The highest phenotypic as well as genotypic coefficients of variation were observed in case of primary branches per plant followed by pod yield per plant, number of pods per plant, nodes to first pod appears and nodes to first flower appearance. The highest phenotypic and genotypic coefficient of variation was observed for node to first pod appear followed by number of seeds per 250 g, number of pods per 250 g and total soluble solid. Similar, results have been reported by Chaudhary et al. (2010) [10], Singh et al. (2012) [7], Dar et al. (2013)^[4] and Sharma and Sharma (2013)^[6]. Moderate PCV along with GCV were recorded for primary branches per plant and pod yield per plant. Similar result was also reported by Srivastava et al. (2009)^[8] and Lal et al. (2011)^[5].

The phenotypic and genotypic coefficients of variations were lower for number of seeds per 250g. Low GCV and PCV for these traits indicated that the genotypes taken for the present study were similar for these traits

Heritability in broad sense of a character is important to the breeder since it indicate the possibility and extent to which improvement is possible through selection. It also indicates direction of selection pressure to be applied for a trait during selection because it measures relationship between parents and their progeny, hence widely used in determining the degree to which a character may be transmitted from parents to offspring. However, high heritability alone is not enough to make efficient selection in advanced generation unless accompanied by substantial amount of genetic advance (Burton, 1953)^[2]. High estimates of heritability along with high genetic advance provides good scope for further improvement in advance generations. Estimates of heritability (broad sense) and genetic advance for different characters has been the heritability in broad sense ranged from 66.54 per cent in case of shelling percentage to 98.20 per cent for pod yield per plant.

High estimates of heritability (>75%) were recorded for 11 characters viz. pod yield per plant (98.20%), number of seeds per 250 g (97.58%), primary branches per plant (97.33%), TSS (97.12%), number of pod per plant (96.67%), Days to 50% flowering (96.53%), number of pods per 250 g (94.77%), number of first pod appears (90.75%), width of pod (90.67%), node to first flower appears (89.91%), length of pod (88.83%). However, moderate heritability (>50% and <75%) was observed for number of seeds per pods (74.50%) followed by weight of seed per pod (71.03%), and Shelling percentage (66.54) and no lower heritability (<50%) was estimated for all fourteen characters. Highest value of genetic advance in percent of mean was shown by primary branches per plant (62.75%) while shelling percentage exhibited lowest value (8.04%) for this parameter. The characters which observed very high estimates of genetic advance were primary branches per plant (62.75), pod yield per plant (50.76), number of pod per plant (49.00), number of seeds per 250 g (41.36), nodes to first pod appearance (34.66), node to first flower appears (33.56), number of pods per 250 g (32.16), days to 50% flowering (31.69), TSS (26.35), Width of pod (21.96), length of pod (16.97) and number of seeds per pods (16.32). Lowest genetic advance in per cent of mean was estimated for weight of seed per 250 g (12.92) and shelling % (8.04).

The result on heritability and genetic advance in per cent of mean of present investigation had been studied. The heritability estimates for different characters ranged from 66.54 to 98.20 per cent. High heritability was recorded for almost all the character except number of seeds per pod, weight of seed per 250 g and shelling percentage. High heritability coupled with high genetic advance in per cent of means were recorded for primary branches per plant, pod yield per plant, number of pods per plant and number of seeds per 250 g indicating that these traits were little influenced by environment. Thus, require low selection intensity for improvement. Similar result was also reported by Srivastava *et al.* (2009) ^[8] and Dar *et al.* (2013) ^[4].

 Table 1: Mean, range, coefficient of variations (PCV & GCV), heritability in broad sense, genetic advance and genetic advance in percent of mean for fourteen character in garden pea germplasm

S. No	Genetic parameters	Range		Grand	ECVs	PCV	GCV	Heritability in broad	Genetic	Genetic advance in percent of mean 5%
110.	characters	LUWESI	inguest	mean				sense (70) (II DS)	auvance 570	percent of mean 370
1.	Days to 50% Flowering	41.40	67.36	50.97	5.13	15.93	15.65	96.53	16.15	31.69
2.	Primary branches per plant	1.53	6.12	3.17	8.85	31.29	30.87	97.33	1.99	62.75

3.	Node to first flower appears	8.66	18.40	12.09	9.96	18.11	17.18	89.91	4.05	33.56
4.	Node to first pod appears	7.53	18.53	12.36	9.76	18.54	17.66	90.75	4.28	34.66
5.	Length of pod (cm)	7.28	10.37	9.05	5.37	9.27	8.74	88.83	1.53	16.97
6.	Width of pod (cm)	1.01	1.70	1.33	6.21	11.75	11.19	90.67	0.29	21.96
7.	Number of seeds per pod	5.26	8.20	6.96	9.30	10.63	9.18	74.50	1.13	16.32
8.	Number of pods per plant	15.80	39.20	27.90	7.77	24.60	24.19	96.67	13.67	49.00
9.	Number of pods per 250 (g)	37.33	68.00	51.50	6.52	16.47	16.03	94.77	16.56	32.16
10.	Number of seeds per 250 (g)	221.66	476.00	346.77	5.21	20.52	20.30	97.58	143.58	41.36
11.	Weight of seeds per 250 (g)	105.76	160.00	138.52	8.23	8.83	7.44	71.03	17.90	12.92
12.	Shelling %	40.93	56.00	51.24	5.88	5.86	4.78	66.54	4.12	8.04
13.	TSS (⁰ B)	9.50	17.66	12.58	3.87	13.17	12.98	97.12	3.31	26.35
14.	Pod yield per plant (g)	69.00	199.26	137.25	5.82	25.09	24.86	98.20	69.68	50.76

*, ** Significant at 5% and 1%, respectively

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