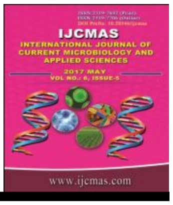
International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 6 Number 5 (2017) pp. 1025-1033**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2017.605.111

Assessment of GCV, PCV, Heritability and Genetic Advance for Yield and its Components in Field Pea (*Pisum sativum* L.)

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ABSTRACT

Keywords

Pisum sativum L., GCV, PCV, Heritability, Genetic advance.

Article Info

Accepted:
12 April 2017
Available Online:
10 May 2017

The present investigation was carried out at Research Farm, ICAR Research Complex for NEH Region Tripura centre Lembucherra Agartala (Tripura) during rabi 2012-13. The experiment comprisingP_1,P_2 F_1, F_2, Bc_1P_1 (B_1) and Bc_1P_2 (B_2) populations of two crosses *viz.*, IM 9214-10 x Rachna (C-1) and IM 9214-10 x Ambika (C-2) was conducted in randomized block design with three replications. The populations were employed for the assessment of genetic variability, heritability and genetic advance for days to first flowering, number of branches per plant, days to maturity, plant height, number of clusters per plant, pod bearing length, seed setting percent, pods per cluster, number of pods per plant, pod length, hundred seed weight and seed yield per plant. Analysis of variance revealed that sufficient genetic variation has been created for seed yield and its attribute for taking different biometrical analyses. Relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study indicating environmental influence on the traits. High heritability coupled with high genetic advance as per cent of F_1 mean was found for plant height, clusters per plant, pod bearing length, pods per plant and seed yield per plant indicating that direct selection can be effective for yield improvement in the populations under study.

Introduction

Proteins are the essential ingredients of our food and are considered to be building block of our body. The deficiency of protein particularly in growing children and nursing mothers causes "Protein caloric malnutrition" IPCMI. Proteins constitute about 20 percent of our body weight and are derived from the dietary foods (Swaminathan, 1990).

Pulses are considered to be the cheapest and economic source of protein. However, the availability of pulses had declined from 64 g to less than 37g as against the recommendation of 80 g per capita per day. It is estimated that the Indian population will touch nearly 1350 million by 2020 A.D. and country' would then need a minimum of 30.0 million tones of pulses, as against today's pulses production of 28.17 million tonnes (Anonymous, 2013).

Among the major pulse crops grown in India, field pea or dry pea (*Pisum sativum* L.) belongs to family leguminoceae and sub family Papilionaceae is considered to be the native of Ethiopia, the Mediterranean and Central Asia. It is a nutritious and protein rich

(19.6%) crop, mostly used for green and dry seeds. Hence, pea is categorized as vegetable type and field pea. The area of field pea in India is about 0.76 million hectares with annual production of 0.84 million tones and productivity of 1100 kg ha^{-1} (Anonymous, 2013 a). Its area, production and productivity in the state of Tripura are 1028 hectare 897 mt tonnes and 873 kg/ ha respectively, (Anonymous, 2013 b).

To meet out challenging demand of pulses it has became necessary to boost up their production in the country. Field pea has high production potential of more than 2.0 tons per ha under better agronomic management (Anonymous, 2013c). Field pea, very much response to low soil pH and one/two irrigations hence, there is plenty of scope for its horizontal and vertical expansion in rice based cropping system of Tripura. Relatively this crop dose not has much problem of pest and diseases except powdery mildew, to which genetic resistance is available.

The farmers of the state are small and marginal hence, there is urgent need to give them varieties which yield better even under average agronomic management. Dwarf types have greater potential under one or two irrigations. Hence, there is need to combine together desirable gene(s) from tall and dwarf types for evolving high yielding, disease resistant and widely adopted varieties for the state of Tripura. To attain the goal, the information on genetic variability, heritability and genetic advance of yield and its attributing traits is essentially needed. Hence, the present study has been undertaken to generate basic information in relation to genetic improvement in seed yield.

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). Genetic improvement in relation to grain yield and harvest index is prime objective in this crop. However, yield is a complex character contributed by several morpho-physiological traits. Hence, the knowledge relating genetic control of yield and its contributing traits is of immense use for initialing an efficient selection scheme for selecting a superior desirable genotype. Further, the study of genetic variability heritability and genetic advance would provide realistic estimates for deciding an efficient and effective breeding programme in this crop. In view point of these facts present investigation was carried out to estimate the extent of genetic variability, heritability and genetic advance created through hybridization, for seed yield and its component characters

Materials and Methods

The present investigation was carried out at Research Farm, ICAR Reesearch Complex for NEH Region Tripura centre Lembucherra Agartala (Tripura) during rabi 2012-13. The experiment comprising P_1, P_2, F_1, F_2, Bc_1P_1 (B_1) and Bc_1P_2 (B_2) Populations of two crosses *viz.*, IM 9214-10 x Rachna (C-1) and IM 9214-10 x Ambika (C-2) was conducted in randomized block design with three replications. The populations were employed for the assessment of genetic variability, heritability and genetic advance for days to first flowering, number of branches per plant, days to maturity, plant height, number of clusters per plant, pod bearing length, seed setting percent, pods per cluster, number of pods per plant, pod length, hundred seed weight and seed yield per plant utilizing the models suggested by Mather (1949) and Hayman (1958). In each replication, each genotype was sown in a plot size 2.0 x 0.90 m^2 consisting of five row. The row to row and plant to plant distance was 30 cm and 10 cm, respectively. Ten competitive plants were selected at random in P_1, P_2, F_1, BC_1 and BC_1 while 60 plants in F_2 for recording the observations on number of branches per plant, plant height, number of clusters per plant, pod bearing length, seed setting percent, pods per cluster, number of pods per plant, pod length, hundred seed weight and seed yield per plant. Data on days to 50% flowering and Days to maturity was however recorded on whole plot basis. The crop was raised as per the recommended package of practices. Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1985). Genotypic and phenotypic coefficients of variability were estimated according to the Burton and Devane (1953) by using the following formulae.

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100 \quad GCV = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

Where,

PCV = Phenotypic Coefficient of variation, GCV = Genotypic Coefficient of variation

$\sigma^2 g$ = Genotypic variance = (Mean sum of squares due to genotypes – Error mean sum of squares) ÷ Replications

$\sigma^2 p$ = Phenotypic variance = $\sigma^2 g + \sigma^2 e$

$\sigma^2 e$ = Environmental variance = (Error mean sum of squares) ÷ Replications

$\bar{x}$ = General mean

PCV and GCV were classified as suggested by Sivasubramanian and Menon (1973).

Less than 10% = Low
10-20% = Moderate
More than 20 % = High

Heritability in broad sense (h2 (b)) was estimated as per the formulae suggested by Allard (1960).

$$h^2 (b) = \frac{(\sigma 2g)}{(\sigma 2p)} \times 100$$

The heritability (h2 (b)) was categorised as suggested by Johnson *et al*., (1955).

0-30% = Low
31-60% = Medium
61% and above = High

Genetic advance (GA) was estimated as per formula given by Allard (1960)

$GA = K \times \sigma p \times h^2 (b)$ Where,

K = Selection differential at 5 per cent selection intensity which accounts to a constant value 2.06

σp = Phenotypic standard deviation

Genetic advance over mean (GAM) was calculated using the following formula and was expressed in percentage.

$$GAM = \frac{(GA)}{\bar{x}} \times 100$$

The genetic advance as per cent over mean was categorized as suggested by Johnson *et al*. (1955).

Less than 10% = Low
10-20% = Moderate
More than 20 % = High

Results and Discussion

Analysis of variance was carried out separately for cross and characters (Table 1). The mean sum of squares due to treatments (different generations) were highly significant for all the characters except number of branches per plant and hundred seed weight in cross-1, and pod length and pods per cluster in cross-2. The mean performance of six generations for each of the twelve characters is given in table 2. F_1 means as compare to their parental values varied in magnitude from cross to cross and character to character. Similarly, F_2 means also deviated from F_1 means. In general, backcrosses gave superior performance as compare to their parents for seed yield and other important attributes related to seed yield.

Heritability in narrow sense and genetic advance over mean estimated as percentage of mean for all the characters and cross wise. The cross-wise result is presented in table 3.

Cross-1

Nine characters *viz.*, days to flowering (75.70%), days to maturity (83.30%), plant height (99.90%), pod bearing length (98.80%), number of clusters per plant (97.00%), seed setting percent (87.90%), number of pods per plant (99.70%), hundred seed weight (84.80%) and seed yield per plant (97.60%) expressed high heritability, while number of branches per plant (52.64%), pods per cluster (47.80%) and pod length (45.40%) expressed moderate heritability under study.

Genetic advance as percentage of mean was found to be the highest for number of pods per plant (78.86%), followed by seed yield per plant (69.20%), pod bearing length (57.95%), plant height (54.20%.), number of clusters per plant (51.30%). It was low for pods per cluster (10.00%), hundred seed weight (9.30%), seed setting percent (7.25%), pod length (5.65%), number of branches per plant (5.36%), days to first flowering (3.74%) and days to maturity (1.66%).

Cross-2

Nine characters viz., days to flowering (66.30%), days to maturity (63.30%), plant height (98.8).%), pod bearing length (94.60%), number of clusters per plant (97.80%), seed setting percent (77.00%), number of pods per plant (90.00%), hundred seed weight (82.50%) and seed yield per plant (96.40%) expressed high heritability. However, number of branches per plant (36.50%), pods per cluster (20.40%) and pod length (10.66%) showed moderate to low heritability.

Genetics advance as percentage of mean was found to be the highest for plant height (64.05%) followed by number of clusters per plant (53.10%), pod beating length (51.54%), number of pods per plant (48.80%), seed yield per plant (46.40%), while it was moderate to low for hundred seed weight (7.40%), seed setting percent (6.40%), pods per cluster (3.65%), days to first flowering (3.40%), number of branches per plant (2.60%), days to maturity (1.62%) and pod length.(0.20%).

Sound genetic information has been an indispensable prelude for modifying the vast array of gene frequencies to enable genetic enrichment in a genotype. The presence of genetic variability is essential and pre-requisite for an effective improvement in a crop species. Besides, genetic variability, heritability which measures the relationship between phenotypic and genotypic appearance is another important consideration for the success of a breeding programme. It is obvious that the selection is usually based on phenotypic observations and the success would naturally depend upon the relationship between phenotype and the genotype. The estimates of heritability are also useful in prediction of genetic improvement following selection and deciding suitable breeding procedures for the improvement of a crop plant. The knowledge of association between yield and yield components are useful in determining suitable selection scheme for maximum genetic gain. This information can also be used for locating the most important yield components.

The purpose of the present investigation was to obtain the basic information which can throw light on the strategies to be adored for genetics improvement of filed pea also known as dry pea. The present investigation was therefore, under taken to ascertain the basic information regarding the genetic variability, heritability and genetic advance for grain yield and yield related components in field pea. In lieu of this, the findings achieved from the present study and their practical utility in genetic improvement of this crop is explains here. Three parents used in the present investigation differing in origin showed sufficient variability for the characters under study (Table 4). The treatments consisting six generations showed significant differences for all the traits in both the crosses except for number of branches per plant, hundred seed weight in cross-1, pods per cluster and length in cross-2. Thus it is evident from data that adequate variability was generated for carrying out the various analyses as well as fulfilling the long term objectives of selecting desirable genotypes, possessing high yield. These findings are in accordance with those of Sharma and Bora (2013) in guar.

Heritability in 'narrow sense' is the ratio of additive genetic variance to the total phenotypic variance and measures the portion of the total variation, which can be utilized for the improvement of reference population with respect to a particular trait, by mass pedigree selection. It indicates the degree to which the progeny of F_2, plant will resemble their parents (Allard, 1960). The broad sense heritability, the proportion of genotypic variance to the phenotypic variance is an important parameter in breeding and genetics, because knowledge of numerical magnitude of heritability is of special importance for planning in breeding programmes and for the examination of experimental results (Pallavi *et al.*, 2013).

Heritability estimates are influenced by methods of estimation, generation under study, sample size and the environmental factors. Usefulness of heritability estimates depends on their reliability of predicting progress under selection. Heritability estimates remain extremely useful in the study of the inheritance of quantitative traits. The recent emphasis is more on evaluation of selection procedure through computation of expected progress. The magnitude of genetic advance is influenced by unit of measurement. In order to avoid this and to facilitate the comparison of progress in various characters of different crosses, genetic advance was calculated as percent gain over the F_2 mean.

Estimates of heritability were grouped in to three categories high (>170 %), medium (50-70 %) and low (<50%); depending on magnitude as per Robinson (1966). In the present investigation high heritability coupled with high genetic advance as percent of mean was found for plant height. Number of clusters per plant, pod bearing length, number of pods per plant and seed yield per plant, in accordance to these findings Bhagmal (1969, Yadva (1989) and Vikash *et al.*, (1999) also reported high heritability coupled with high genetic advance for these characters.

High heritability associated with low genetic gain was recorded for seed setting percent and hundred seed weight. Vaishnav (2000) reported high heritability and moderate genetic gain for seed setting percent. In contrary to the present findings Singh *et al.*, (1977), Yadav (1989), Kumar *et al.*, (1995) and Vaishnav (2000) reported high heritability coupled with high genetic gain for seed size in pea. This might be due to narrow variation in the test weight of the parents used in the crossing programme.

Table.1 Analysis of variance for yield and its attributes in field pea

Source of variation	df	First flower (days)	No of branches Plant^{-1}	Maturity (days)	Plant height (cm)	No of clusters plant^{-1}	Pod bearing length (cm)	Seed setting (%)	Pods cluster^{-1}	Number of pods plant^{-1}	Pod length (cm)	100 seed weight (g)	Seed yield plant^{-1} (g)
C-1: IM 9214-10 × Rachna													
Replication	2	0.0273	0.1088	0.4375	2.5430	0.4066	0.1486	0.8710	0.0016	0.6571	0.0720	0.1203	0.1668
Treatment	5	2.756**	0.1622	3.7875*	1015.973**	7.2306**	68.227**	22.9135**	0.0386*	65.40**	0.1418*	2.792	18.865**
Error	10	0.2664	0.0755	0.2375	0.5054	0.0733	0.2715	1.0065	0.0103	0.0745	0.0405	0.1571	0.1526
C-2: IM 9214-10 × Ambika													
Replication	2	0.6914	0.2338	0.8906	0.1015	0.06222	0.2271	0.0039	0.0072	0.2772	0.0816	0.4257	0.1433
Treatment	5	2.7679**	0.3498*	5.3416**	1424.687**	7.2818**	42.7472**	21.1802**	0.0222	26.9245**	0.0936	2.1602**	9.604**
Error	10	0.4011	0.1025	0.8666	0.8250	0.05356	0.7952	1.9200	0.0125	0.9372	0.0869	0.1424	0.1173

*, ** Significant at 5 and 1 percent level of significance

Table.2 Cross wise mean performance of different generations for yield and attributes in field pea

	First flower (days)	No of Branches/plant	Maturity (days)	Plant height (cm)	Clusters plant^{-1}	Pod bearing length (cm)	Seed setting (%)	Pods cluster^{-1}	Number of pods plant^{-1}	Pod length (cm)	100 seed weight (g)	Seed yield/pla (g)
C-1: IM 9214-10 × Rachna												
P_1	43.73	3.67	121.80	60.00	4.67	7.33	68.67	1.20	8.00	4.33	18.73	5.17
P_2	42.20	3.27	125.20	76.00	4.80	18.07	72.97	1.40	9.93	4.73	19.43	5.90
F_1	42.40	3.67	123.53	79.67	8.80	19.33	75.33	1.53	19.03	4.33	17.70	12.07
F_1	44.00	3.23	124.33	63.44	6.73	17.80	73.77	1.37	17.00	4.83	18.65	6.47
BC_1	44.30	3.20	123.87	79.60	6.27	17.87	77.67	1.40	8.47	4.67	20.40	8.07
BC_2	44.33	3.13	123.80	85.07	5.33	20.53	69.33	1.47	10.60	4.73	19.85	6.33
C-2: IM 9214-10 × Ambika												
P_1	45.43	3.47	120.87	63.20	4.60	8.00	69.00	1.23	8.60	4.40	20.03	5.62
P_2	45.13	3.67	124.20	88.67	4.47	19.53	69.67	1.43	16.33	4.70	19.28	6.40
F_1	43.27	3.27	123.47	96.20	8.30	15.33	69.83	1.37	12.83	4.67	20.20	9.53
F_1	43.47	3.13	124.60	65.33	4.13	15.83	72.17	1.33	9.37	4.50	19.81	6.70
BC_1	43.80	3.53	124.03	64.17	4.50	14.00	72.33	1.43	13.70	4.43	20.73	8.30
BC_2	43.33	3.70	123.33	71.47	5.17	13.73	76.17	1.47	9.93	4.80	21.73	10.00

Table.3 Estimation of heritability and genetic advance in two crosses of field pea (*Pisum sativum* L.)

Characters	Cross -1		Cross -2	
	h^2 (ns)	GA %	h^2 (ns)	GA %
First flower (days)	75.70	3.73	66.30	3.40
No of branches plant^{-1}	52.64	5.36	36.50	2.60
Maturity (days)	83.30	1.66	63.30	1.62
Plant height (cm)	99.90	54.20	98.80	64.05
Clusters plant^{-1}	97.00	51.30	97.80	53.10
Pod bearing length (cm)	98.80	57.95	94.60	51.54
Seed setting (%)	87.90	7.25	77.00	6.40
Pods cluster^{-1}	47.80	10.00	20.40	3.65
Number of pods plant^{-1}	99.70	78.86	90.00	48.80
Pod length (cm)	45.40	5.65	10.66	0.20
100 seed weight (g)	84.80	9.30	82.50	7.40
Seed yield plant^{-1} (g)	97.60	69.20	96.40	46.40

Table.4 Genetic parameters of variability for yield and its components in field pea

➢ **Parameters**	**Range**		**Mean**	**Coefficient of Variation**	
Characters	**Minimum**	**Maximum**		**Genotypic**	**Phenotypic**
First flower (days)	43.33	46.80	44.70	02.97	05.96
No of branches plant^{-1}	02.33	03.55	03.10	01.05	17.35
Maturity (days)	122.00	125.00	123.80	00.30	00.91
Plant height (cm)	41.86	78.67	65.50	14.27	20.57
Clusters plant^{-1}	04.60	05.33	04.90	00.61	17.88
Pod bearing length (cm)	07.73	22.33	16.60	14.53	25.53
Seed setting (%)	68.00	76.66	72.00	00.39	04.80
Pods cluster^{-1}	01.20	01.60	01.40	04.11	08.38
Number of pods plant^{-1}	08.00	14.70	11.10	00.29	37.84
Pod length (cm)	04.30	04.90	04.60	02.88	05.78
100 seed weight (g)	17.40	22.06	19.80	04.96	06.02
Seed yield plant^{-1} (g)	04.50	09.33	06.80	08.60	21.31

Table.5 Estimation of heritability and genetic advance in two crosses of field pea (*Pisum sativum* L.)

Characters	Cross -1		Cross -2	
	h^2 (ns)	GA %	h^2 (ns)	GA %
First flower (days)	H	L	M	L
No of branches plant^{-1}	M	L	L	L
Maturity (days)	H	L	M	L
Plant height (cm)	H	H	H	H
Clusters plant^{-1}	H	H	H	H
Pod bearing length (cm)	H	H	H	H
Seed setting (%)	H	L	H	L
Pods cluster^{-1}	L	L	L	L
Number of pods plant^{-1}	H	H	H	H
Pod length (cm)	L	L	L	L
100 seed weight (g)	H	L	H	L
Seed yield plant^{-1} (g)	H	H	H	H

In consistency in heritability estimates noted for days to first flowering, days to maturity might he due to environmental effects on these traits.

Heritability values were high in C-1 but were moderate in C-2 for days to flowering and maturity. In accordance to these, Nandpuri and Kumar (1973) and Sable *et al.*, (2003) also observed high heritability (h^2n) and low genetic advance for days to flowering while Yadava (1989) and Vaishnav (2000) found high heritability associated with low genetic gain for days to maturity. Number of branches seemed to be high inconsistent and very much influenced by environment, as evidenced by its high phenotypic coefficient of variation and low genotypic coefficient of variation (Table 5). It showed moderate heritability in cross-I and low in cross-2 however, genetic advance was low in both the crosses, giving an indication to the plant breeders for paying proper attention while exercising selection for high number of branches. Similar results in tall and dwarf type field pea have also been noted by Vaishnav (2000).

As stated earlier that heritability estimates is also influenced by environmental factor which is true for this study too. Abrupt weather conditions during crop season. Highly influenced the crop growth and other economic traits even though high estimates of heritability in narrow sense showed presence of adequate additive genetic variance that can easily be exploited for the genetic improvement of the quantitative traits such as plant height, pod number, seed yield and seed size. High heritability coupled with high genetic gain obtained for plant height, number of branches, number of pods, seed yield per plant and hundred seed weight gave an indication that desirable improvement in seed yield can easily be achieved on implementation of effective selection scheme for above traits.

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How to cite this article:

Meena, B.L., S.P. Das, S.K. Meena, R. Kumari, A.G. Devi and Devi, H.L. 2017. Assessment of GCV, PCV, Heritability and Genetic Advance for Yield and its Components in Field Pea (*Pisum sativum* L.). *Int.J.Curr.Microbiol.App.Sci*. 6(5): 1025-1033.
doi: https://doi.org/10.20546/ijcmas.2017.605.111