

Studies On Genetic Variability and Relationship Among Yield Contributing Traits in Field Pea (*Pisum sativum* L.)

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Abstracts: This study was conducted at the Pulses Research Institute (PRI), Ayub Agricultural Research Institute (AARI), Faisalabad, during the Rabi season of 2020-21. The experiment included populations derived from two crosses: DP-11 × DP-09 (Cross-1) and DP-07 × DP-03 (Cross-2), namely P1 (parent-1), P2 (parent-2), F1, F2, Bc1P1 (Backcross-1), and Bc1P2 (Backcross-2) in a randomized block design with three replications. The objectives were to assess genetic variability, heritability, and genetic advances for various agronomic traits including days to first flowering, days to maturity, plant height, total number of clusters per plant, total number of branches per plant, total pods per cluster, total number of pods per plant, pod length, hundred seed weight, and total seed yield per plant. Analysis of variance (ANOVA) indicated significant genetic variation for seed yield and its related attributes, supporting subsequent biometrical analyses. Phenotypic coefficients of variation exceeded genotypic coefficients for all traits studied, indicating substantial environmental influence on trait expression. Traits such as plant height, total number of clusters per plant, total pods per plant, and total seed yield per plant exhibited high heritability and genetic advance as a percentage of the F1 mean, suggesting these traits are amenable to direct selection for yield improvement within the studied populations. In conclusion, this research underscores the potential for genetic improvement in pulse crops through targeted selection based on the identified traits.

Keywords: Pea, Yield Improvement, Cross-Breeding, Agronomic Traits

1. INTRODUCTION

Dry pea is a valuable source of vegetable protein, containing 21-27% protein, which is essential for human nutrition as the building blocks of our body (Parveen, Jamil, Pasha, & Ahmad, 2022). Proteins constitute about 20% of our body weight and are primarily derived from dietary foods (Nasir, Zaidi, Tabassum, & Asfaq, 2024). Pulses are considered the most economical source of protein, yet their availability has significantly declined. Dry pea plants possess a nodule system that fixes atmospheric nitrogen into the soil, enriching it for subsequent crops (Hossain et al., 2022). This characteristic makes peas particularly important for crop rotation, as noted by (Siddika, Islam, Rasul, Mian, & Ahmed, 2013). Among pulse crops, field pea or dry pea (*Pisum sativum* L.) belongs to the family Leguminosae and is believed to have originated in Ethiopia, the Mediterranean region, and Central Asia (Warkentin et al., 2015). It is a nutritious, protein-rich crop used for both green and dry seeds, and is categorized into vegetable-type and field pea (Parveen et al., 2022).

In Pakistan, field pea covers approximately 46.5 thousand hectares with an average yield of 662 kg ha⁻¹ (Anonymous, 2014-15). To meet the increasing demand for pulses, it is crucial to boost their production. Field pea

has high production potential under optimal agronomic management. It thrives in low soil pH conditions and requires only one or two irrigations, indicating significant scope for expansion (Kaur et al., 2018). Additionally, this crop is relatively resistant to pests and diseases, with the exception of powdery mildew, for which genetic resistance is available (T. Khan et al., 2013). Enhancing field pea production through improved agronomic practices and crop management can play a vital role in addressing the protein needs of the population while supporting sustainable agricultural practices (Powers & Thavarajah, 2019). There is an urgent need to provide farmers with varieties that yield well even under average agronomic management. Dwarf types, in particular, show greater potential with just one or two irrigations (Sharma & Khan, 1996). Therefore, it is necessary to combine desirable genes from both tall and dwarf types to develop high-yielding, disease-resistant, and widely adapted varieties. Achieving this goal requires information on genetic variability, heritability, and genetic advances in yield and its attributing traits.

The present study aims to generate essential data on genetic improvement in seed yield. Understanding genetic variability, heritability, and genetic advance of traits under improvement is a prerequisite for launching any breeding program (Janaki, Naidu, Ramana, & Rao, 2015). Genetic improvement in relation to grain yield and harvest index is a major objective for this crop. However, yield is a complex trait influenced by several morphological and physiological characteristics. Therefore, knowledge about the genetic control of yield and its contributing traits is crucial for initiating an efficient selection scheme to identify superior genotypes. Moreover, studying genetic variability, heritability, and genetic advance provides valuable estimates for designing effective and efficient breeding programs. In light of these considerations, the present study was conducted to estimate the extent of genetic variability, heritability, and genetic advance created through hybridization for seed yield and its component traits.

MATERIALS AND METHODS

The trial was conducted at the Pulses Research Institute, Ayub Agricultural Research Institute (AARI), Faisalabad, during the Rabi season of 2020-21. The experiment involved P1, P2, F1, F2, Bc1P1 (Backcross-1), and Bc1P2 (Backcross-2) populations from two crosses: DP-11 × DP-09 (Cross-1) and DP-07 × DP-03 (Cross-2). It was arranged in a randomized block design with three replicates. The aim was to assess genetic variability, heritability, and genetic advance for traits such as days to first flowering, number of branches per plant, number of clusters per plant, days to maturity, plant height, pods per cluster, pods per plant, pod length, hundred seed weight, and total seed yield per plant, using the models suggested by Mather (1949) and Hayman (1958). Each genotype was sown in a plot measuring 4.0m × 1.2m, consisting of four rows. The row-to-row and plant-to-plant distances were 30 cm and 15 cm, respectively. Five plants were randomly selected from P1, P2, F1, Bc1P1, and Bc1P2 populations, while 40 plants were selected from the F2 population to record observations on the aforementioned traits. Data on days to 50% flowering and days to maturity were recorded on a plot basis. The crop was grown following recommended practices. Analysis of variance (ANOVA) was conducted using the procedure outlined by Panse and Sukhatme (1985). Genotypic and phenotypic coefficients of variation were estimated according to Burton and Devane (1953) using the following formulae.

$$PCV = \sqrt{\sigma^2 p / X} * 100, \quad GCV = \sqrt{\sigma^2 g / X} * 100$$

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

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

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

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

\bar{X} = General mean

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

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

Heritability in broad sense was worked out as per the formulae suggested by Allard (1960).

$$h^2(b) = \frac{V_G}{V_G + V_E} = \frac{V_G}{V_P} \times 100$$

The heritability was categorized by Johnson *et al.* (1955).

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

The genetic advance as % over mean was categorized as worked out by Johnson *et al.*, (1955).

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

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

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

Analysis of variance (ANOVA) was worked out separately for crosses and characters (Table 1). Heritability in narrow sense and genetically advanced over mean estimated as percentage of mean for all the characters and cross wise. The cross-wise result is presented in (Table 2).

RESULTS AND DISCUSSION

The mean sum of square due to treatments (different generations) were high significantly for all the characters except total number of branches per plant and hundred seed weight in cross-₁, and pod length and total number of pods per cluster in cross-₂. F₁ means as compare to their parental values varied from cross to cross and character to character. Similarly, F₂ means also deviated from F₁ means. In general, backcrosses gave superior performance as compare to their parents for total seed yield and other important attributes to total seed yield.

cross-1(c-1)

(M. M. H. Khan, Rafii, Ramlee, Jusoh, & Al Mamun, 2021) confirmed the same results that seven characters e.g. total number of days to flowering, total number of days to maturity, plant height, total number of clusters per plant, total number of pods per plant, hundred seed weight and total seed yield per plant expressed high heritability, while total number of branches per plant, total number of pods per cluster and pod length expressed moderate heritability in current study.

Genetic Advance (GA) as percentage of mean was found to be the highest for total number of pods per plant, followed by total seed yield per plant, plant height, and total number of clusters per plant. It was low for total pods per cluster, hundred seed weight, Pod length, total number of branches per plant, total days to first flowering and total number of days to maturity.

cross-2(c-2)

(RAHMAN, 2017) confirmed the same results as conducted in this institute that seven characters e.g. total days to flowering, total days to maturity, plant height, total number of clusters per plant, total number of pods per plant, hundred seed weight and total seed yield per plant expressed high heritability. However, total number of branches per plant, total pods per cluster and pod length showed moderate to low heritability. Genetics advance (GA) as % age of mean was found to be the high for plant height followed by total number of clusters per plant, total number of pods per plant, total seed yield per plant, while it was moderate to low for hundred seed/grains weight, total number of pods per cluster, total number of days to first flowering, total number of branches per plant, total days to maturity and pod length.

Valuable genetic information has been an indispensable indicator for modifying the vast array of gene frequencies to enable genetic enrichment in a genotype (Xu et al., 2017). The presence of genetic variability is essential and pre-requisite for an effective improvement in a crop species. Besides, genetically variability, heritability which measures the relationship between phenotypic and genotypic appearance is another important consideration for the success of a breeding program. It is clear that the selection is usually based on phenotypic observations and success would depend upon the relationship between phenotype and genotype. The estimates of heritable are useful in indication 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 proper selection scheme for maximum genetic information. This information can also be used for locating the most important yield components.

The purpose of the present study was to obtain the basic information which can throw light on the strategies to be used for genetics improvement of field pea. The present study was therefore, undertaken to ascertain the basic information regarding the genetic variability, heritability and genetic advance for grain yield and yield related components in field pea. In this regard, the findings achieved from the present study and their practical utility in genetic improvement of this crop is explained here. Three parents used in the present study differing in origin showed sufficient variability for the characters under study (Table 3). The treatments consisting six(6) generations showed significant differences for all the traits in both the crosses except for total number of branches per plant, hundred seed weight in cross-1, total number of pods per cluster and pod length in cross-2. 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 (Ahmad et al., 2022).

Heritability in 'narrow sense'(h²_{ns}) is the ratio of additive genetic variance to the total phenotypic variance and measures the portion of the total variation, which can be used 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 F₂, plant will resemble their parents (Allard, 1999). The broad sense heritability, the components of genotypic variation to the phenotypic variance is an important parameter in breeding and genetics, because knowledge of numerical limit of heritability is of special importance for planning and execution in breeding programmes and for the examination of trial results (Pallavi, Singh, & Pandey, 2013).

Heritability estimates are affected by methods of estimation, generation under study, sample size and the environmental factors. Heritability estimates remain extremely useful in the study of the inheritance of quantitative

traits. The emphasis is more on evaluation of selection procedure through computation of expected progress. The magnitude of genetic advance is influenced by unit of measurement. Genetic advance was calculated as % gain over the F_2 mean. Estimates of heritable were grouped in to three (3) categories high (>170 %), medium (50-70 %) and low (<50%); depending on magnitude as per Robinson (1966). In the present study high heritability coupled with high genetic advance as percent of mean was found for plant height. Total number of clusters per plant, total number of pods per plant and total seed yield per plant, in accordance to these findings (Yadav, 1989) also reported high heritability coupled with high genetic advance for these characters. High heritability associated with low genetic gain was recorded for hundred seed weight. (Vaishnav, 2000) reported high heritability and moderate genetic gain for seed setting percent. In contrary to the present findings (Vaishnav, 2000) (Vavilov, 1951) 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 program.

Table.1 Analysis of variance for yield and its attributes in field pea (*Pisum sativum* L.)

Source of variation	df	First flower (days)	No of branches Plant-1	Maturity (days)	Plant height (cm)	No of clusters plant-1	Number of pods per plant -1	Pod length (cm)	Pods cluster-1	100 seed weight (g)	Seed yield plant-1 (g)
Cross-1: DP-11x DP-09											
Replications	2	0.0273	0.1088	0.4275	1.8430	0.4066	0.6571	0.0720	0.016	0.1203	0.1668
Treatment	5	1.656**	0.1522	2.7275*	1100.973**	6.306**	62.40**	0.1218*	0.386*	2.792	18.865**
Error	10	0.2664	0.0755	0.2375	0.554	0.0633	0.745	0.0405	0.0103	0.1571	0.1526
Cross-2: DP-07 x DP-03											
Replications	2	0.6914	0.2138	0.8806	0.115	0.06222	0.2672	0.0816	0.0172	0.4257	0.1433
Treatments	5	1.679**	0.3298*	4.3416**	1204.687**	5.2818**	24.945**	0.0836	0.0122	2.1602**	9.604**
Error	10	0.4011	0.1125	0.8166	0.8350	0.05256	0.9272	0.0869	0.0125	0.1424	0.1173

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

Table.2 Genetic parameters of variability for yield and its components in field pea (*Pisum sativum* L.)

parameters	Range		Coefficient of Variation	
	Minimum	Maximum	Genotypic	Phenotypic
First flower (days)	44.33	48.80	02.70	05.96
No of branches plant-1	02.33	04.55	01.50	16.35
Maturity (days)	129.0	155.0	00.35	00.91
Plant height (cm)	39.86	90.67	18.27	22.57
Clusters plant-1	04.60	06.32	00.69	15.88
Pods cluster-1	01.10	03.60	07.11	08.38
Number of pods plant-1	07.00	19.70	00.59	39.40
Pod length (cm)	03.30	07.90	03.88	05.78
100 seed weight (g)	11.40	25.06	05.96	06.23
Seed yield plant-1 (g)	03.50	11.33	09.60	24.31

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

characters	cross-1		cross-2	
	h2(ns)	GA%	h2(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
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

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Conflict of Interest

There were no conflicting interests disclosed by the authors regarding the publication of the current research work.

Data Availability

All data generated or analyzed during this study are included in this published article.

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