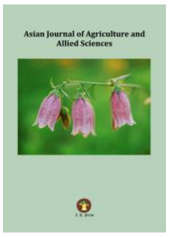

Asian Journal of Agriculture and Allied Sciences

Volume 8, Issue 1, Page 45-56, 2025; Article no.AJAAS.12674

Assessment of Genetic Variability and Performance of Field Pea (*Pisum sativum*) Advanced Genotypes Across Environments

Gebeyaw Achenef [a*], Temesgen Abo [a], Gizachew Yilma [a], Deressa Tesfaye [a], Nigat Tilahun [b], Kedir Yimam [a] and Alehegn Workie [c]

[a] *Ethiopian Institute of Agricultural Research, Kulumsa Research Centers, Ethiopia.*
[b] *Ethiopian Institute of Agricultural Research, Holeta Research Centers, Ethiopia.*
[c] *Ethiopian Institute of Agricultural Research, DebreMarkos Research Centers, Ethiopia.*

Authors' contributions

This work was carried out in collaboration among all authors. Author GA writing and editing the original draft of the final manuscript. Author GY wrote methodology, did the investigation and conceptualization. Author KY supervise, editing, did data collection, did data cleaning and inspection, did the data analysis. Author DT supervise data collection and did the validation. Author NT did the conceptualization, investigation, coordination and data cleaning. Author AW did the data collection and supervised the study. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.56557/ajaas/2025/v8i151

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://prh.ikprress.org/review-history/12674

Original Research Article

Received: 03/11/2024
Accepted: 07/01/2025
Published: 10/01/2025

**Corresponding author: E-mail: gebesday08@gmail.com;*

Cite as: *Achenef, Gebeyaw, Temesgen Abo, Gizachew Yilma, Deressa Tesfaye, Nigat Tilahun, Kedir Yimam, and Alehegn Workie. 2025. "Assessment of Genetic Variability and Performance of Field Pea (Pisum Sativum) Advanced Genotypes Across Environments". Asian Journal of Agriculture and Allied Sciences 8 (1):45-56. https://doi.org/10.56557/ajaas/2025/v8i151.*

ABSTRACT

Field peas (*Pisum sativum* L.) belong to the Leguminosae family. The crop provides valuable and accessible protein, complementing cereals and providing valuable food and feed to many poor people. The foundation of plant breeding lies in genetic variability, which is generated by the genetic differences among individuals within a population. This variability is essential for developing new crop varieties and improving traits. Therefore, this experiment was conducted at Bekoji and Debre Markos research sites. It consisted of 35 advanced field pea genotypes evaluated under rain fed conditions during the 2023 cropping season utilizing α-lattice design with two replications. The study aims to identify patterns of genetic variation through morpho-agronomic assessments, offering valuable insights for future breeding programs. The analyses of variance for all traits studied indicated significant differences ($P < 0.001$) between testing locations. The traits of grain yield and plant height showed significant differences at ($P < 0.01$). Most traits, except for days to flowering, including grain yield, number of pods per plant, number of seeds per pod, days to maturity, and ascochyta blight, did not show significant differences due to genotype × environment interaction. The study examined variability, heritability, genetic advance, and genetic advance as a percentage of the mean for all the characters under investigation. Selection based on highly heritable traits often leads to more successful outcomes. By using heritability along with other variability measures, we can predict gains under specific selection intensities, enhancing the effectiveness and sustainability of crop improvement. The number of pods per plant and seeds per pod also demonstrated moderate genetic advances, making them important selection criteria. In contrast, plant height exhibited low heritability (H^2b) values and a low genetic advance. The phenotypic coefficient of variation was generally higher than the genetic coefficient of variation for most of the traits, indicating substantial environmental influences on genetic expression. The findings also indicate that a narrow base population will not generate wide genetic variation for crop improvement. This lack of diversity can limit the potential for developing new varieties and enhancing desirable traits in plants, emphasizing the importance of a broader genetic base in breeding programs.

Keywords: Genetic advance; genotype; heritability; traits; variability.

1. INTRODUCTION

Field pea (*Pisum sativum* L.) is a member of the Leguminosae family, characterized by a chromosome number of 2n=14. In Ethiopia, field peas are predominantly cultivated in mid to high-altitude regions, specifically between 1800 and 3000 meters above sea level, where annual rainfall varies from 700 to 1000 mm. Ethiopia is recognized globally as the second most diverse region for field pea varieties. The crop is cultivated by small-scale farmers on marginal lands with limited management practices, especially when compared to cereals. They hold significant economic value for the livelihoods of farming communities in Ethiopia (Tolessa, 2017).

Field peas provide an important source of food and feed, offering valuable and affordable protein as a complement to cereals for many poor individuals, particularly those who cannot afford animal-based proteins. The dry seed of field pea is highly nutritious, with nutritional composition including protein content ranging from 19-27%, starch at 20-50%, sugars between 4-10%, fat from 0.6% to 1.5%, cellulose comprising 2-10%, minerals at 4%, and water content of 9-15% (Naveen, 2023; Gudadinni et al., 2017). Due to their essential role in promoting human and soil health, field peas are often grown alongside cereals, not only to support diverse food systems but also to maintain a balanced agricultural production system.

Genetic variability, derived from the genetic differences among individuals within a population, serves as the foundation of plant breeding. Effective management of this diversity can yield significant and lasting improvements in plant performance while providing resilience against seasonal variations (Sharma et al., 2017). Genetic variation is essential for any crop improvement program; it represents the initial step, unless variation is already present (Elings, 2000). The creation of genetic variation begins with the critical process of identifying and isolating parent materials that possess the desired traits for end users. Subsequently, the transfer of genes responsible for key characteristics from one parent to another occurs, followed by the cultivation of selected progeny. The effectiveness of this process is pivotal to the success of the breeding program. Moreover, contributors to the understanding of pea genetic variations in Ethiopia include the collection of germplasm, the introduction of exotic materials, and hybridization efforts. In summary, genetic variation is generated through the collection of landraces, introduction from exotic sources, and the hybridization of selected parent strains.

Advanced field pea genotypes were developed through the process of hybridization. A comprehensive understanding of the extent and patterns of genetic variation within these genotypes will provide valuable opportunities for selecting optimal parental materials in future pea breeding programs in Ethiopia. Genetic variability is a significant factor and serves as a prerequisite for crop improvement initiatives aimed at achieving high-yield progenies (Tiwari & Lavanya, 2012). Estimating genetic variability is essential for identifying the sources of specific traits within the existing germplasm. Moreover, heritable variances offer insights into the potential for enhancing the traits under investigation. Heritability represents the proportion of phenotypic variation that can be transmitted from parent to progeny.

A higher degree of heritable variation increases the likelihood of successfully fixing desired traits through selection methods (Vinod & Lila, 2013). Significant variability has been noted in various agronomic characteristics of peas, including plant height, days to flowering, pod length, and seed weight (Pallavi et al., 2013). However, the limited production of peas is largely attributed to the suboptimal productivity potentials of existing varieties. Thus, it is crucial to comprehend yield and its component attributes for the current advanced field pea genotypes to enhance the genetic potential in the future hybrid line development. Developing high-yielding and disease resistance/tolerance varieties of field pea is the major objectives of plant breeders to improve production and productivity for small scale farmers in Ethiopia. To meet this objective, we initiated this study to explore genetic variability and estimate genetic parameters of specific traits in pea, which could facilitate the selection of suitable genotypes useful as a parent material for field pea genetic improvement.

2. MATERIALS AND METHODS

2.1 Testing Site Descriptions

The experiment was conducted in 2023 at Bekoji and Debremarikos research sites during the main growing season. Bekoji is located at 39°14'46"E longitude and 07°31'22"N latitude, with an elevation of 2780 meters above sea level. It has an annual rainfall of 1020 mm and average minimum and maximum temperatures of 7.9°c and 16.6°c respectively. The trial site's soil type is clay soil with a good drainage system.

2.2 Treatments and Design

Thirty two elite breeding lines were selected after completed observation nursery at the national field pea breeding program developed through hybridization and three varieties were selected as standard checks [shiro-type (Bursa) and kik-type (Jeldu and Etetu)] field pea genotypes. At each site the experiment was carried out using 7 × 5 simple lattice design with two replications; each replication containing seven incomplete blocks and each incomplete block containing five genotypes. Each plot had four rows of 4 m length, with spacing of 20 cm between rows and 5 cm between plants. Each genotype was planted in a plot size of 1.8m^2 including space between plots. More information’s regarding to the genotypes descriptions given in Table 1.

2.3 Collected Data

Data were collected on both individual plants and a plot basis. For the individual plant observations, data were gathered from five randomly selected plants of each genotype across each replication. The recorded metrics included plant height (in centimeters), the number of pods per plant, and the number of seeds per pod, all of which were subsequently averaged.

On the plot basis, data collection encompassed grain yield, days to 50% flowering, days to 90% maturity, and the assessment of disease incidence, specifically for Ascochyta blight and powdery mildew. Disease severity was evaluated using a scale ranging from 1 to 9, where a rating of 1 indicates immunity or the absence of disease symptoms, and a rating of 9 indicates a high level of susceptibility.

Table 1. Descriptions of 35 field pea genotypes used in the experiment

Code	Genotype	Status	Code	Genotype	Status
G1	EH018009-1	Breeding lines	G18	EH018005-6	Breeding lines
G2	EH018009-3	Breeding lines	G19	EH018012-4	Breeding lines
G3	EH018002-1	Breeding lines	G20	EH018011-4	Breeding lines
G4	EH018009-6	Breeding lines	G21	EH018004-2	Breeding lines
G5	EH018008-6	Breeding lines	G22	EH018008-5	Breeding lines
G6	EH018012-2	Breeding lines	G23	EH018011-3	Breeding lines
G7	EH018007-1	Breeding lines	G24	EH018004-3	Breeding lines
G8	EH018001-3	Breeding lines	G25	EH018005-8	Breeding lines
G9	EH018001-6	Breeding lines	G26	JELDU	Variety (2019)
G10	EH018008-1	Breeding lines	G27	EH018006-1	Breeding lines
G11	EH018005-3	Breeding lines	G28	EH018014-2	Breeding lines
G12	EH018003-1	Breeding lines	G29	BURSA	Variety (2015)
G13	EH018006-4	Breeding lines	G30	EH018013-3	Breeding lines
G14	EH018014-3	Breeding lines	G31	EH018001-1	Breeding lines
G15	ETETU	Variety (2021)	G32	EH018005-1	Breeding lines
G16	EH018009-2	Breeding lines	G33	EH018003-2	Breeding lines
G17	EH018001-2	Breeding lines	G34	EH018010-2	Breeding lines
			G35	EH018004-1	Breeding lines

Note: *Numbers in parentheses indicated the year of the variety released*

2.4 Data Analyses

The above listed trait data were subjected to a separate and combined analysis of variance for suggested by (Johnson et al., 1955). Before we processed to combined analysis the error homogeneity between environments were assessed using F-max ratio and all traits showed homogeneous. The estimation of genetic parameters, including phenotypic variance, genotypic variance, heritability, and both phenotypic and genotypic coefficients of variation, was conducted for each genotype. Additionally, genetic advance and genetic advance as a percentage of the mean were calculated. These estimates were derived using the equations suggested by (Johnson et al., 1955; Kuswantoro et al., 2022).

Environmental variance ($\sigma\ ^2e$) = MS_e

Genotypic variance ($\sigma\ ^2g$) = $\frac{\mathrm{MSg{\times}e{-}\ MSe}}{\mathrm{r}}$

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

Phenotypic coefficient of variation $PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}} * 100$

Genotypic coefficient of variation $GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} * 100$ Where MSg= Mean square of genotypes, MSe=Mean square of error, $\sigma\ ^2p$ = phenotypic variance, $\sigma\ ^2g$ = genotypic variance, $\sigma\ ^2e$ = environmental variance, r = number of replication and $\bar{X}$ = grand mean.

Broad sense heritability (H^2) for all traits were calculated based on the formula suggested by (Elings, 2000) as: $H^2 = \frac{\sigma^2 g}{\sigma^2 p} * 100$

Where H^2= heritability in the broad sense, $\sigma\ ^2g$ = genotypic variance, $\sigma\ ^2p$ = phenotypic variance. The heritability values were described by (Robinson et al., 1955) stated (<30 %, 30-60% and > 60%) low, moderate and high heritability respectively. Genetic advance (GA) and genetic advance as percent of the mean (GAM), presumed selection of the superior 5% of the accessions, were estimated suggested by (Johnson et al., 1955; Hanson et al., 1956).

$$GA = K^* \sqrt{\sigma^2 p} * H^2$$

and $$GAM = \frac{GA}{\bar{X}} * 100$$

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

After conducting a comprehensive assessment of the assumptions concerning normality and the homogeneity of error variance utilizing the F-max ratio and examining genotype performance pattern across location (Fig. 1) and the model was checking based on a plot of residuals versus fitted values as shown in Fig. 2. We then proceeded with a combined analysis of variance. The findings for eight traits across 35 field pea genotypes, as detailed in Table 2, present valuable insights. We observed significant differences ($P < 0.001$) in all yield and yield component traits across the testing locations. Notably, grain yield and plant height exhibited significant differences at $P < 0.01$, while days to flowering and powdery mildew resistance were significant at $P < 0.001$. Additionally, the number of seeds per pod and the number of pods per plant showed significant differences ($P < 0.005$). However, it is worth noting that days to maturity and ascochyta blight did not display significant differences among the genotypes (Table 2).

These results not only highlight the variability among the genotypes but also provide a foundation for further exploration of traits that contribute to improved yield and resilience in field peas. The results depicted the presence of genetic variability among the studied genotypes, as well as a significant impact of the locations on genotype performance. Considering the influence of genotype-environment interaction, most of the traits were not showed different performance across environments except days to flowering (Table 2). A similar finding was reported by (Ofga & Petros, 2017). Although there was a significant difference in the genotype by location interaction for few traits at ($P \leq 0.05$) in Table 2, it does not have a major impact on genotype performance, except in the case of the disease Ascochyta blight (AB) records. Therefore, the success of genetic enhancement is linked to the extent and nature of variability for specific traits.

3.2 Genotypic Mean Performance of Traits

The average performance of various genotypes demonstrated a significant range of variation for most of the traits analyzed (Table 3). For instance, grain yield, quantified in kilograms per hectare (kg/ha), exhibited substantial variability, with genotypes G12 reflecting lower yield potential compared to genotype G3, which showcased a considerably higher yield capacity. Regarding the trait measuring days to 50% flowering, notable differences were observed among the genotypes, particularly between G35 and G11, which displayed earlier flowering times relative to genotype G16. This disparity underscores the diverse adaptability of these genotypes to differing environmental conditions.

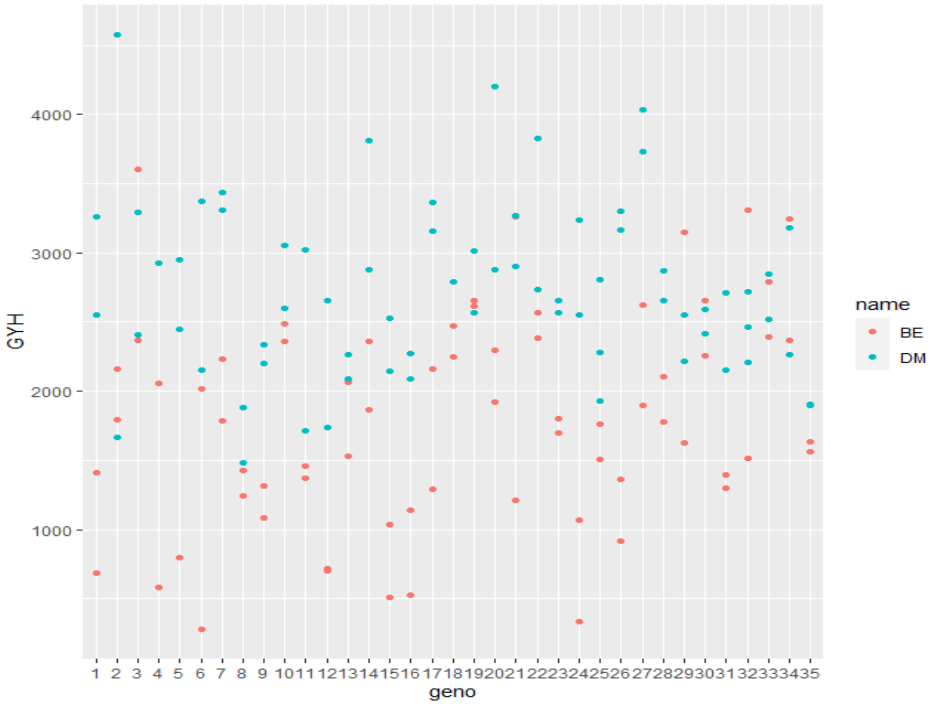

Fig. 1. Scatter plot visualization of the pattern of genotypes across the two locations BE =Bekoji, DM =Debremarkos research sites

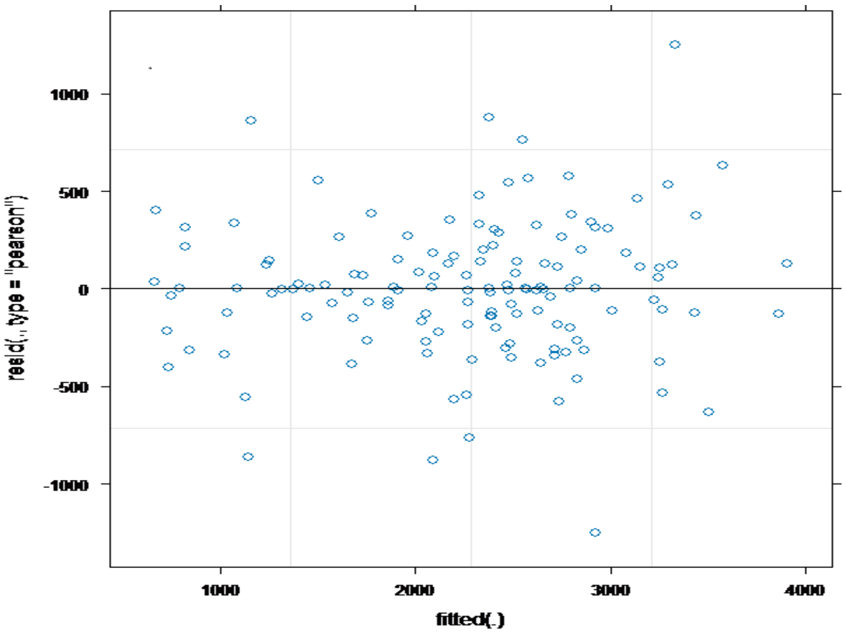

Fig. 2. Model checking based on residual Vs. fitted value of 35 field pea genotypes conducted across two locations

Table 2. Mean square of Pooled Analysis of Variance for eight traits evaluated at Bekoji and Debremarkos testing locations during 2023

Source of Var.	Df.	GY	PH	PPP	SPP	DF	DM	AB	PM
Genotype (G)	**34**	831893**	345.3**	10.5*	1.0*	71.4***	27^{NS}	1.1 ^{NS}	4.2***
Location (L)	**1**	25138775***	12653.4***	143.3***	17.9***	905.3***	17316.1***	115.2***	158.6***
Replication(rep)	**2**	375487	149.8 ^{NS}	15.8	7.2 ^{NS}	30.2**	10.6 ^{NS}	6.0***	2.8*
G x L	**34**	435107	250.4*	5.0^{NS} ^{NS}	0.3 ^{NS}	12.6**	7.2 ^{NS}	0.7 ^{NS}	1.6*
L x rep x block	**24**	290457	190.6 ^{NS}	5.5 ^{NS}	0.7 ^{NS}	12.5*	12.5 ^{NS}	0.6 ^{NS}	1.7*
Residuals	**44**	323917	142.2	5.4	0.5	6.4	4.2	0.6	0.8

***Note:** *, ** and *** level of significance at (P < 0.05, (P < 0.01) and (P < 0.001) respectively, Df. Degrees of freedom, GY = Grain yield, PH = Plant height, PPP = Number of pods per plant, SPP = Number of seeds per pod, DF = Days to flower, DM = Days to maturity, AB = Ascochyta blight and PM = powdery mildew, NS = Not significant*

Table 3. Mean performances of 35 Field pea genotypes evaluated at Bekoji and DebreMarkos research station in 2023 main cropping season

Code	Genotype	DF	DM	PH	PPP	SPP	GY	AB	PM
G1	EH018009-1	74.0	133.2	168.0	8.5	5.5	2183	4.0	4.9
G2	EH018009-3	69.9	129.6	153.2	14.4	3.8	2305	4.1	4.0
G3	EH018002-1	74.0	135.9	160.0	8.3	4.2	2918	5.8	4.1
G4	EH018009-6	73.1	131.6	140.0	7.4	4.2	2071	5.3	3.2
G5	EH018008-6	70.1	131.1	127.3	6.3	3.7	2064	5.5	3.7
G6	EH018012-2	78.0	134.9	133.7	10.5	3.9	1956	5.0	4.4
G7	EH018007-1	70.3	132.3	146.1	10.6	4.3	2691	5.3	3.4
G8	EH018001-3	76.6	134.7	164.4	8.6	3.5	1508	4.5	5.9
G9	EH018001-6	67.6	130.6	132.4	11.1	4.1	1734	5.6	3.2
G10	EH018008-1	76.8	136.2	143.7	10.7	4.5	2625	5.2	4.2
G11	EH018005-3	67.2	135.2	157.9	9.1	4.0	1893	4.4	5.4
G12	EH018003-1	75.8	131.6	152.2	8.3	4.1	1452	4.7	3.0
G13	EH018006-4	74.8	136.3	150.2	9.6	4.4	2070	4.6	6.5
G14	EH018014-3	75.9	132.6	151.4	7.3	5.4	2731	5.5	6.1
G15	ETETU	79.5	130.5	145.9	8.8	3.8	1553	4.5	4.2
G16	EH018009-2	86.6	136.2	154.0	8.5	3.6	1507	4.2	5.0
G17	EH018001-2	72.1	134.5	149.2	6.6	5.2	2492	5.7	5.0
G18	EH018005-6	71.2	131.6	150.6	10.0	4.1	2401	5.8	4.9
G19	EH018012-4	67.0	131.7	137.9	8.9	4.6	2712	5.4	4.7
G20	EH018011-4	69.7	131.2	139.9	10.7	4.4	2825	5.5	5.0
G21	EH018004-2	75.6	137.4	153.2	11.7	4.2	2659	5.0	3.9
G22	EH018008-5	71.3	134.0	162.9	8.0	4.5	2879	6.0	5.6
G23	EH018011-3	69.1	131.5	141.5	9.0	4.5	2179	5.6	3.7
G24	EH018004-3	75.3	135.3	142.8	7.6	4.9	1799	6.1	4.6
G25	EH018005-8	70.9	129.2	141.5	8.4	4.2	1870	5.7	2.9
G26	JELDU	71.4	131.9	148.3	5.8	4.2	2186	5.5	3.7
G27	EH018006-1	71.3	131.7	151.9	9.6	4.2	3072	5.7	3.5
G28	EH018014-2	73.8	135.0	162.5	9.3	4.3	2351	5.0	4.0
G29	BURSA	71.8	135.0	150.0	10.6	4.4	2386	5.0	3.5
G30	EH018013-3	79.4	137.7	145.0	8.4	3.7	2577	5.3	4.4
G31	EH018001-1	74.0	137.5	148.4	7.3	4.3	1890	4.4	4.6
G32	EH018005-1	72.3	137.0	145.4	8.3	4.3	2376	4.7	3.7
G33	EH018003-2	72.1	131.1	140.5	8.7	3.8	2638	5.8	3.2
G34	EH018010-2	68.6	130.5	135.2	8.8	4.0	2765	6.0	3.4
G35	EH018004-1	67.2	129.8	141.3	9.7	3.0	1749	5.5	3.0
	Minimum	67	129.2	127.3	5.8	3	1452	4	2.9
	Maximum	86.6	137.7	168	14.4	5.5	3072	6	6.1
	Mean	73.0	133.3	147.7	9.0	4.2	2259.1	5.2	4.2
	CV (%)	22.4	8.1	25.9	17.1	3.5	1.5	15.2	20.8
	LSD (0.05)	2.9	17.1	3.3	1	3.6	718.9	1.1	1.3

FD: Days to 50% Flowering; MD: Days to 90% Maturity; PH: Plant Height (Cm); PPP: Number of Pods per Plant^{-}; SPP: Number of Seeds per Pod^{-}; GY: Grain Yield (Kg Ha^{-1}); AB: Ascochyta Blight (1-9); PM: Powdery Mildew (1-9) scale

Days to maturity (DM), genotype G25 was identified to mature approximately eight days earlier than genotype G30 (Table 3). Genotype G25 is selective candidate in regions characterized by shorter growing seasons or moisture stress conditions. Consequently, G25 is recommended as valuable parent material for future breeding programs aimed at developing field pea varieties that withstand moisture stress, thereby optimizing yield under challenging agricultural circumstances Moreover, the extensive range of variability highlights the considerable genetic diversity present among the genotypes concerning the traits under study.

In contrast, traits such as plant height (cm) and resistance to powdery mildew (PM) also exhibited significant variations in mean performance. This finding suggests that specific genotypes may exhibit enhanced resilience and productivity under a variety of agricultural practices (Table 3). A thorough understanding of trait variability is essential for making informed breeding decisions, thereby enhancing the overall genetic potential of field pea cultivars.

3.3 Genotypic and Phenotypic Variance

The estimates pertaining to genotypic variation (σ^2g), phenotypic variation (σ^2p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (H^2), genetic advance (GA), and genetic advance as a percentage of the mean (GAM) for various traits are presented in Table 4. Specifically, the values for the phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) are categorized as low (below 10%), medium (10% to 20%), and high (above 20%) (Tesfaye, 2021). The findings indicate that phenotypic variance consistently surpasses genotypic variance across all traits, thus highlighting the significant impact of environmental factors on these characteristics. The highest levels of both genotypic and phenotypic variances observed in quantitative traits, particularly in grain yield, suggest a greater likelihood of successful selection (Mohammadi & Pourdad, 2008). The detailed data concerning the genotypic and phenotypic variations for various traits can be found in Table 4.

3.4 Genotypic and Phenotypic Coefficient of Variation

All traits studied, with the exception of the number of pods per plant and the number of seeds per pod exhibited a higher phenotypic coefficient of variation (PCV) than the genotypic coefficient of variation (GCV) (Table 4). Both the GCV and PCV for grain yield (kg/ha) were high, indicating a broad genetic base. This finding aligns with previous studies by (Tiwari & Lavanya, 2012; Ahmad et al., 2014). Additionally, (Tolessa, 2017) noted high PCV values for grain yield, powdery mildew, and the number of pods per plant in field pea hybrid genotypes.

In contrast, our study identified a low phenotypic coefficient of variation and an intermediate genotypic coefficient of variation values for the number of pods per plant and seeds per pod. The majority of other traits exhibited low genotypic and phenotypic coefficients of variation, both falling below 10% (Table 4). This observation is consistent with the findings of [Kumar et al., 2023; Pandey et al., 2017) Additionally, (Yadav et al., 2009; Lavanya et al., 2010) reported high GCV and PCV values for grain yield, accompanied by low to moderate values for yield components in their field pea experiments. Overall, the GCV and PCV serve as measures to compare variability within the traits. The PCV was slightly greater than the GCV for all characters, suggesting an influence of environmental factors on these traits, as shown in Table 4. Although phenotypic variance surpassed genotypic variance, the difference was minor, indicating that the traits are stable yet still somewhat affected by environmental conditions.

3.5 Heritability, Genetic Advance and Genetic advance as percent of Mean

Heritability values for the browed sense (H^2b) exhibited variability ranging from low to moderate, contingent upon the specific traits examined. These values were observed between 26% for plant height and 52% for the number of seeds per pod, with powdery mildew closely following at 51% (Table 4). Heritability serves as an indicator of the extent to which genotypic selection may be effectively derived from phenotypic performance. The observed low H2b values, in conjunction with a low genetic advance as a percentage of the mean (GAM) for plant height, suggest that a limited proportion of the observed variation is attributable to genetic factors. However, it is important to note that this does not necessarily imply that additive genetic variance is insignificant (Tolessa, 2017). In such scenarios, it is reasonable to expect gradual progress in the enhancement of these traits through direct selection, due to their quantitative mode of inheritance.

In contrast, low H^2b and GAM values have also been documented for powdery mildew and the number of pods per plant, whereas high H2b values have been noted for plant height (Fikreselas, 2012; Kumar et al., 2013). (Getie, 2022) Indicates that high estimates of heritability, in conjunction with moderate GAM values, have been observed for the number of seeds per pod in field peas. Low heritability, GAM, genetic coefficient of variability (GCV), and phenotypic coefficient of variability (PCV) indicate a low level of additive genetic components, making it challenging to directly select traits for genetic improvement in field pea breeding. The research conducted by (Kosev & Georgieva, 2016)

Table 4. Estimate of variance components, heritability and genetic advance for 8 traits of 35 field pea advanced lines conducted at DebereMarkos and Bekoji research site during 2023 cropping season

Characters	Mean	$\sigma^2 g$	$\sigma^2 g\times e$	$\sigma^2 e$	$\sigma^2 ph$	$H^2 b$	GA (5%)	GAM (5%)	GCV	PCV
DF	73	3.1	3.1	6.4	6.3	50	2.6	3.6	2.4	2.9
DM	133.3	3.1	0	13.3	6.5	49	0.26	0.2	1.3	2.2
PH	147.7	22.4	54.8	144.3	85.9	26	4.98	3.4	3.2	7.6
PPP	9	1.2	0.4	5.2	2.7	45	1.5	16.7	12.2	5.5
SPP	4.2	0.1	0	0.5	0.2	52	0.53	12.6	10.5	2.4
GY	2259.1	96080.6	64451.7	310850.1	206018.9	47	4.4	0.2	65.5	95.5
AB	5.2	0.1	0	0.7	0.3	43	0.5	9.6	1.4	2.5
PM	4.2	0.4	0.3	0.9	0.8	51	0.96	22.9	3.1	4.4

*$\sigma^2 g$ =Genetic variance, $\sigma^2 g\times e$ = Genotype by environment interaction variance, $\sigma^2 e$ = Environmental variance, $\sigma^2 ph$ = Phenotypic variance, $H^2 b$ = Heritability in broad sense, **GA** = genetic advance **GAM** = genetic advance as the percent of mean, **GCV** = genetic coefficient of variation and **PCV** = Phenotypic coefficient of variation*

revealed moderate heritability estimates for the number of pods per plant and plant height. The authors concluded that heritability estimates serve as valuable indicators for breeders during the selection process aimed at enhancing these traits within specific environmental contexts.

In instances where heritability reaches 100%, the phenotypic performance would perfectly represent the genotypic value; however, even under such a hypothetical scenario, the heritability value alone does not provide a clear indication of the potential genetic progress achievable through the selection of superior individuals. The extent of genetic progress is contingent upon the variances present. Consequently, the utility of heritability estimates is significantly amplified when considered alongside the selection differential, defined as the difference between the mean of the selected lines and the overall mean of the population.

Genetic advance quantifies the anticipated genetic progress resulting from the selection of the best-performing genotypes for a specific trait (Jones, 2000; Singh et al., 2024). It is essential to evaluate heritability estimates and genetic advance in tandem, as high heritability does not necessarily correspond to high genetic gain. The expected genetic advance is expressed as a percentage of the mean when selecting the top 5% of genotypes, representing the highest yielders. The observed range of genetic advance as a percentage of the mean varied from 0.2% for days to maturity and grain yield to 22.9% for powdery mildew (Table 4).

Our findings align with those of (Khan et al., 2017) who reported moderate heritability accompanied by a low genetic advance as a percentage of the mean for days to 50% flowering. In contrast, all traits, except for plant height, demonstrated moderate heritability alongside low genetic advance for traits such as days to 50% flowering, days to maturity, and grain yield (ascochyta blight). This suggests that these traits are influenced by non-additive gene effects, presenting challenges for improvement through selection. The previous researcher (Luthra et al., 2023) indicates that, heritability and significant genetic advancements in yield and yield component traits are essential factors. Consequently, implementing a strategy that focuses on selecting superior genotypes based on these characteristics will facilitate effective crop improvement, ultimately leading to increased yield and enhanced yield attributes.

Furthermore, (Toppo et al., 2017) also reported moderate heritability estimates, accompanied by moderate genetic advance for seeds number per plant and pod number per plant. Conversely, the traits of days to 50% flowering and days to maturity exhibited lower heritability values in conjunction with lower genetic advance, indicative of a greater influence of dominance and epistatic gene actions in the expression of these traits. As a result, efforts to improve these traits through selection yield suboptimal responses. Low or moderate heritability estimates in a broad context lead to limited genetic advance or gain, primarily due to a narrow genetic base.

4. CONCLUSION

The achievement of any crop improvement depends on a thorough understanding of variation in genetics, heritability, and the types of gene action involved in inheriting desirable traits. The tested genotypes in this study showed statistically significant differences at the ($P < 0.001$) level, indicating a substantial amount of genetic variability. This confirms a positive response for the effectiveness of selection based on traits with high and medium phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) values.

From our investigation, high genotypic and phenotypic coefficients of variation were observed for grain yield, suggesting that acceptable improvements could be achieved through selective breeding of this trait. However, no traits exhibited high heritability along with a high genetic advance as a percentage of the mean for effective trait selection between treatments. This lack of genetic variation across breeding lines necessitated negative selection during the crossing of filial generations (from F1 to F6), leading to a more uniform direction in the breeding process.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

ACKNOWLEDGEMENTS

The authors acknowledge Ethiopian Institute of Agricultural Research as the source of funding for the study. The authors would also like to acknowledge Holeta DebreMArkos and Kulumsa Agricultural Research for providing the research materials and managing the trials.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

Ahmad, H. B., Rauf, S., Rafiq, Ch. M., Mohsin, A. U., & Iqbal, A. (2014). Estimation of genetic variability in pea (*Pisum sativum* l.). Journal of Global Innovations in Agricultural and Social Sciences, 2(2), 62–64. https://doi.org/10.17957/jgiass/2.2.496

Elings, A. (2000). Principles of plant breeding Second Edition, ed by Robert W. Allard John Wiley & Sons, Inc (New York, Chichester, Weinheim, Brisbane, Singapore, Toronto) pp 254, price: £45.50 ISBN 0-471-02309-4. Journal of the Science of Food and Agriculture, 80(5), 631–631. https://doi.org/10.1002/(sici)1097-0010(200004)80:5<631::aid-jsfa596>3.3.co;2-r

Fikreselas, M. (2012). Variability, Heritability and Association of Some Morpho-agronomic Traits in Field Pea (Pisum sativum L.) Genotypes. Pakistan Journal of Biological Sciences, 15(8), 358–366. https://doi.org/10.3923/pjbs.2012.358.366

Garima Tiwari, G. T., & Lavanya, G. R. (2012). Genetic variability, character association and component analysis in F4 generation of fieldpea (*Pisum sativum* var. arvense L.).

Getie, M. (2022). Genetic diversity and association of traits in field pea (Pisum sativum L.) Accessions in Mecha district, north western Ethiopia (Doctoral dissertation).

Gudadinni, P., Bahadur, V., Ligade, P., Topno, S. E., & Prasad, V. M. (2017). Study on Genetic Variability, Heritability and Genetic Advance in Garden Pea (Pisum sativum var. hortense L.). International Journal of Current Microbiology and Applied Sciences, 6(8), 2384–2391. https://doi.org/10.20546/ijcmas.2017.608.282

Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza 1. Agronomy journal, 48(6), 268-272.

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of Genetic and Environmental Variability in Soybeans1. Agronomy Journal, 47(7), 314–318. Portico. https://doi.org/10.2134/agronj1955.00021962004700070009x

Jones, E. (2000). Principles of Plant Breeding – Second Edition. Edited by Robert W. Allard, John Wiley & Sons Ltd. (ISBN-0-4710-2309-4); Price: £ 45.50. Plant Science, 156(1), 117–118. https://doi.org/10.1016/s0168-9452(00)00225-9

Khan, M. R. A., Mahmud, F., Reza, M. A., Mahbub, M. M., Shirazy, B. J., & Rahman, M. M. (2017). Genetic diversity, correlation and path analysis for yield and yield components of pea (Pisum sativum L.). World Journal of Agricultural Sciences, 13(1), 11-16.

Kosev, V., & Georgieva, N. (2016). Evaluation of genotypic and genetic variances of quantitative traits in pea (Pisum sativum L.). Emirates Journal of Food and Agriculture, 28(11), 755. https://doi.org/10.9755/ejfa.2016-06-677

Kumar, D., Malik, S., Singh, S. K., & Kumar, M. (2013). Genetic Variability, Heritability and Genetic Advance for Seed Yield and Yield Components in Garden Pea (Pisum sativumL.). Vegetos- An International Journal of Plant Research, 26(2), 182. https://doi.org/10.5958/j.2229-4473.26.2.072

Kumar, R., Singh, B., Tomar, H., Kumar, V., Chaudhary, A. K., & Marwah, A. (2023). Genetic Heritability, Variability, Genetic Advance, Correlation and Path Analysis Assessment in Garden Pea (Pisum sativum L.). International Journal of Plant & Soil Science, 35(14), 69-79.

Kuswantoro, H., Santoso, J., & Suryanto, A. (2022). Genetic variability, correlation and path coefficient among agronomic characters of soybeans [Glycine max (L.) Merr.] lines. IOP Conference Series: Earth and Environmental Science, 1114(1), 012037. https://doi.org/10.1088/1755-1315/1114/1/012037

Lavanya, G. R., Singh, D., & Vinoth, R. (2010). Genetic variability, character association and component analysis in field pea, Pisum sativum var. arvense. *Madras Agric J*, *97*(10-12), 329-331.

Luthra, S., Singh, B. P., Singh, R., Nagar, B. L., & Singh, S. K. (2023). Genetic Variability in Garden Pea (Pisum sativum L.): A Review. International Journal of Environment and Climate Change, 13(11), 3859–3865. https://doi.org/10.9734/ijecc/2023/v13i113566

Mohammadi, R., & Pourdad, S. S. (2008). Estimation, interrelationships and repeatability of genetic variability parameters in spring safflower using multi-environment trial data. Euphytica, 165(2). https://doi.org/10.1007/s10681-008-9789-z

Naveen, S. (2023). Assessment of Genetic Variability, Correlation and Path Coefficient Analysis for Yield and Yield Attributing Traits in Field Pea (Pisum sativum var. arvense L.). International Journal of Science and Research (IJSR), 12(4), 106–116. https://doi.org/10.21275/sr23331095014

Ofga, B., & Petros, Y. (2017). Genetic Variability and association among agronomic characters in selected field pea (Pisum sativum L.) genotypes at Bale Zone, Sinana Research Center, Oromia Region, Ethiopia. International Journal of Genetics and Genomics, 5(6), 63-75.

Pallavi, P., Singh, A., & Pandey, K. K. (2013). Estimation of heritability on pea (*Pisum sativum* L.)

Pandey, M., Singh, V. B., Yadav, G. C., Pandey, P., & Yamuna Prasad. (2017). Genetic variability, heritability and genetic advance in vegetable pea (Pisum sativum L. var. hortense). Vegetable Science, 44(01), 139–141. https://doi.org/10.61180/vzzyms50

Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1955). Genetic variances in open pollinated varieties of corn. Genetics, 40(1), 45.

Sharma, P. P., Vyas, M., & Meghawal, D. R. (2017). Estimation of genetic variability and correlation analysis in field pea (Pisum sativum L.) genotypes. Journal of Plant Development Science, 9, 53-56.

Singh, G. P., Singh, V. K., Kumar, A., Bhardwaj, A., & Rai, A. K. (2024). Assessment of Genetic Diversity in Garden Pea (Pisum sativum L.) and Identification of Promising Lines for Hybridization. Archives of Current Research International, 24(8), 90–98. https://doi.org/10.9734/acri/2024/v24i8852

Tesfaye, A. (2021). Genetic Variability, Heritability, and Genetic Advance Estimates in Garlic (Allium sativum) from the Gamo Highlands of Southern Ethiopia. International Journal of Agronomy, 2021, 1–8. https://doi.org/10.1155/2021/3171642

Tiwari, G., & Lavanya, G. R. (2012). Genetic variability, character association and component analysis in F4 generation of fieldpea (Pisum sativum var. arvense L.). *Karnataka Journal of Agricultural Sciences*, *25*(2).

Tolessa, T. (2017). Genetic variation, heritability, and advances from selection in elite breeding materials of field pea (Pisum sativum L.) genotypes. Agricultural research and map technology. Open Access Journal, 8(4). https://doi.org/10.19080/artoaj.2017.08.555744

Toppo, H., Sharma, R. N., & Thakur, A. (2017). Path analysis for quality traits in field pea (Pisum sativum L.). Agricultural Science Digest-A Research Journal, 37(4), 324-326.

Vinod, K. S., & Lila, B. (2013). Studies on genetic variability and heterosis in vegetable pea (Pisum sativum L.) under high hills condition of Uttarakhand, India. African Journal of Agricultural Research, 8(18), 1891–1895. https://doi.org/10.5897/ajar09.427

Yadav, R., Srivastava, R. K., Kant, R., & Singh, R. (2009). Studies on genetic variability, heritability and and character association in fieldpea. *Crop Res*, *38*(1), 184-188.

Peer-review history:
The peer review history for this paper can be accessed here:
https://prh.ikprress.org/review-history/12674