Studies on estimates of heritability and genetic advance for certain quantitative traits in Fieldpea (*Pisum sativum* L.)

Abstract

Twenty two field pea genotypes were evaluated for estimation of variability, heritability and genetic advance. The Fieldpea genotypes were sown in, Randomized Block Design with three replications at the experimental farm of department of Genetics and Plant Breeding, Faculty of Agriculture, Kamla Nehru Institute of Physical and Social Sciences Sultanpur 228118 (U.P.) India, during Rabi, season 2022-2023. Phenotypic data were recorded for nine characters *viz*. days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, 100-grain weight, grain yield per plant and biological yield per plant. It was reported that in general the value of phenotypic coefficient of variance (PCV) is slightly higher than the value of genotypic coefficient of variance (GCV) indicating the importance of environment in the phenotypic performance of the genotypes studied. The maximum value of GCV was observed for plant height (31.94), grain yield per plant (20.02). High estimates of heritability in broad sense (h^2b) were recorded for plant height (97.28), days to 50% flowering (83.96), 100-grain weight (78.48) and days to maturity (64.83). High estimates of genetic advance as percent of mean were recorded for plant height (64.89), 100-grain weight (25.28) and grain yield per plant (25.15). Thus, the characters (plant height, days to 50% flowering, 100-grain weight etc) having high value of GCV, heritability as well as genetic advance may be exploited in Fieldpea breeding program for further improvement in grain yield.

Key words: pea genotypes, pulse crops, Fieldpea

Introduction

"Fieldpea (*Pisum sativum* L.) is one of the most popular types of pulse crops worldwide. It belongs to family Leguminosae (Fabaceae) with chromosome no. 2n= 14. It is the third most important pulse crop at global level, after common bean and chickpea and third most popular Rabi pulse of India after chickpea and lentil"[17,18,19].

"India occupy fourth position in area (10.53 %) and 5th position in production (6.96 %)" (**FAO Stat., 2021**). "In India field pea is grown over an area of 7.45 lakh ha with a production of about 9. 10 lakh tonnes during period" (**Anonymous, 2021**). "Uttar Pradesh is the major field pea growing state. It alone produces about (46%) of pea produced in India. Besides, Uttar Pradesh, Madhya Pradesh, Jharkhand and Assam are the major pea producing states" (**Anonymous, 2021**).

"Pea is a rich source of protein, amino acids and carbohydrates. Peas are used alone and mixed with other vegetables. Pea is of Mediterranean origin, the Near East and Ethiopia are considered as its secondary center of origin" (**Blixt 1970**). "Peas are mainly utilized as a pulse and vegetables. Peas are much valued in rotations with cereals because their cultivation breaks cereal disease cycles, facilitates weed control and improves soil condition and fertility" (**Chittaranjan, 2007**).

Fieldpea has highest genetic yielding potential but due to various climatic factors the overall production is not better therefore it is necessary to identify such genotypes that are able to provide maximum yield under various ecological conditions. For above mentioned problems it is desirable to evaluate genetic variability in the existing genotypes because genetic variability is a prerequisite for any breeding programme. Heritability estimates provide the information about transmissibility of the characters from parents to their offspring that enabled us to select elite genotypes from the mixed parental population, while estimation of genetic advance help in understanding the type of gene action involved in the expression of various quantitative traits. Taking a lot of such type of problems in consideration, the investigation carried out with the aim to estimate genetic variability, heritability and genetic advance in Fieldpea for different quantitative traits.

Material and methods

The experiment under present investigation was conducted during Rabi 2022-23 at experimental field of, Department of Genetics and Plant Breeding, Faculty of Agriculture, Kamla Nehru Institute of Physical and Social Sciences Sultanpur 228118 (U.P.) India. The collections of 22 germplasm comprising indigenous genotypes, constituted the experimental materials for the study. The genotypes were obtained from the pulse section, Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, 224229 (U.P.) India. Five plants from each plot were randomly selected for recording of observations on nine characters. Averages of the data from selected plants of each plot in respect of different characters were used for various statistical analyses. The data were recorded for the following characters.

Fig 1: Experimental field work

Days to 50% flowering, days to maturity, number of branches per plant, plant height (cm), number of pods per plant, 100-grain weight (g), biological yield per plant (g), grain yield per plant (g) and harvest index (%)

Statistical Analysis:

Replication wise mean data of 22 genotypes for 9 characters was used for statistical and biometrical analysis for the following parameters.

- Analysis of variance for Replicated Block Design was done as per the formula given by **Panse and Sukhatme (1961).**
- Estimation of variability as per suggested by **Burton and De vane (1953).**
- Heritability was estimated as suggested by **Hanson *et al.* (1956).**
- Genetic advance was suggested by **Johnson *et al.* (1955).**

Result and discussion

The analysis of variance for the design of experiment involved 22 field pea genotypes including four checks with three replications for the nine characters in Randomized Block Design. The mean squares resulting from replications, treatments, and error for all characters are shown in (**Table-1**).The variation due to treatments were found to be highly significant for all the characters, whereas, the variation due to replications were found non-significant for all characters. **Jaiswal *et al.*, 2015** also reported highly significant variation in Fieldpea for the studied characters.

Table 1: Analysis of variance of randomized block design for different characters in Fieldpea genotypes

Source of varianc	**Degree of freedom**	**Days of 50% flowering**	**Days to maturity**	**Plant height (cm)**	**Pods / plant**	**branches / plant**	**100-Seed weight (g)**	**Biological yield / plant (g)**	**grain Yield /plant (g)**	**Harvest index (%)**
Treatments	21	48.245	26.7193	2033.83	51.120	0.59976	22.7272	139.34	59.023	124.697
Replication	2	5.015	1.4091	65.83	129.523	2.10335	**0.**4482	576.35	95.083	18.883
ERROR	42	2.888	**4.**0916	18.75	44.058	0.44715	1.9033	77.64	21.264	52.513

Table-2: Range, mean, GCV, PCV, heritability and genetic advance estimates for different character in Fieldpea

Characters	Range (Min-Max)	Mean Value	Coefficient of variation (%)		Heritability in broad sense	Genetic advance	Genetic advance in percent of mean (5%)
			PCV (%)	GCV (%)			
Days to 50% flowering	57-77	67.15	6.32	5.79	83.96	7.3395	10.93
Days to maturity	80-94	85.14	4.01	3.23	64.83	4.5553	5.35
Plant height (cm)	60-190	81.15	32.38	31.94	97.28	0.9728	64.89
Number of branches/ plant	1.66-5.6	3.16	22.34	7.14	10.22	0.1486	4.70
Number of pods/ plant	14.20-43.8	23.81	28.61	6.44	05.07	0.7118	2.99
100-seed weight (g)	11.50-24.9	19.02	15.64	13.85	78.48	4.8080	25.28
Grain yield/plant (g)	10-33.33	17.72	32.83	20.02	37.18	4.4565	25.15
Biological yield/plant^{-1}(g)	18.80-61.5	34.65	28.59	13.09	20.94	4.2752	12.33
Harvest index (%)	32.73-88.33	52.15	16.78	9.41	31.42	5.6643	10.86

The estimates of GCV, PCV, heritability and genetic advance are presented in **Table 2**. Genotypic coefficient of variation (GCV) estimates the actual amount of genetic variability present in a material while; phenotypic coefficient of variation (PCV) estimates the amount of genotypic and environmental variability present in the material. Heritability measures how much of this genotypic diversity is passed down from parents to next generation. Broad Sense Heritability was given by **Lush (1949)**. Our ability to utilize genotypic variability in breeding programs is determined by this factor. Gene frequency influence genotypic variance and its components. Due to varying gene frequencies between population estimates of heritability also varies between populations for a given character.

For every character under investigation, the phenotypic, genotypic, and environmental coefficients of variation were noted as well. For every characteristic, it was often observed that the phenotypic coefficient of variation was higher than the genotypic coefficient of variation, showing that the environment had an impact on the traits. **Bashir *et al.*, 2017** and **Meena *et al.*, 2017** also reported that “relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study”. The highest value of Phenotypic Coefficient of Variation was observed in seed yield per plant followed by plant height, pods per plant, biological yield per plant, no. of branches per plant moderate value was observed for no. of branches per plant, harvest index, 100 seed weight, days to 50 % flowering while lowest value are recorded for days to maturity. The highest value of Genotypic coefficient of variation was observed in plant height followed by grain yield per plant, 100 seed weight and biological yield per plant moderate values were observed for harvest index, seeds per pods, branches per plant while lowest values was observed for days to 50% flowering and days to maturity. Findings are in accordance with earlier workers **Verma *et al.*, 2023** and **Jaiswal *et al.*, 2015**.

Highest estimates of broad sense heritability (h^2b) was recorder for plant height (97.28%), days to 50 % flowering (83.96 %), 100 grain-weight (78.48 %), days to maturity (64.83 %), grain yield per plant (37.18 %), harvest index (31.42%), biological yield per plant(20.94%), number of branches per plant (10.22) and number of per plant (05.07 %) heritability in broad sense, respectively. Similar findings were reported earlier by **Kumar *et al*., 2001, Sultana *et al*., 2003, Sirohi *et al*. 2006, Jaiswal *et al*., 2015, Verma *et al*., 2023.**

“Individual genotype selection does not provide any indication of how much genetic change will occur based on heritability alone. As a result, understanding genetic development and heritability is critical. Genetic progress is an improvement over the base population in the mean of selected families” (**Lush 1949** and **Johnson *et al*. 1955**). It can also be expressed as a shift in gene frequency towards the superior side as a result of selection pressure. The genetic advance in per cent of mean varied from 0.1486-7.3395 for no. of branches per plant and days to 50 % flowering respectively. Highest genetic advance (Ga) was found for days to 50 % flowering (7.3395) followed by for harvest index (5.6643), 100-grain weight (4.8080), days to maturity (4.553), grain yield per plant (4.4565), biological yield per plant (4.2752), number of branches per plant (0.1486) and no. of pod per plant (0. 7118). Similar findings were reported earlier by **Sultana *et al*., 2003, Jaiswal *et al*., 2015, Verma *et al*., 2023.**

Conclusion

Thus, from the above discussion it can be concluded that the characters such as plant height, days to 50% flowering, 100-grain weight etc that showed high value of GCV, heritability as well as genetic advance may be exploited as direct selection parameters for further improvement in grain yield in Fieldpea breeding.

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