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Evaluation of genetic variability for yield and yield attributing traits in field pea (*Pisum sativum* L.) under diverse environmental conditions

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Abstract

The present investigation aimed to assess the extent of genetic variability, heritability and genetic advance for yield and its attributing traits in 70 field pea (*Pisum sativum* L. var. *arvense*) genotypes evaluated across four environments (E-I, E-II, E-III, and E-IV) and in pooled analysis at the Breeder Seed Production Unit (Soybean), Department of Genetics and Plant Breeding, College of Agriculture, JNKVV, Jabalpur (Madhya Pradesh). High estimates of both genotypic and phenotypic coefficients of variation (GCV and PCV) were recorded for number of pods per plant, number of effective nodes per plant, biological yield per plant and seed yield per plant across all environments and in pooled analysis. The close correspondence between GCV and PCV for these traits indicated that they are primarily governed by genetic factors with limited environmental influence. Moderate variability was observed for hundred seed weight, number of seeds per pod, pod length, and plant height, suggesting the influence of both genetic and environmental components. Broad-sense heritability estimates were generally high for most traits, signifying that a major portion of the total phenotypic variance was due to genetic factors. The hundred seed weight exhibited the highest heritability (98.55%) and substantial genetic advance (26.15%), followed by seed yield per plant, biological yield per plant, and number of pods per plant, which also displayed high heritability coupled with high genetic advance. This combination of high heritability and genetic advance indicated the predominance of additive gene effects and high transmissibility of these traits. Overall, seed yield per plant, biological yield per plant and pods per plant emerged as the most dependable selection indices for yield improvement and stability in field pea breeding across diverse environments.

Keywords: Field pea, germplasm lines, GCV, PCV, heritability, genetic advance, diverse environment

Introduction

Field pea (*Pisum sativum* L. var. *arvense*) is a self-pollinated, cool-season legume of substantial global significance, ranking third among pulse crops after dry bean and chickpea. In India, it occupies a prominent position among the rabi pulses, following chickpea and lentil in acreage and production. The crop is well adapted to temperate and high-altitude tropical environments, thriving in an optimum temperature range of 7°C to 30°C during its vegetative and reproductive phases (Sahoo, 2018) [22]. *Pisum sativum* is taxonomically classified under the family *Fabaceae*, subfamily *Papilionoideae*, and exhibits a diploid chromosome number of 2n = 14 (Anand *et al.*, 2024a) [2]. Its center of origin and diversity is traced to four primary regions—Central Asia, the Near East, Ethiopia, and the Mediterranean basin—making it one of the oldest domesticated legumes with rich genetic diversity (Vavilov, 1926; Smýkal *et al.*, 2014) [28, 32].

Two major cultivated types are recognized within *Pisum sativum*: the garden pea (*P. sativum* var. *hortense*), primarily consumed as a green vegetable, and the field pea (*P. sativum* var. *arvense*), which is harvested at physiological maturity for dry grain utilization. Field pea serves as an important component in cereal-based cropping systems owing to its high nutritional value and ecological benefits. It is a rich source of plant-based protein (18-30%), particularly lysine, along with carbohydrates (56.5%), dietary fiber, and essential vitamins such as thiamine (B1) and pantothenic acid (B5) (Gautam *et al.*, 2017; Sahoo, 2018) [8, 22]. Apart from its use as human food, field pea also contributes to agricultural sustainability through its multifaceted roles as animal fodder, green manure, and a nitrogen-fixing legume that enhances soil fertility and reduces dependence on synthetic fertilizers (Anand *et al*., 2024a) [3].

Globally, pea cultivation covered 7.19 million hectares during 2020-21, producing approximately 14.64 million tonnes with an average yield of 2,036 kg ha^{-1}. In India, peas were cultivated over an area of 617,000 hectares, producing 797,000 tonnes at an average productivity of 1,292 kg ha^{-1}. Madhya Pradesh, one of the major pea-producing states, accounted for 101,000 hectares with a production of 123,000 tonnes and a mean productivity of 1,217 kg ha^{-1} (Anonymous, 2021; Anonymous, 2022) [4, 5]. Despite its nutritional and economic relevance, the productivity of field pea in India remains substantially lower than the global average. This yield gap is primarily attributed to a narrow genetic base, inadequate availability of high-yielding and disease-resistant cultivars, susceptibility to terminal heat stress during the reproductive phase, and poor seed quality. Additionally, the predominance of rainfed cultivation and limited varietal diversity constrain genetic improvement efforts (Gautam *et al*., 2017; Shukla, 2015) [8, 24].

Enhancing the yield potential and stability of field pea necessitates the identification and utilization of genetically diverse and agronomically superior genotypes. Genetic variability forms the cornerstone of any successful crop improvement program, as it provides the foundation for selection and hybridization. The estimation of key genetic parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability (in the broad sense), and genetic advance is crucial for understanding the extent and nature of genetic control governing quantitative traits. These parameters collectively enable breeders to predict the effectiveness of selection and to devise efficient breeding strategies for yield improvement (Singh *et al*., 2014; Sahoo, 2018) [22, 26].

Given the influence of environmental factors on the expression of quantitative traits, multi-environment evaluation plays a pivotal role in identifying stable and adaptable genotypes. Understanding the magnitude of genetic variability and heritability across diverse environmental conditions helps delineate the relative contribution of genotypic and environmental components to phenotypic performance. Such insights facilitate the identification of traits with greater additive genetic control, which can be effectively exploited through selection.

In this context, the present investigation was undertaken to assess the extent of genetic variability, heritability, and genetic advance for yield and its contributing traits in a diverse set of field pea genotypes evaluated under multiple environments. The findings are expected to provide valuable insights for breeders in selecting promising genotypes and developing ideotypes suited for diverse agro-climatic regions of India, thereby contributing to the genetic improvement and productivity enhancement of field pea.

Material and Methods

The present investigation was carried out at the Breeder Seed Production Unit (Soybean), Department of Genetics and Plant Breeding, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur (Madhya Pradesh). The experimental material comprised 70 field pea (*Pisum sativum* L. var. *arvense*) genotypes, including three check varieties (JP-885, IPF-99-25, and IPFD-12-2), obtained from the Field Pea Improvement Project, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (M.P.).

The genotypes were evaluated across four environments: Rabi 2020-21 (EI and EII) and Rabi 2021-22 (EIII and EIV), representing variations in seasonal conditions. The experimental site is characterized by medium black soils with uniform topography, good drainage, and no waterlogging issues, ensuring favorable conditions for field pea growth. Uniform recommended agronomic and plant protection practices were followed in all environments to minimize experimental error and maintain crop health.

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications to ensure the reliability of results and accurate estimation of genetic parameters. Each genotype was sown in a single row of standard length, maintaining uniform spacing between and within rows as per the crop's recommended geometry.

Observations were recorded on twelve agro-morphological traits, namely: days to 50% flowering, days to maturity, plant height (cm), number of nodes per plant, number of effective nodes per plant, number of pods per plant, pod length (cm), number of seeds per pod, hundred seed weight (g), biological yield per plant (g), harvest index (%), and seed yield per plant (g). These traits were selected based on their direct or indirect contribution to yield potential and adaptability under varying environments.

To quantify the extent of variability among genotypes, key genetic parameters were estimated. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed following the method of Burton (1952) [7], while the partitioning of variance components was carried out as per Burton and De Vane (1953) [7]. The broad-sense heritability (H^2) was estimated according to the formula proposed by Hanson *et al*. (1956) [11]. The expected genetic advance (GA) and genetic advance as a percentage of mean (GAM) were calculated following Johnson *et al*. (1955) [13].

These genetic parameters were employed to assess the magnitude of genetic variability, the heritable fraction of total variability, and the potential response to selection. The combined interpretation of GCV, PCV, heritability, and genetic advance provided insights into the nature of gene action governing various traits and facilitated the identification of traits with the highest breeding potential for yield improvement in field pea.

Results and Discussion

Genotypic and Phenotypic Coefficient of Variation

This study identified substantial genetic variability among 70 field pea (*Pisum sativum* L. var. *arvense*) genotypes evaluated across four environments (E-I, E-II, E-III, and E-IV) and in pooled analysis. The phenotypic coefficient of variation (PCV) consistently exceeded the genotypic coefficient of variation (GCV) for all traits, indicating environmental influence on phenotypic expression. However, the narrow differences between PCV and GCV for most traits suggest that environmental effects were limited and that the observed variability was primarily genetic, making these traits suitable for selection.

High estimates of both GCV and PCV were recorded for the number of pods, nodes, and effective nodes per plant, as well as for biological and seed yield per plant, across all environments and in pooled data. The close correspondence between GCV and PCV for these characters suggests minimal environmental interference and a predominance of genetic control. Such findings align with Tiwari and Lavanya (2012) [29], who emphasized the high genetic variability of seed yield per plant, days to 50% flowering, and plant height. These results highlight the potential of these traits as effective selection indices for yield improvement.

Moderate variability was recorded for hundred seed weight, number of seeds per pod, pod length, and plant height, suggesting that these traits are influenced by both genetic and environmental factors. Similar findings were reported by Ahmad *et al*. (2014) [1], and Pallavi *et al*. (2013) [19], who documented moderate-to-high GCV and PCV for seed yield and component traits, including pods per plant and 100-seed weight.

Traits associated with crop phenology *i.e.* days to 50% flowering, days to maturity, and harvest index (HI)—displayed relatively low variability across environments. These results indicate a narrow genetic base for phenological attributes and limited opportunities for improvement through simple selection, consistent with the findings of Saxena *et al*. (2014) [23]. In a few cases, however, moderate variation in flowering and HI was observed, echoing the reports of Kannoj (2016) [14], who also noted partial environmental influence on such traits.

The trend of slightly higher PCV than GCV, observed in this study, is well-documented in legumes (Prasad *et al*. (2018) [21] and Singh *et al*. (2019) [27]. This pattern signifies that, although environmental effects contribute to the expression of quantitative traits, their overall impact remains limited, thus preserving the reliability of genetic selection. Comparable observations were made by Tolessa *et al*. (2017) [31] and Barcchiya *et al*. (2018) [6] who reported high variability for plant height, pods per plant, and seed yield per plant, affirming the presence of considerable exploitable genetic variation.

Several other studies, including those by Prasad *et al*. (2019) [21], and Meena *et al*. (2017) [18], also documented wide genetic diversity for pods per plant, seed yield, biological yield, and seed weight, confirming that yield-associated traits in field pea exhibit extensive variability and should be prioritized in breeding programs.

Overall, the results demonstrate that yield-contributing traits, such as pods per plant, nodes per plant, biological yield, and seed yield per plant, are predominantly governed by additive genetic effects with high variability, suggesting their suitability for direct selection. Conversely, traits such as pod length, seed weight, and seeds per pod, showing moderate variability, may require complementary breeding approaches, while phenological traits with low variability might benefit from hybridization or molecular introgression to broaden their genetic base.

Heritability and Genetic Advance as Percentage of Mean (GAM)

Heritability represents the proportion of total phenotypic variance attributable to genetic causes and provides an estimate of the potential effectiveness of selection. In the present study, broad-sense heritability estimates were generally high (>70%) for most traits across individual environments and in pooled analysis, underscoring the predominance of genetic factors in trait expression and suggesting that selection would be reliable across environments.

Among the evaluated traits, hundred-seed weight exhibited the highest heritability (92.86-97.15% across environments and 98.55% in pooled data), followed by plant height, seed yield per plant, biological yield per plant, and number of pods per plant. These results suggest that these traits are under strong genetic control and can be efficiently improved through direct phenotypic selection.

Although traits such as pod length, harvest index, and number of seeds per pod also exhibited high heritability, their estimates were slightly lower (e.g., 67.04% for pod length in pooled analysis). This suggests that environmental factors contribute more to their expression compared to other yield traits.

Similar findings have been reported by Kumar *et al*. (2013) [16], Saxena *et al*. (2014) [23], and Gupta *et al*. (2018) [10], who also documented high heritability for plant height, pods per plant, and seed yield per plant in pea, indicating the predominance of additive genetic variance. Similarly, Tiwari and Lavanya (2012) [30] observed high heritability for seed yield per plant and days to 50% flowering in field pea. Barcchiya *et al*. (2018) [6] also noted moderate to high heritability but substantial environmental influence for pod length and seed number.

The estimates of genetic advance as a percentage of mean (GAM) showed a strong positive association with heritability, especially for yield-contributing traits. High GAM values were recorded for plant height, seed yield per plant, biological yield per plant, number of pods per plant, number of nodes per plant, number of effective nodes per plant, and hundred seed weight across environments, ranging from 26.15% (HSW, pooled) to 60.30% (plant height, EI). High heritability coupled with high GAM indicates the predominance of additive gene action, suggesting that simple selection methods would be effective for genetic improvement.

These findings align with those of Jeberson *et al*. (2016) [12], Khan *et al*. (2017) [15], Singh *et al*. (2017) [25], and Sahoo (2018) [22], who similarly reported high GAM for plant height, pods per plant, seeds per plant, and 100-seed weight, thereby demonstrating the reliability of direct selection in pea improvement. Lal *et al*. (2019) [17] and Gupta *et al*. (2018) [10] further confirmed high GAM for pods per plant, seed yield per plant, and HSW, highlighting substantial additive genetic variance.

In contrast, days to 50% flowering, days to maturity, and pod length exhibited high heritability but moderate GAM values (10-14%), indicating a preponderance of non-additive gene effects or strong environmental modulation. Similarly Pathak *et al*. (2019) [20], Tiwari and Lavanya (2012) [30], and Saxena *et al*. (2014) [23] suggest that while these traits are genetically controlled, the expected response to direct selection is comparatively limited.

The combination of high heritability and high GAM observed for seed yield per plant, biological yield per plant, pods per plant, and hundred seed weight collectively demonstrates the predominance of additive gene effects and high transmissibility of these traits, making them ideal targets for direct selection. On the other hand, phenological and efficiency traits such as flowering, maturity, and harvest index—though heritable—showed moderate GAM, implying the involvement of non-additive gene effects. For these, selection may be less effective, and approaches such as heterosis breeding, recurrent selection, or marker-assisted introgression could be more advantageous.

Table 1: Genetic parameters of variability for yield and its component traits in Niger genotypes under EI, EII, EIII, EIV and Pooled Analysis

Characters	Environment	Grand Mean	Range		Coefficient of Variation		h^2 (bs)	GAM at 5%
			Min	Max	GCV (%)	PCV (%)		
DFF	E I	55.83	31.00	69.33	13.69	13.72	85.33	28.12
	E II	59.47	36.00	73.00	13.44	13.47	87.56	27.62
	EIII	56.79	30.00	71.00	13.26	13.33	84.21	27.20
	EIV	62.60	37.33	76.33	11.95	12.01	87.12	24.51
	Pooled	58.67	45.67	68.25	7.28	8.05	78.98	13.57
DM	E I	86.07	57.00	100.00	8.90	8.92	82.56	18.28
	E II	91.49	64.33	102.00	7.69	7.72	87.30	15.78
	EIII	86.10	58.33	101.00	9.20	9.22	85.56	18.89
	EIV	94.83	64.33	106.33	7.36	7.38	79.38	15.10
	Pooled	89.62	77.75	100.58	5.61	6.00	79.77	10.81
PH	E I	82.00	32.44	134.89	29.28	29.29	84.91	60.30
	E II	75.30	28.33	121.28	27.09	27.14	80.74	55.71
	EIII	83.37	34.94	133.72	28.57	28.58	86.91	58.83
	EIV	81.96	33.19	130.27	28.16	28.20	87.74	57.93
	Pooled	80.66	51.58	112.75	15.74	17.16	73.10	29.76
NNPP	E I	51.72	8.96	138.67	48.78	48.79	76.91	36.45
	E II	46.21	6.02	103.12	50.30	50.35	73.82	33.54
	EIII	52.61	10.27	140.93	48.03	48.06	80.91	38.89
	EIV	47.10	9.72	118.63	48.73	48.76	81.91	40.31
	Pooled	49.41	19.03	84.83	28.82	30.99	78.12	35.22
NENPP	E I	14.32	7.19	36.00	43.97	44.07	81.56	41.35
	E II	11.83	4.48	31.73	49.02	49.34	86.86	45.33
	EIII	14.99	7.40	36.17	42.23	42.49	76.94	36.45
	EIV	10.55	5.93	30.55	38.63	39.00	82.33	42.81
	Pooled	12.92	8.31	24.20	28.71	30.62	72.35	34.46
NPPP	E I	18.09	4.67	54.46	64.35	64.41	82.82	32.42
	E II	15.77	4.04	47.85	68.37	68.47	87.74	40.63
	EIII	18.12	4.67	54.46	64.70	64.87	87.56	32.94
	EIV	14.08	5.17	42.11	61.20	61.46	87.30	25.54
	Pooled	16.51	5.73	34.14	42.68	45.04	79.02	23.31
PL	E I	5.40	3.45	7.45	14.25	15.09	78.50	27.72
	E II	4.84	3.45	6.72	14.66	15.42	79.55	28.72
	EIII	4.89	3.07	6.56	15.63	16.68	73.26	30.16
	EIV	4.65	2.21	6.14	13.79	15.08	72.57	25.97
	Pooled	4.95	3.64	6.54	9.77	10.73	67.04	18.34
NSPP	E I	5.06	3.51	9.43	17.88	18.38	83.25	35.82
	E II	4.68	3.08	8.51	20.15	20.82	82.46	40.18
	EIII	4.99	3.68	8.43	14.02	15.50	76.98	26.13
	EIV	4.09	2.55	7.43	17.85	18.96	77.97	34.61
	Pooled	4.71	3.46	5.67	11.31	12.51	80.90	21.06
HSW	E I	14.98	10.42	26.42	19.00	19.12	92.86	38.88
	E II	13.24	9.39	22.58	19.63	19.82	96.33	40.05
	EIII	15.30	11.41	25.59	18.65	18.81	94.50	38.09
	EIV	13.62	9.93	22.55	17.57	17.77	97.15	35.81
	Pooled	14.28	10.93	21.01	13.35	14.04	98.55	26.15
BYPP	E I	28.93	6.60	71.27	54.57	54.59	80.91	32.36
	E II	26.27	5.74	65.52	56.95	57.01	83.82	37.21
	EIII	28.59	7.75	73.01	52.34	52.44	81.65	35.62
	EIV	27.71	6.94	59.83	53.01	53.07	87.82	39.06
	Pooled	27.88	9.82	46.33	37.41	39.11	80.52	34.74
HI	E I	44.76	40.61	57.37	8.54	9.01	79.11	16.68
	E II	37.62	30.10	52.77	15.58	16.13	82.10	31.00
	EIII	45.13	40.24	57.78	8.72	9.43	75.24	16.61
	EIV	38.25	30.27	51.14	15.58	16.01	83.34	31.23
	Pooled	41.44	31.14	50.16	10.62	11.17	79.64	20.81
SYPP	E I	12.75	3.25	32.05	52.65	52.73	84.74	34.28
	E II	9.57	2.22	27.13	54.90	55.15	87.21	36.57
	EIII	12.60	4.07	30.22	48.61	48.70	78.65	32.95
	EIV	10.31	2.66	25.24	50.74	50.87	88.56	44.25
	Pooled	11.31	4.43	20.62	38.74	40.18	81.75	36.93

Classes of Heritability (%): High >70.0%, Medium 50.0 - 70.0%, Low <50.0%
Classes of GAM at 5%: High >20.0%, Medium 10.0-20.0%, Low <10.0% Where,
EI- *Rabi* 2020-21 (Early); EII -*Rabi* 2020-21 (Late), EIII- *Rabi* 2021-22 (Early); EIV - *Rabi 2021-22* (Late); Pooled analysis (EI, EII, EIII and EIV)
DFF- days to 50% flowering, DM- days to maturity, PH- plant height (cm), NNPP- number of nodes per plant, NENNP- number of effective nodes per plant, NPPP- number of pods per plant, PL- Pod Length (cm), NSPP- number of seeds per pod, HSW- Hundred seed weight (g), BYPP- biological yield per plant (g), HI- harvest index (%), SYPP- seed yield per plant (g)

Conclusion

The present investigation conducted across four environments revealed substantial genetic variability among 70 field pea genotypes, indicating wide potential for genetic improvement through selection. High estimates of GCV and PCV for yield-contributing traits such as pods per plant, biological yield per plant, and seed yield per plant across all environments and in pooled analysis reflected strong additive gene action with minimal environmental influence. Hundred seed weight consistently exhibited very high heritability and genetic advance, suggesting its stability and reliability across environments. Conversely, phenological traits showed comparatively lower variability and moderate genetic gain. Overall, seed yield, biological yield, and pods per plant emerged as the most dependable selection indices for yield-oriented breeding in field pea.

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