International Journal of Bio-resource and Stress Management
https://ojs.pphouse.org/index.php/IJBSM

Crossref

IJBSM February 2025, 16(2): 01-10
Article AR5549

**Research Article**
Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2025.5549

# Genetic Variability Studies in Field Pea (*Pisum sativum* L.) for Yield and Associated Characters Evaluated at Asasa South-East Highlands of Ethiopia

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0009-0002-5625-9823

## ABSTRACT

The current study was conducted during June to October, 2019 cropping season at Asasa, Ethiopia to evaluate forty-nine field pea genotypes were evaluated in simple lattice design to assess genetic variability for morpho-agronomic traits. The analysis of variance showed significant differences among genotypes for most of the traits. The genotypes variations for grain yield in the range between 383.0 to 5605 kg ha$^{-1}$. A total of 10 genotypes had higher grain yield than high yielding check variety, Burkitu (4521 kg ha$^{-1}$) of which EH 010011-3, EH 08003-2 and EH 08016-2 had 24, 14.80 and 14.11% yield advantages, respectively, over higher yielding check variety. The mean performance of genotype EH010011-3 was highest at Asasa with mean grain yield 5605 kg ha$^{-1}$. The genotypic coefficient of variation ranged from 1.0% for days to maturity to 20.01% for grain yield, whereas the phenotypic coefficient of variation ranged from 1.37% for days to maturity to 27.41% for grain yield ha$^{-1}$. The estimated broad sense heritability ranged from 51.21% for thousand seed weight to 53.93% for days to maturity. Genetic advance as percent of mean ranged from 1.52% for days to maturity to 33.88% for grain yield. The study showed the existence of reasonable genetic variability among the field pea genotypes that could be exploited in breeding programs.

**KEYWORDS:** Genotypic, phenotypic, heritability, pea, genotype, yield, variability, variance

***Citation* (VANCOUVER)*:*** Abo and Mohamed, Genetic Variability Studies in Field Pea (*Pisum sativum* L.) for Yield and Associated Characters Evaluated at Asasa South-East Highlands of Ethiopia. *International Journal of Bio-resource and Stress Management,* 2025; 16(2), 01-10. HTTPS://DOI.ORG/10.23910/1.2025.5549.

***Data Availability Statement:*** Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

***Conflict of interests:*** The authors have declared that no conflict of interest exists.

RECEIVED on 22nd June 2024 RECEIVED in revised form on 10th January 2025 ACCEPTED in final form on 22nd January 2025 PUBLISHED on 07th February 2025

## 1. INTRODUCTION

Field pea (*Pisum sativum* L.) is self-pollinated an annual herbaceous legume crop that belongs to family Leguminosae and genus Pisum (Duke, 1981). The center of origin for field pea is considered the Mediterranean to central Asia as well as the highlands of Ethiopia (Davies, 1976). In Ethiopia field pea is cultivated since ancient time in Ethiopia and its wild and primitive forms of the species was concealed in the highlands of Ethiopia. Due to this fact Ethiopia considered as one of the centers of diversity for field pea. Field pea grow around the world for its fresh green seeds, tender green pods, dried seeds, and soil restorative purposes (McPhee, 2003).

In Ethiopia, (*Pisum sativum*) is grown in high altitude area (1800-3200) m.a.s.l. (Yirga and Tsegay, 2013). Among the highland pulse crops Field pea is the third most important staple food legume crop in Ethiopia next to faba bean and common bean, among the highland pulses. Field pea covers about 216,786.33 hectares of arable lands with a total production of 3,608,112.40 quintals with average yield of 1.664 t $ha^{-1}$. It constitutes 12.73% of the total area covered by pulses (Anonymous, 2019).

Field pea supplies 344 calories, 20.1 g protein and 64.8 g carbohydrates 100 $g^{-1}$ edible portion. In combination with wheat, rice and other cereals it provides a balanced diet (Santalla et al., 2001) though pea protein is deficient in sulphur-containing amino acids (Cysteine and methionine) (McPhee, 2003).

A field pea plays a great role in soil fertility restoration as suitable rotational crop. Especially with barely and bread wheat which serves to restore soil fertility and minimize insect pests and disease of the cereals.

Despite the importance of field pea in Ethiopia, the major yield-limiting constraints in field pea production in Ethiopia are aphids, low yielding local varieties, lodging, diseases (ascochyta blight, powdery mildew) and pod shattering (Yirga, 2019). The high diversity of the field pea accession associated with the robust representation of its center of domestication, that is, the Near East and Mediterranean (Warkentin et al., 2015) and other centers of diversity, including Central Asia and Ethiopia (Van der, 1988).

The existence of wide range of field pea germplasm in Ethiopia makes the country the secondary center of genetic diversity. This indicates that has Ethiopia the potential for improving field pea for desired traits either through selection and/or hybridization breeding programs. In field pea, studies showed that the landraces and accessions in the breeding programs are focused on selection and evaluation from the existing diversity (Burstin et al., 2015).

The crossing among the highly divergent parents can produce varieties with broad genetic base (Russell, 1978), (Singh, 1990) raises the yield ceilings imposed by a narrow genetic base. In addition, assessing the genotype×environment interaction will be crucial since most of the traits are governed through polygenic inheritance that affected mostly by the environment (Ofga and Petros, 2017). Yield is highly affected by different yield component traits that required a clear understanding how these traits affect yield and designing a selection procedure. This indicate sometimes direct selection for the target trait (grain yield) which is a polygenic trait may not be effective in an unless yield contributing traits are considered during selection (Srivastava et al., 2017). So, to have a successful breeding program, the breeder should study the genetic variability of the base population, understand the nature of inheritance of the traits and understand the interrelationship among traits of interest to design the breeding strategy. Thus the investigation was aimed to estimate the genetic variability among the field pea genotypes for yield and yield related traits.

## 2. MATERIALS AND METHODS

### 2.1. *Description of the study area*

The experiments were conducted during June to October 2019 cropping season at Asasa research sites of Kulumsa Agricultural Research Center, Ethiopia. Asasa is located at 07°06'12'' N latitude and 38°11'32'' E longitude with an altitude of 2340 m.a.s.l. The site receives an average annual rainfall of 620 mm with the average annual minimum and maximum temperatures of 5.8°C and 23.6°C, respectively. The soil type of Asasa is gleysol and its pH is 6.25 light sandy soils with low water holding capacity.

### 2.2. *Experimental materials and design*

Forty-nine field pea genotypes obtained from Kulumsa and Holeta Agricultural Research Centers were used for this study. The list and description of the materials used for the study are presented in (Table 1). A plot size of 4×0.8 $m^2$ (3.2 $m^2$) was used in this study where each plot was consisted of four rows with 80 plants within each row, with an inter-row spacing of 20 cm and 5 cm between plants within the row. The spacing between plots and blocks distances was 1.0m and 1.5 m, respectively. The experiment was laid out in 7×7 simple lattice designs at Asasa and each genotype was assigned randomly in blocks of each replication. All agronomic management practices were applied equally and properly as per the recommendations of Kulumsa Agricultural Research Center for Asasa.

### 2.3. *Data collection*

Data on agronomic and morphological traits were collected on plot and individual plant basis. In this experiment the following data was recorded in plot and average *plant basis.*

Table 1: Description of field pea accessions

| Acc. code | Genotype name | Seed source | Acc. code | Genotype name | Seed source |
|---|---|---|---|---|---|
| G-1 | Bursa | Breeder seed | G-26 | EH 010009-2 | PVT 2018 |
| G-2 | Burkitu | Breeder seed | G-27 | EH 08003-1 | NVT 2018 |
| G-3 | EH 05048-5 | NVT 2018 | G-28 | EK 08023-5 | NVT 2018 |
| G-4 | EH 08034-2 | NVT 2018 | G-29 | EH 08016-2 | NVT 2018 |
| G-5 | EH 010006-2 | PVT 2018 | G-30 | EH 08027-1 | NVT 2018 |
| G-6 | EH 08021-1 | NVT 2018 | G-31 | EH 08027-3 | NVT 2018 |
| G-7 | EH 09021-5 | NVT 2018 | G-32 | EK 08017-5 | NVT 2018 |
| G-8 | EH 08003-2 | NVT 2018 | G-33 | EK 08016-4 | NVT 2018 |
| G-9 | EH 08036-4 | NVT 2018 | G-34 | EH 08003-7 | NVT 2018 |
| G-10 | EH 010005-2 | PVT 2018 | G-35 | EK 08024-4 | NVT 2018 |
| G-11 | EH 08027-2 | NVT 2018 | G-36 | EK 08017-3 | NVT 2018 |
| G-12 | EH 08036-1 | NVT 2018 | G-37 | PDFPT p-313-050 | ICARDA |
| G-13 | EH 08041-3 | NVT 2018 | G-38 | PDFPT p--313-015 | ICARDA |
| G-14 | EH 07005-1 | NVT 2018 | G-39 | PDFPT p-313-017 | ICARDA |
| G-15 | EH 010011-3 | PVT 2018 | G-40 | PDFPT p-313-26 | ICARDA |
| G-16 | EH 07002-1 | NVT 2018 | G-41 | PDFPT p-313-020 | ICARDA |
| G-17 | EH 08021-4 | NVT 2018 | G-42 | PDFPT p-313-052 | ICARDA |
| G-18 | EH 010004-1 | PVT 2018 | G-43 | PDFPT p-313-062 | ICARDA |
| G-19 | EH 07006-5 | NVT 2018 | G-44 | PDFPT p-313-098 | ICARDA |
| G-20 | EH 010009-1 | PVT 2018 | G-45 | PDFPT p-313-022 | ICARDA |
| G-21 | EH 08042-2 | NVT 2018 | G-46 | GIZ 02019 - 1 | GERMANY |
| G-22 | EH 07007-5 | NVT 2018 | G-47 | GIZ 02019 - 2 | GERMANY |
| G-23 | EH 08041-4 | NVT 2018 | G-48 | PDFPT p-313-028 | ICARDA |
| G-24 | EH 08042-4 | NVT 2018 | G-49 | PDFPT p-313-065 | ICARDA |
| G-25 | EH 08041-1 | NVT 2018 | | | |

Seed Source: Kulumsa and Holeta Agricultural Research Centers

#### *2.3.1. Data collected on plot basis*

#### *2.3.1.1. Days to 50% flowering (DTF)*

The number of days from the date of sowing to the date at which about 50% of the plants in a plot showed blooming on about 50% of their flower buds.

#### *2.3.1.2. Days to 90% maturity (DTM)*

The number of days from the date of sowing to a stage when 90% of plants have reached their physiological maturity was assessed by yellowish foliage color and shedding start on the lower stem, pods and seeds hardened.

#### *2.3.1.3. Thousand seed weight (TSW) (g)*

The weight in gram of 1000 seeds randomly taken from each plot.

#### *2.3.1.4. Grain yield (g plot$^{-1}$)*

The net plot grain yield in gram per plot Gy (g plot$^{-1}$).

#### *2.3.1.5. Grain yield ha$^{-1}$ (kg ha$^{-1}$)*

The net plot grain yield adjusted at 10.0% moisture content was converted in to yield per hectare in a kilogram.

#### *2.3.1.6. Grain filling period (GFP)*

The number of days from days to 50% flowering to days to 90% physiological maturity.

#### *2.3.1.7. Above ground total biomass plot$^{-1}$ (TBPP)*

The mean weight of above ground parts sun dried and weighted to get the biological yield per plot in grams

#### *2.3.1.8. Harvest index (HI)*

Ratio of grain yield which is oven dried over total biomass of oven dried.

This was calculated by the following formula:

Harvest index (HI)=(Seed yield plot$^{-1}$ (g)/Biomass plot$^{-1}$ (g)) ×100

### *2.3.2. Data collected on plant basis*

#### *2.3.2.1. Plant height (PH)*

Average height of five randomly selected plants in each plot measured (cm) from the ground surface to the top of the main stem at physiological maturity (where the color of their pods changed from green to lemon yellow).

#### *2.3.2.2. Pod length (PL)*

Average length of 25 fully matured pods randomly taken from each five sample plants per each test genotype was measured from the pod apex to the peduncle in centimeters.

#### *2.3.2.3. Number of pods plant$^{-1}$ (PPP)*

Average number of mature pods, counted at harvest on five randomly taken plants.

#### *2.3.2.4. No. of seeds pod$^{-1}$ (SPP)*

Average number of seeds per pod, counted at harvest on five randomly taken plants, in five randomly taken pods plant$^{-1}$.

### *2.4. Data analysis*

#### *2.4.1. Analysis of variance*

The data collected from each location were subjected to analysis of variance (ANOVA) and computed with R statistical software. The data were collected in simple lattice (partially balanced or incomplete block) design (Gomez and Gomez, 1984) and analysis of variance for individual location was computed considering the general linear model as follows.

Yijl=μ+rj+gi+pl(j)+εijl

Where:

Yij=the observed value of the trait Y for the i$^{th}$ genotype in J$^{th}$ replication

μ=The general mean of trait Y,

rj=The effect of J$^{th}$ replication

gi=The effect of i$^{th}$ genotypes and (j)=block within replicate effect

εijl=The experimental error associated with the trait y for the i$^{th}$ genotype in l$^{th}$ block with in replication and j$^{th}$ replication (Table 2).

#### *2.4.2. Estimation of phenotypic and genotypic variances*

The phenotypic and genotypic variances of each trait estimated from the analysis of variance. The expected mean squares under the assumption of random effects model was computed from linear combinations of the mean squares. The phenotypic and genotypic coefficients of variations were computed as per the methods suggested by Burton and De Vane, 1953. The genetic variance of the components was estimated by considering the effects in the model as random variable using the lme4 package (Bates et al., 2015) of R software v 3.6. The genotypic variance ($\sigma^2_g$) and the environmental variance ($\sigma^2_e$) were obtained directly from variance component table generated by the software.

Table 2: Analysis of variance model for individual location

| Source of variation | DF | SS | Mean square | F value |
|---|---|---|---|---|
| Replications | r-1 | SSr | MSr | MSr/Mse |
| Treatments | t-1 | SSt | MSt | MSt/Mse |
| Block within replication (b) | r (b-1) | SSb | SSb | MSb/ Mse |
| Intra block error | (b-1) (rb-b-1) | SSe | Mse | |
| Total | TSS | | | |

r: Number of replication; t: Number of treatment; df: Degree of freedom; b: block; SS: Sum of squares, MS: mean squares; SSr and MSr are sums of squares and mean of replication, respectively; SSt and MSt are sums of squares and mean of treatments respectively; SSb and MSb are sums of squares and mean of blocks within replication respectively, SSe and MSe are sums of squares and mean of intra-block error, respectively and SST is sum of squares of the total.

#### *2.4.3. Genotypic variance for individual location*

The genotypic variance was estimated according to the method suggested by Burton and Devane (1953) considering mean square expectations from the analysis of variance as follows:

$^2$ used for field data which analysed by lattice design.

Where;

$\sigma^2$g=Genotypic variance,

Msg=Genotype/treatment mean square,

Mse=Error mean square,

r=Number of replications and

k=Number of plots with in block.

Phenotypic variance ($\sigma^2_{ph}$)=$\sigma^2_g$+ $\sigma^2_e$

Where; $\sigma^2$g=Genotypic variance and $\sigma^2_e$=error variance or error mean square.

#### *2.4.4. Estimation of genotypic and phenotypic coefficient of variations*

The genotypic and phenotypic coefficients of variability were undertaken according to the formulae of (Singh and Chaudhary, 1985).

Genotypic coefficient of variation (GCV) (%)=($\sigma_g$/grand mean)×100

Phenotypic Coefficient of variation (PCV) (%)=($\sigma_{ph}$/grand mean)×100

Where, $\sigma_g$ and $\sigma_{ph}$ are genotypic and phenotypic standard deviations, respectively.

### 2.4.5. *Estimation of heritability and genetic advance*

Heritability in broad sense for all traits was computed as suggested by (Hanson et al., 1956).

Heritability in broad sense ($H^2_b$) (%)=($\sigma^2_g/\sigma^2_{ph}$)×100

Then, the genetic advance for selection intensity (k) at 5% (2.06) was estimated by the formula (Johnson et al., 1955a); (Allard, 1960); (Rasmusson and Glass, 1967):

$EGA=k\times\sigma_{ph}\times H^2_b$

Where, EGA represents the expected genetic advance under selection; $\sigma_{ph}$ is the phenotypic standard deviation; $H^2_b$ is heritability in broad sense and k is selection intensity.

The genetic advance as percent of population mean was also estimated following the procedure.

Genetic advance per population mean (GMA) (%)=(EGA/grand mean)×100

## 3. RESULTS AND DISCUSSION

### 3.1. *Analysis of variance*

Analysis of variance (ANOVA) was computed for 8 traits of 49 field pea genotypes result are presented in Table 3. The results of ANOVA revealed that the genotypes had significant differences for days to flowering, days to maturity, grain filling period, plant height, thousand seed weight, total biomass, harvest index and yield at Asasa; and the results showed the presence of significant differences among field pea genotypes for all the traits.

The results from ANOVA showed the existence of significant variations among the 49 field pea genotypes for all the traits. The presence of significant differences among the field pea genotypes for most of morpho-agronomic traits was an indication of the potential of exploiting the observed variations in field pea improvement programs. The existence of significant differences among the field pea genotypes for days to flowering, days to maturity, plant height, 1000 seed weight and seed yield plant$^{-1}$ was also reported by other workers in Ethiopia (Assen, 2020); (Seboka and Erena, 2013); (Fikreselassie, 2012); (Siddika et al., 2013). (Kumar et al. (2013) also observed significant differences among the field pea genotypes for days to flowering, plant height,100 seed weight and seed yield plant$^{-1}$.

Table 3: The analysis of variance table for the eleven characters tested at Asasa as simple lattice design

| Traits | Rep (1) | Block (rep) (12) | Genotype (48) | Error (36) | CV (%) | F-ratio |
|---|---|---|---|---|---|---|
| Days to flowering | 2.95 | 0.7 | $27.96^{**}$ | 1.23 | 1.6 | 1.09 |
| Days to maturity | 0.01 | 1.86 | $4.58^{**}$ | 1.50 | 0.94 | 1.11 |
| Grain filling period | 2 | 3.79 | $24.08^{**}$ | 3.46 | 2.78 | 1.40 |
| Plant height (cm) | 9880.2 | 511.3 | $2616.7^{**}$ | 402.9 | 9.97 | 1.81 |
| No. of pods plant$^{-1}$ | 353.02 | 8.77 | $6.73^{ns}$ | 5.14 | 18.94 | 29.37 |
| Pod length (cm) | 0.06 | 0.09 | $0.28^{ns}$ | 0.21 | 7.01 | 1.17 |
| No. of seeds pod$^{-1}$ | 0.31 | 0.30 | $0.41^{ns}$ | 0.29 | 10.67 | 1.52 |
| Thousand seed weight (g) | 467.31 | 238.09 | $924.5^{**}$ | 135.85 | 14.25 | 1.68 |
| Biomass g plot$^{-1}$ | 636837 | 946580 | $2083924^{**}$ | 447200 | 11.94 | 2.01 |
| Yield kg ha$^{-1}$ | 192023 | 713268 | $1589336^{**}$ | 559359 | 6.49 | 2.84 |
| Harvest index (%) | 0.04 | 15.72 | $35.24^{**}$ | 8.37 | 18.75 | 2.82 |

ns, * and **, non-significant, significant at $p<0.05$ and $p<0.01$, respectively. Rep=Replication, Block (rep)=Block in replication, Geno=genotype, and F-ratio=Ratio of higher to lower error mean squares

### 3.2. *Mean performances of genotypes*

#### 3.2.1. *Phenology and growth traits*

The 49 field pea genotypes had days to flowering and days to maturity in the range between 57 and 74 and 129 and 135 days respectively. The two genotypes (GIZ-02019-2) and PDFPTp-313-062) showed early flowering (57 days), but these genotypes had non- significant difference with PDFPTp-313-015. The genotype, EH 08027-2 showed delayed flowering (74 days), but had non-significant difference with EH 08003-2, EH 08027-3, EH 08042-4, EH 08036-4 and EH 08034-2. The three genotypes (PDFPTp-313-015, GIZ-02019-1 and GIZ-02019-2) took 129 days after sowing to attain maturing while EH 08027-1, EH 08041-3 and EH 08027-3 took 135 days to attain maturity. But, most of the genotypes had non-significant differences for days to flowering and days to maturity. The grain filling period of genotypes ranged from 58 to 75 days. Thirty-seven genotypes had 65 to 69 days of grain filling period with non-significant difference, while five genotypes had 71 to 75 days of GFP with non-significant difference (Table 4 and 5).

It was observed significant variation among field pea genotypes, and the difference between early and delayed flowering and maturity was 17 and 6 days, respectively, while the difference between short and long duration of grain filling period was 17 days. These differences among field pea genotypes could be exploited in improvement programs

Table 4: Mean performance of 49 field pea genotypes for yield components and grain yield evaluated at (Asasa) in 2019 cropping season

| Genotype | DTF | DTM | GFP | PHT | TSW | GY | BM | HI |
|---|---|---|---|---|---|---|---|---|
| Bursa | 63.0 | 134.0 | 70.0 | 174.0 | 164.0 | 4182.0 | 5734.0 | 24.0 |
| Burkitu | 63.0 | 134.0 | 70.0 | 195.0 | 173.0 | 4521.0 | 5089.0 | 30.0 |
| EH 05048-5 | 64.0 | 132.0 | 68.0 | 207.0 | 206.0 | 4936.0 | 5718.0 | 27.0 |
| EH 08034-2 | 73.0 | 131.0 | 58.0 | 224.0 | 159.0 | 3559.0 | 4177.0 | 27.0 |
| EH 010006-2 | 65.0 | 133.0 | 68.0 | 194.0 | 158.0 | 3779.0 | 5320.0 | 23.0 |
| EH 08021-1 | 64.0 | 132.0 | 68.0 | 210.0 | 167.0 | 1644.0 | 2284.0 | 24.0 |
| EH 09021-5 | 63.0 | 134.0 | 71.0 | 220.0 | 156.0 | 3946.0 | 3919.0 | 32.0 |
| EH 08003-2 | 70.0 | 134.0 | 63.0 | 232.0 | 185.0 | 5190.0 | 6527.0 | 26.0 |
| EH 08036-4 | 70.0 | 134.0 | 62.0 | 214.0 | 153.0 | 3988.0 | 5253.0 | 26.0 |
| EH 010005-2 | 67.0 | 133.0 | 67.0 | 232.0 | 187.0 | 4301.0 | 6044.0 | 23.0 |
| EH 08027-2 | 74.0 | 133.0 | 59.0 | 202.0 | 138.0 | 3247.0 | 5644.0 | 18.0 |
| EH 08036-1 | 67.0 | 134.0 | 67.0 | 247.0 | 189.0 | 4000.0 | 5665.0 | 22.0 |
| EH 08041-3 | 65.0 | 135.0 | 70.0 | 219.0 | 183.0 | 3517.0 | 5170.0 | 21.0 |
| EH 07005-1 | 69.0 | 131.0 | 62.0 | 173.0 | 216.0 | 4586.0 | 5819.0 | 25.0 |
| EH 010011-3 | 67.0 | 132.0 | 66.0 | 215.0 | 217.0 | 5605.0 | 5263.0 | 33.0 |
| EH 07002-1 | 65.0 | 134.0 | 69.0 | 256.0 | 198.0 | 4059.0 | 5159.0 | 26.0 |
| EH 08021-4 | 65.0 | 132.0 | 68.0 | 228.0 | 178.0 | 4495.0 | 4402.0 | 32.0 |
| EH 010004-1 | 65.0 | 133.0 | 68.0 | 226.0 | 191.0 | 4357.0 | 4744.0 | 29.0 |
| EH 07006-5 | 67.0 | 133.0 | 66.0 | 195.0 | 190.0 | 3075.0 | 4665.0 | 21.0 |
| EH 010009-1 | 65.0 | 132.0 | 67.0 | 233.0 | 190.0 | 4304.0 | 4903.0 | 28.0 |
| EH 08042-2 | 65.0 | 133.0 | 68.0 | 263.0 | 191.0 | 3346.0 | 4473.0 | 23.0 |
| EH 07007-5 | 67.0 | 131.0 | 65.0 | 200.0 | 203.0 | 4652.0 | 5346.0 | 27.0 |
| EH 08041-4 | 69.0 | 134.0 | 66.0 | 200.0 | 189.0 | 3649.0 | 5368.0 | 23.0 |
| EH 08042-4 | 72.0 | 132.0 | 60.0 | 234.0 | 176.0 | 3625.0 | 5139.0 | 22.0 |
| EH 08041-1 | 67.0 | 132.0 | 66.0 | 221.0 | 159.0 | 4887.0 | 5918.0 | 26.0 |
| EH 010009-2 | 64.0 | 134.0 | 70.0 | 218.0 | 206.0 | 3231.0 | 3832.0 | 27.0 |
| EH 08003-1 | 66.0 | 134.0 | 69.0 | 212.0 | 189.0 | 3818.0 | 5941.0 | 21.0 |
| EK 08023-5 | 64.0 | 132.0 | 68.0 | 188.0 | 180.0 | 4941.0 | 4466.0 | 34.0 |
| EH 08016-2 | 63.0 | 132.0 | 69.0 | 203.0 | 233.0 | 5159.0 | 5189.0 | 31.0 |
| EH 08027-1 | 69.0 | 135.0 | 66.0 | 254.0 | 167.0 | 3842.0 | 5748.0 | 22.0 |
| EH 08027-3 | 73.0 | 135.0 | 62.0 | 205.0 | 144.0 | 3359.0 | 6427.0 | 16.0 |
| EK 08017-5 | 65.0 | 134.0 | 69.0 | 215.0 | 180.0 | 3742.0 | 5182.0 | 23.0 |

Table 4: Continue...

| Genotype | DTF | DTM | GFP | PHT | TSW | GY | BM | HI |
|---|---|---|---|---|---|---|---|---|
| EK 08016-4 | 64.0 | 132.0 | 69.0 | 226.0 | 223.0 | 3412.0 | 4585.0 | 25.0 |
| EK 08024-4 | 63.0 | 133.0 | 70.0 | 215.0 | 206.0 | 3573.0 | 3673.0 | 29.0 |
| EK 08017-3 | 63.0 | 131.0 | 69.0 | 234.0 | 196.0 | 4773.0 | 4942.0 | 32.0 |
| PDFPTp-313-050 | 64.0 | 134.0 | 70.0 | 223.0 | 183.0 | 4058.0 | 4822.0 | 28.0 |
| PDFPTp-313-015 | 58.0 | 129.0 | 71.0 | 113.0 | 153.0 | 2514.0 | 2889.0 | 28.0 |
| PDFPTp-313-017 | 65.0 | 132.0 | 68.0 | 190.0 | 169.0 | 4320.0 | 5289.0 | 26.0 |
| PDFPTp-313-26 | 65.0 | 133.0 | 68.0 | 214.0 | 149.0 | 3251.0 | 3970.0 | 27.0 |
| PDFPTp-313-020 | 66.0 | 130.0 | 64.0 | 199.0 | 149.0 | 4009.0 | 4379.0 | 29.0 |
| PDFPTp-313-052 | 64.0 | 131.0 | 68.0 | 196.0 | 162.0 | 4808.0 | 5389.0 | 28.0 |
| PDFPTp-313-062 | 57.0 | 132.0 | 75.0 | 223.0 | 181.0 | 4456.0 | 5542.0 | 26.0 |
| PDFPTp-313-098 | 61.0 | 133.0 | 72.0 | 220.0 | 173.0 | 4097.0 | 4468.0 | 32.0 |
| PDFPTp-313-022 | 64.0 | 130.0 | 67.0 | 234.0 | 164.0 | 3747.0 | 4644.0 | 25.0 |
| GIZ-02019-1 | 64.0 | 129.0 | 65.0 | 94.0 | 168.0 | 383.0 | 568.0 | 21.0 |
| GIZ-02019-2 | 57.0 | 129.0 | 72.0 | 93.0 | 189.0 | 4200.0 | 4177.0 | 32.0 |
| PDFPTp-313-028 | 64.0 | 133.0 | 68.0 | 185.0 | 177.0 | 3484.0 | 4884.0 | 24.0 |
| PDFPTp-313-065 | 66.0 | 131.0 | 65.0 | 127.0 | 169.0 | 4485.0 | 4273.0 | 32.0 |
| Mean | 65.4 | 132.5 | 67.2 | 206.1 | 179.7 | 3939.8 | 4854.6 | 26.2 |
| LSD (5%) | 2.25 | 2.49 | 3.77 | 40.71 | 23.64 | 1517.0 | 1356.2 | 6.48 |

DTF: days to flowering; DTM: Days to maturity; PH: Plant height; GFP: Grain filling period; HI: Harvest index; GY (kg ha$^{-1}$): Yield in kg ha$^{-1}$; TSW: Thousand seed weight; BM (g): Biomass in g plot$^{-1}$

Table 5: Estimates of mean, range, variance components, coefficient of variability, heritability and genetic advance of the eight characters studied at Asasa in 2019

| Traits | Mean | Range | $\sigma g^2$ | $\sigma ph^2$ | $\sigma e^2$ | GCV (%) | PCV (%) | $H^2$ (%) | GA (5%) | GAM (5%) |
|---|---|---|---|---|---|---|---|---|---|---|
| Days to flowering | 66 | 57-74 | 15.24 | 16.47 | 1.09 | 5.91 | 6.15 | 92.53 | 7.74 | 11.72 |
| Days to maturity | 132 | 129-135 | 1.76 | 3.26 | 1.56 | 1.00 | 1.37 | 53.93 | 2.0 | 1.52 |
| Plant height (cm) | 208 | 93-263 | 11.75 | 15.21 | 426.1 | 5.12 | 5.82 | 77.26 | 6.21 | 9.26 |
| Grain filling period | 67 | 58-75 | 1261.87 | 1664.77 | 3.48 | 17.08 | 19.62 | 75.80 | 63.71 | 30.63 |
| Harvest index (%) | 26 | 16-34 | 449.53 | 585.38 | 9.69 | 11.78 | 13.44 | 76.79 | 38.27 | 21.26 |
| Yield kg ha$^{-1}$ | 3907 | 383-5605 | 932932.7 | 1380132.68 | 541666 | 20.01 | 24.33 | 67.60 | 1635.90 | 33.88 |
| Thousand seed weight (g) | 180 | 138-233 | 587086.9 | 1146445.89 | 135.5 | 19.61 | 27.41 | 51.21 | 1129.52 | 28.91 |
| Biomass g plot$^{-1}$ | 4828 | 568-6527 | 15.32 | 23.6859 | 478276 | 15.05 | 18.72 | 64.66 | 6.48 | 24.93 |

$\sigma g^2$: Genotypic variance; $\sigma gl^2$: Variance for genotype×location interaction; $\sigma e^2$: Error variance; $\sigma ph^2$: Phenotypic variance; GCV (%): Percentage of genotypic coefficient of variation; PCV (%): Percentage of phenotypic coefficient of variation; ($H^2$) (%): Percentage of broad sense heritability; GA (5%): Absolute genetic advance at 5% selection intensity and GAM (5%): Percentage of genetic advance as percent of mean

depending on the breeding objective. In agreement to these research results, (Fikreselassie, 2012) observed significant differences among field pea genotypes for days to flowering and days to maturity. (Kumar and Jain, 2003) also observed significant variation among field pea genotypes for grain filling period.

The plant height of genotypes was in the range between 93 cm (GIZ-02019-2) and 263 cm (EH 08042-2). Among the tested genotypes, the four genotypes had shorter plant height (93 to 127 cm), but most of the genotypes had tall plant height in the range between 173 to 263 cm (Table 4 and 5). The presence of highly significant variation among field pea genotypes on plant height was reported by [Ofga, 2019] and [Sorphi et al., 2006]. Similar result also reported in field pea by [Tolessa, 2017]. The improvement of field pea focused to develop medium to short plant height field pea variety due to the fact that tall plant height associated with high incidence of lodging that consequently resulted in low productivity and low quality grain (shriveled). Therefore, combined, the four genotypes with the plant height less than 127cm in this study can be used in the crossing block to develop varieties high yielding and tolerant to lodging.

### *3.2.2. Yield components and grain yield*

The tested genotypes showed the performance differences for thousand seed weight in the range between 144.0 g (EH 08027-3) and 233.0 g (EH 08016-2). The genotype, EH 08016-4 with 223.0g and other four genotypes with 206 to 223 g thousand seed weight had non-significant difference with EH08016-2 and EH 08027-3, respectively. The two check varieties, Burkitu and Bursa had 173 and 164 g thousand seed weight, respectively. A total of 30 and 29 genotypes had higher thousand seed weight than Burkitu and Bursa, respectively (Table 4 and 5). The observed wide range of variations among genotypes for thousand seed weight showed the higher chance to identify genotypes with seeds of heavy weight and to develop as improved variety for the trait.

The three genotypes, EH 010011-3, EH 08003-2 and EK 08016-2 had significantly higher grain yield of 5605, 5190 and 5159 kg ha$^{-1}$, respectively. The two check varieties, Burkitu and Bursa had 4521 and 4182 kg ha$^{-1}$, respectively. A total of 11 genotypes had yield advantages of 1.85 to 33.79% over Bursa and 10 genotypes had 0.06 to 31.36% over Burkitu high yield variety. The lowest grain yield of 383 kg ha$^{-1}$was registered for GIZ-02019-1 (Table 4). The study showed the presence of significant difference among genotypes for grain yield that would gave a chance to selection of genotypes for higher yield than improved varieties. Moreover, eight genotypes that had higher grain yield than better performing Bursa variety also had higher thousand seed weight than this variety and Burkitu. Therefore, in this study, it was possible the selection of genotypes for higher yield and heavier seed weight to improve grain yield and seed size. (Sorphi et al., 2006) also reported significant differences among field pea genotypes for grain yield.

The genotype, EH 08003-2 had the highest biomass yield of 6527 g plant$^{-1}$, however, 24 genotypes had biomass yield non-significant difference with biomass yield of this genotype. In contrast, GIZ-02019-1 had the lowest biomass yield of 568 g plot$^{-1}$ (Table 4). The high yield Bursa variety also had the 4th higher biomass yield of 5734 g plot$^{-1}$, while Burkitu variety had 5089 g plot$^{-1}$ biomass yield and 24 genotypes had biomass yield higher than the biomass yield of this variety. On the other hand, the harvest index of genotypes ranged from EH 08027-3 (16 g plot$^{-1}$) to EK 08023-5 (34 g plot$^{-1}$). The two check varieties, Burkitu and Bursa had 30 g plot$^{-1}$ and 24 g plot$^{-1}$ harvest index, respectively. A total of 8 and 31 genotypes had harvest index higher than Burkitu and Bursa varieties, respectively (Table 4).

The genotypes that had large photosynthetic area might have a higher chance to convert the light and nutrient from soil to dry biomass. This might also contribute to the production higher grain yield by the genotypes. For instance, 8 of 10 genotypes that had yield advantages over better yielding Bursa variety also had higher biomass yield non-significant difference with this variety. However, the production of higher biomass and grain yield might not guarantee the genotypes to have higher harvest index. In support of this suggestion, (Sorphi et al., 2006) indicated that the genotypes with higher biomass have higher potential to convert light and soil nutrients to grain yield than the genotypes with lower biomass. (Sivasubramanian and Menon, 1973). Similarly, observed significant differences among field pea genotypes for biomass yield and harvest index.

### *3.3. Estimates of variability*

### *3.3.1. Genotypic and phenotypic variations*

The estimated phenotypic (PCV) and genotypic (GCV) coefficient of variations for eight traits of 49 field pea genotypes evaluated at Asasa in 2019 are presented in (Table 5). The estimates of PCV and GCV for eight traits of genotypes are presented in Table 5. The GCV and PCV were estimated in the range between 1.00% for days to maturity and 20.01% for grain yield and 1.37 for days to maturity and 27.41%, for thousand seed weight respectively, at Asasa. The lowest and highest GCV estimated for days to maturity and grain yield kg ha$^{-1}$ and the lowest and highest PCV estimated for days to maturity and thousand seed weight (g plot$^{-1}$) (Table 5). The lowest GCV and PCV were estimated for days to maturity and the highest values were estimated for grain yield kg ha$^{-1}$ (Table 5).

PCV and GCV can be categorized as low (<10%), moderate (10–20%) and high (>20%). Correspondingly, low PCV and GCV values were computed for phenology traits (days to flowering, days to maturity and plant height) and moderate values for both PCV and GCV were recorded for grain filling period, biomass g plot$^{-1}$ and harvest index. High PCV and GCV were estimated for grain yield kg ha$^{-1}$ and thousand seed weight (g plot$^{-1}$) at Asasa (Table 5).

The estimates of PCV and GCV being low and moderate for all traits except high PCV was estimated for thousand seed weight for pooled data and near to similar trends were observed for estimates of PCV and GCV for most of the traits suggested that the traits were more influenced by environmental factors and selection based on phenotypic expression of the genotypes might not be effective to improve the traits. The high estimates for these genetic parameters allow breeders to implement direct selection whereas for the traits with low and moderate estimates of these genetic parameters indicate that the breeder should employ alternative methods to create variability such as crossing. Similar result also reported for field pea genotypes evaluated at different locations (Sorphi et al., 2006).

### *3.3.2. Heritability and genetic advance*

Heritability ($H^2$) in broad sense and genetic advance as percent of mean (GAM) ranged between 51.21 (thousand seed weight) to 92 (days to flowering) and 1.52 (Days to maturity) to 33.88% (grain yield), respectively (Table 5). The ANOVA result showed that high estimate of heritability were observed for days to 50% flowering, grain filling period, plant height, harvesting index, total biomass and grain yield.

[Johnson et al., 1955a] Suggested that heritability values are low (<30%), moderate (30-60%) and high (>60%), and genetic advance as percent of mean categorized as low (<10%), moderate+(10-20%) and high (>20%). Based on this delineation, the estimates of $H^2$ and GAM of Asasa, result of analysis variance showed that both $H^2$ and GAM estimates were high for total biomass, harvesting index, grain yield, grain filling period and thousand seed weight. The high estimate of genetic advance for these traits showed the possibility of improving the populations through selection. (Seboka and Erena, 2013) Reported lower estimates of heritability for grain yield, hundred seed weight, number of pods plant$^{-1}$, plant height, number of seed plant$^{-1}$ and days to 50% flowering. (Demeke et al., 2022) Reported high broad sense heritability in days to flowering, days to maturity and 100-seed weight.

Similar to our findings, (Demeke et al., 2022) reported high genetic advance as percent of the mean for biomass yield, grain yield, thousand seed weight, plant height, grain filling period and days to flowering. (Dabi et al., 2019). Also reported high genetic advance as percent of the mean for grain yield.

The finding from our study revealed that high heritability value coupling with high genetic advance as percent of mean recorded for plant height, grain yield, thousand seed weight and total biomass. This implies these traits could be improved though direct selection or can be used as indirect selection criteria to improve seed yield or other traits if they produced strong positive correlation with the target trait. The importance of considering both the genetic advance and heritability of traits was suggested than considering them separately in how much progress can be made through selection. Thus, selection based on performances of field pea genotypes is possible for the traits that high $H^2$ and GAM were estimated. High heritability coupled with higher genetic advance were observed for grain yield, total biomass, grain filling period and harvesting index at Asasa (Table 5).

## 4. CONCLUSION

This study was conducted to assess the extent of genetic variability for yield and yield related traits in field pea. Analysis of variances showed highly significant difference among genotypes ($p \leq 0.01$). The highest heritability was obtained for days to flowering, plant height, grain filling period, yield and harvest index. The genotypes variations for grain yield in the range between 383.0 to 5605 kg ha$^{-1}$. Grain yield provide the highest genetic advance as percent of mean that can be exploited in selection.

## 5. ACKNOWLEDGEMENT

The author would like to thank breeding and genetics research division staffs of Kulumsa Agricultural Research Center who managed the field experiments. The financial support provided from government fund by Ethiopian Institute of Agricultural Research (EIAR) is also duly acknowledged.

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