



E-ISSN: 2278-4136

P-ISSN: 2349-8234

www.phytojournal.com

JPP 2021; 10(1): 1053-1055

Received: 09-11-2020

Accepted: 18-12-2020

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Study of genetic variability in field pea (*Pisum sativum* L.)

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Abstract

The investigation was carried out at Research cum Instructional form of S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur (C.G.) at during the year 2019-20. Studies undertaken to estimate the genetic parameters for eleven characters with 21 diverse genotypes of field pea. The analysis of variance shows large variability present among the genotypes studied. High to moderate GCV and PCV estimates for the traits number of primary branches per plant, number of pods per plant, and plant height (cm). High heritability coupled with high genetic advance as percentage of mean were observed for the characters like plant height (cm), number of primary branches per plant, pods per plant, and seed yield per plant (g).

Keywords: *Pisum sativum*, field pea, Kumhrawand, Jagdalpur

Introduction

Field pea (*Pisum sativum* L.) belongs to family fabaceae (leguminosae) with chromosome number of pea $2n = 14$. Field pea is important crop for Rabi session crops in India. Field pea also called "dry pea" buy as a dry form shelled product for also human or domestic animal food, unlike the garden pea buy as a fresh and canned vegetable. Pea are highly nutritious and are rich source of digestible protein (27.8%) along with carbohydrates (42.65%), minerals (calcium, phosphorus), vitamins, dietary fiber and anti-oxidant compounds and sugars (5.67g/100 g edible portion) (Urbano *et al.* 2003) [14]. Field pea not only provides grain and forage also provide nitrogen to the soil through biological nitrogen fixation by help rhizobium bacteria it lead to increase the crop production and the improvement of soil health. Besides pulse residues are nutritious feed for livestock and milk cattle and thus, offer an added advantage to the poor farmer families.

Materials and methods

The investigations were undertaken at Research cum Instructional form of S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur (C.G.) at during the year 2019-20. The Experimental material comprised of 6 parents (Adarsh KPMR-400, Prakash, Paras, Indira Matar, and Ambika. and their 15 crosses of field pea *viz.*, Adarsh x KPMR-400, Adarsh x Prakash, Adarsh x Paras, Adarsh x Indira Matar, Adarsh x Ambika, KPMR-400 x prakash, KPMR-400 x Paras, KPMR-400 x Indira Matar, KPMR-400 x Ambika, Prakash x Paras, Prakash x Indira Matar, Prakash x Ambika, Paras x Indira Matar, Paras x Ambika, Indira Matar x Ambika. Genetically pure seeds were grown in a RBD with three replications in a plot size of 1.35 m² (1.5m x 90m). All recommended agronomic and plant protection practices were followed. The data were recorded for 11 characters *viz.*, days to 50% flowering, days maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, harvest index and seed yield per plant.

Genotypic and phenotypic coefficients of variations were estimated by using the formula suggested by Burton and De Vane (1953) [3]:

$$GCV (\%) = \frac{\sigma_g^2}{\text{mean}} \times 100$$

$$PCV (\%) = \frac{\sigma_p^2}{\text{mean}} \times 100$$

Where, σ_g^2 = Genotypic variance σ_p^2 = Phenotypic variance.

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Heritability in broad sense for each character was analysed by using the method suggested by Hanson *et al.* (1956) [4]:

$$\text{heritability (h}^2\text{) (bs) \%} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2 (bs) % = heritability in broad sense, σ^2_g = Genotypic variance, σ^2_p = Phenotypic variance

Genetic Advance as percentage of the mean (GAM) estimated by using the formula suggested by Johnson *et al.* (1955) [5] as:

$$\text{Genetic Advance as percentage of mean} = \frac{GA}{GM} \times 100$$

Where,

GA = genetic advance, GM = general mean

Result and discussion

The success of any breeding programme lies upon the thorough knowledge of genetic variability, heritability and type of gene action involved in the inheritance of improvement of desirable characters. Thus, success of genetic enhancement is attributed to the magnitude and nature of variability present for a specific character.

Genotypic and phenotypic coefficients of variation was high in case of number of primary branches per plant (37.44, 38.61), number of pods per plant (24.85, 26.52), and plant height (22.12, 22.73), which indicates the presence of high amount of variation among the genotypes. Lowest genotypic and phenotypic coefficient of variation estimate was found in traits days to 50% flowering (3.06, 4.18) days to maturity (2.04, 2.58) and 100 seed weight (3.99, 5.38). The other characters which recorded Moderate PCV and GCV have in seed yield per plant (18.06%, 16.97%) followed by number of secondary branches (16.65%, 13.13%), number of seeds per pod (12.08%, 10.72%), and harvest index (11.95%, 10.31%), respectively. Ahmad *et al.* (2014) [1] reported high genotypic and phenotypic coefficient of variation for pods per plant, seed yield per plot and cluster per plant. Similar heritability reported by Toppo *et al.* (2014) and Pathak and Jamwal (2002) [16, 10].

Heritability estimates ranged from 53.56% (days to 50% flowering) to 94.73% (plant height). High heritability coupled with high genetic advance as percentage of mean indicated presence of additive gene action in these traits *viz.*, plant height (94.73%, 44.35%), number of primary branches per plant (94.01%, 74.77%), seed yield per plant (88.28%, 32.84%) and number of pod per plant (87.77%, 47.96%). High heritability coupled with low genetic advance as percent of mean it is indicated non-additive gene action in these traits *viz.* number of seed per pod (78.83%, 19.61%) and harvest index (74.40% 18.31%), respectively, the high heritability is being exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. Moderate heritability and low genetics advance as percent of mean was recorded for the characters days to maturity (62.45%, 3.32%), test weight (55.07%, 6.10%) and days to 50% flowering (53.56%, 4.61%). The findings of present study were in agreement with the findings of Saxena *et al.* (2014) and Kumar *et al.* (2013) [11, 8].

The value of phenotypic coefficient of variation (PCV) is higher than genotypic coefficient of variation (GCV) recorded for the traits plant height, followed by number of primary branches per plant, seed yield per plant(g), number of pods per plant, number of seeds per pod, harvest index, pod length(cm), days to maturity, number of secondary branches per plant, test weight of 100 seeds, and days to 50% flowering suggested that, the apparent variation is not only due to genotypic but also due to the influence of environment. Selection for such traits sometimes may be misleading.

Conclusion

High heritability coupled with high genetic advance as percentage of mean indicated presence of additive gene action in these traits *viz.*, plant height, number of primary branches per plant, seed yield per plant and number of pod per plant, additive gene action is pronounced in the expression of these characters early generation selection would be effective in breeding programme. High heritability is found with high genetic advance as percentage of mean for traits plant height, days to maturity, pod per plant and seed yield per plant which is indicative of aforesaid characters are governed under non additive gene action.

Table 1: Analysis of variance for yield and yield attributing traits

Source of variation	DF	DFF	PH (cm)	DM	NPB/P	NSB/P	PL/P (cm)	P/P	NS/P	HI (%)	TW (g)	SY/P
Replication	2	0.90	36.10	0.78	0.09	0.02	0.14	0.15	0.16	5.83	0.84	0.26
Genotypes	20	10.35**	980.75**	11.64**	1.85**	0.96**	1.15**	48.33**	1.05**	16.26**	2.56**	12.09**
Error	40	2.32	17.87	1.94	0.04	0.16	0.15	2.14	0.09	1.67	0.55	0.51
CD		2.52	7.00	2.31	0.33	0.67	0.64	2.43	0.49	2.14	1.22	1.19
C.V. (%)	--	2.85	5.22	1.58	9.45	10.25	6.48	9.27	5.56	6.05	5.61	6.18

*, ** significant at 5% and 1% level of significance. DF = Degrees of freedom, DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, NPB/P= Number of primary branches per plant, NSB/P =Number of secondary branches per plant, NP/P= Number of pods per plant, PL= Pod length, NS/P= Number of seeds per pod, SY/P= Seed yield per plant, HI= Harvest index, TW (g) = Test weight of 100 Seed weight

Table 2: Genetic parameters of variation for seed yield and its component traits in field pea

S. No.	Characters	Mean	Min	Max	Heritability (%)	GA% mean	GCV (%)	PCV (%)
1	DFF	53.48	49.67	56.33	53.56	4.61	3.06	4.18
2	PH (cm)	80.98	49.67	101.99	94.73	44.35	22.12	22.73
3	DM	88.11	85.33	92.00	62.45	3.32	2.04	2.58
4	NPB/P	2.08	1.20	4.10	94.01	74.77	37.44	38.61
5	NSB/P	3.92	3.47	6.13	62.15	21.32	13.13	16.65
6	PL/P (cm)	5.95	4.90	7.00	69.14	16.61	9.70	11.66
7	P/P	15.79	11.97	26.71	87.77	47.96	24.85	26.52

8	NS/Pod	5.30	4.37	6.57	78.83	19.61	10.72	12.08
9	HI (%)	21.39	18.15	26.21	74.40	18.31	10.31	11.95
10	TW (g)	20.51	19.08	22.73	55.07	6.10	3.99	5.38
11	SY/P(g)	11.58	9.32	17.89	88.28	32.84	16.97	18.06

GCV= Genotypic coefficient variance, PCV= Phenotypic coefficient variance, h^2 bs = Heritability in broad sense, DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, NPB/P= Number of primary branches per plant, NSB/P =Number of secondary branches per plant, NP/P= Number of pods per plant, PL= Pod length, NS/P= Number of seeds per pod, SY/P= Seed yield per plant, HI= Harvest index, TW (g) = Test weight of 100 Seed weight

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