

Genetic Variability and Heritability for Various Quantitative Traits in Field Pea (*Pisum sativum* L.) Genotypes in Southern Highlands of Ethiopia

Temesgen Abo^{1, *}, Wassu Mohamed², Tesfahun Alemu³

¹Kulumsa Agricultural Research Center (EIAR), Addis Ababa, Ethiopia

²School of Plant Sciences, Haramaya University, Haramaya, Ethiopia

³Holeta Agricultural Research Center (EIAR), Addis Ababa, Ethiopia

Abstract

In Ethiopia, field pea (*Pisum sativum* L.) is the major source of protein for resource poor farmers. The development of varieties for yield and disease resistance is one of the important activities to support farmers and improve the productivity of the crop. Therefore, this study was conducted to assess genetic variability and association among agronomic traits of field pea genotypes. Forty-nine field pea genotypes were evaluated in simple lattice design at Bekoji and Asasa in 2019 cropping season. Data collected for morpho-agronomic traits were subjected for analysis of variance. The analysis of variance showed significant differences among genotypes for most of the traits. The genotypes variations for grain yield in the range between 442.4 to 5148.3 kg ha⁻¹. A total of 10 genotypes had higher grain yield than high yielding check variety, Bursa (3919.23 kg ha⁻¹) of which EH 010011-3, EH 05048-5 and EK 08017-3 had 31.36, 10.69 and 10.38% yield advantages, respectively, over higher yielding check variety. The mean performance of genotype EH010011-3 was highest at Assasa and Bekoji with mean grain yield 5190 kg/ha and 4498 kg/ha respectively. Asasa was showed high environment mean yield (4028.9 kg/ha) compared to Bekoji (2866.6 kg/ha). The genotypic coefficient of variation ranged from 1.09% for days to maturity to 17.25% for grain yield, whereas the phenotypic coefficient of variation ranged from 1.23% for days to maturity to 21.67% for grain yield/ha. The estimated broad sense heritability ranged from 63% for grain yield to 94.0% for days to 50% flowering. Genetic advance as percent of mean ranged from 1.99% for days to maturity to 28.89% for total biomass. The study showed the existence of reasonable genetic variability among the field pea genotypes that could be exploited in breeding programs.

Keywords

Genetic Advance, Heritability, *Pisum sativum*, Traits, Variability

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1. Introduction

Field pea (*Pisum sativum* L.) is self-pollinated an annual herbaceous legume crop that belongs to family Leguminosae and genus *Pisum* [11]. It is a diploid species ($2n=2x=14$ chromosomes) and has determinate (bush or dwarf) or indeterminate (climbing) growth habit (majority of pea plants) [27]. The center of origin for field pea is considered the

Mediterranean to central Asia as well as the highlands of Ethiopia [9]. In Ethiopia field pea is cultivated since ancient time in Ethiopia [10] 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 [15]. Field pea grow around the world for its fresh green seeds, tender green pods, dried seeds, and soil restorative purposes [20].

* Corresponding author

E-mail address: temesgenabo2009@gmail.com (T. Abo), wasmoha@yahoo.com (W. Mohamed), setotaw2006@gmail.com (T. Alemu)

In Ethiopia, *Pisum sativum var. sativum* is grown in high altitude area (1800-3200) m.a.s.l [14]. 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 [7].

In Ethiopia, field pea is mainly used to prepare “*shiro wet*”, a stew eaten with local bread made of teff, i.e. “*Injera*”. The crop is commonly grown in association with faba bean (*Vicia faba*), and is important food, cash and “hunger break” crop in highlands of the country. Field pea supplies 344 calories, 20.1 g protein and 64.8 g carbohydrates/100g edible portion [2]. It is known as poor man’s meat in the developing world since it provides valuable cheap protein. In combination with wheat, rice and other cereals it provides a balanced diet [22] though pea protein is deficient in sulphur- containing amino acids (Cysteine and methionine) [20].

A Field pea has a dual advantage in fixing atmospheric nitrogen and serves as a “break crop” [12].

Besides to plan appropriate selection method understanding the association among traits and its effect on the target trait (like yield) will be important. Yield it is highly affected by different yield component traits that required a clear understanding how these traits affect yield and designing a selection procedure. This indicates sometimes direct selection for the target trait (grain yield) which is a polygenic trait may not be effective in unless yield contributing traits are considered during selection [24]. 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. Despite

the large number of filed pea accessions held in the gene bank of Ethiopia, limited information available on the magnitude and pattern of genetic variability for these materials. Therefore, this study was conducted in the field pea populations of the breeding program with the following specific objectives.

Objectives:

- 1) Estimate the genetic variability among the field pea genotypes for yield & yield related traits.
- 2) Estimate heritability and genetic advance of important agronomic characters of field pea genotypes.
- 3) Assess the extent of association among agronomic characters of field pea genotypes.

2. Materials and Methods

2.1. Description of the Study Area

The experiments were conducted at Bekoji and Asasa research sites of Kulumsa Agricultural Research Center during 2019 main cropping season. Bekoji is located 39°14'46"E longitude and 07°31'22"N latitude with an altitude of 2780 m.a.s.l. It receives an average annual rainfall of 1020 mm with the average annual minimum and maximum temperatures of 7.9°C and 16.6°C, respectively. The soil type of the trial site is eutric nitisols with a good drainage system. It contains 5.5% organic matter, 0.25% nitrogen and its pH is 5.35 (KARC, 2000 unpublished paper). 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 (Kulumsa Agricultural Research Center meteorology station unpublished paper).

Table 1. Description of Field pea accessions.

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

Seed Source: Kulumsa and Holeta Agricultural Research Centers.

2.2. Experimental Materials and Design

Forty-nine field pea genotypes obtained from Kulumsa and Holeta Agricultural Research Centers was used for this study. The list and description of the materials used for the study are presented in (Table 1). A plot size of 4m x 0.8m (3.2 m²) 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 m and 1.5 m, respectively. The experiment was laid out in 7 x 7 simple lattice designs at each location and each genotype was assigned randomly in blocks of each replication.

3. Results and Discussion

3.1. Analysis of Variance

Analysis of variance (ANOVA) was computed for 8 traits of 49 field pea genotypes for each location and results are presented in Table 5. 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 both locations; and the results showed the presence of significant differences among field pea genotypes over locations for all traits.

The results from ANOVA showed the existence of significant variations among the 49 field pea genotypes for all traits except location by genotype for thousand seed weight and harvest index. The results also showed the phenology growth, yield components and yield of genotypes were significantly influenced by locations and genotype x location. 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 per plant was also reported by other workers in Ethiopia [17]; [19]; [13]; [21]; [26]. [1] and [6] also observed significant differences among the field pea genotypes for days to flowering, plant height, 100 seed weight and seed yield per plant.

Table 2. Mean squares from the combined analysis of variance for eight traits of 49 field pea genotypes.

Trait	Rep*Loc (2)	Location (1)	Rep*Loc* Block (24)	Genotype (48)	Geno*Loc (48)	Error (72)	CV (%)
DTF	1.89	4508**	1.65	40.51**	4.16**	1.06	1.47
DTM	0.03	18828**	1.59	17.57**	7.95**	1.34	0.81
GFP	1.62	4990**	3.61	29.48**	14.49**	2.66	2.26
PLH	4548	185371**	332	2611**	1037**	172	9.42
TSW	246	11524**	191	1647**	214 ^{ns}	213	7.80
GY	980974	70323798**	470855	1964092**	614939*	360209	18.04
TBM	1528418	52562500**	454254	2828548**	853021**	396334	14.53
HI	3.44 ^{ns}	339**	8.30 ^{ns}	48.15**	8.86 ^{ns}	6.54	10.33

ns, *and **, nonsignificant, significant and highly significant at P<0.05 and P<0.01, respectively.

Rep= replication, Loc= location, Block)= block within replication, Geno= genotype, and CV (%) = coefficient of variation in percent. Numbers in parenthesis in each source of Variations represent degree of freedom.

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 64 and 78 and 137 and 145 days respectively. The two genotypes (GIZ-02019-2 and PDFPTp-313-015) showed early flowering (64 days), but these genotypes had non-significant difference with PDFPTp-313-062. The genotype, EH 08027-2 showed delayed flowering (78 days), but had non-significant difference with EH 08003-7, 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 137 days after sowing to attain maturing while EH 08027-1, EH 08041-4 and EH 08027-3 took 145 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 65 to 75 days. Nine genotypes had 65 to 69 days of grain filling period with non-significant difference while 34 genotypes had 71 to 75 days of GFP with non-significant difference (Tables 3 and 5).

It was observed significant variation among field pea genotypes, and the difference between early and delayed flowering and maturity was 14 and 8 days, respectively, while the difference between short long duration of grain filling period was 10 days. These differences among field pea genotypes could be exploited in improvement programs depending on the breeding objective. In agreement to this research results, [26] and [21] observed significant differences among field pea genotypes for days to flowering and days to maturity. [13] Also observed significant variation among field pea genotypes for grain filling period.

The plant height of genotypes was in the range between 89 cm (GIZ-02019-2) and 209 cm (EH 08042-2). Among the

tested genotypes the four genotypes had shorter plant height (89 to 128 cm) but most of the genotypes had tall plant height in the range between 151 to 209 cm (Table 5). The presence of highly significant variation among field pea genotypes on plant height was reported by [18] and [3]. Similar result also reported in field pea by [23]. 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 (shrivelled). Therefor the four genotypes with the plant height less than 128 cm in this study can be used in the crossing block to develop varieties high yielding and tolerant to lodging.

Table 3. Mean performance of 49 field pea genotypes for phenology and growth traits evaluated across two locations (Bekoji and Asasa) in 2019.

Genotype	Days to flowering	Days to maturity	Grain filling period	Plant height (cm)
Bursa	68.92 ^{i-m}	143.91 ^{a-g}	74.25 ^{a-c}	173.00 ^{a-g}
Burkitu	68.20 ^{j-m}	141.99 ^{a-i}	73.34 ^{a-f}	174.75 ^{a-g}
EH 05048-5	69.17 ^{i-l}	142.66 ^{a-j}	73.25 ^{a-f}	172.50 ^{b-g}
EH 08034-2	76.22 ^{a-c}	142.67 ^{a-j}	66.38 ^{l-m}	198.75 ^{a-d}
EH 010006-2	69.69 ^{h-k}	141.19 ^{d-j}	71.93 ^{a-j}	167.75 ^{c-g}
EH 08021-1	69.65 ^{h-k}	143.19 ^{a-h}	73.67 ^{a-e}	175.00 ^{a-g}
EH 09021-5	67.95 ^{j-m}	140.74 ^{f-j}	73.09 ^{a-g}	182.75 ^{a-g}
EH 08003-2	74.70 ^{b-d}	141.73 ^{b-i}	66.42 ^{l-m}	181.25 ^{a-g}
EH 08036-4	75.57 ^{b-c}	143.98 ^{a-g}	67.72 ^{i-m}	190.50 ^{a-e}
EH 010005-2	72.73 ^{d-f}	143.07 ^{a-h}	70.51 ^{c-l}	200.50 ^{a-d}
EH 08027-2	78.00 ^a	142.50 ^{a-i}	64.55 ^m	177.50 ^{a-g}
EH 08036-1	72.22 ^{e-g}	144.01 ^{a-f}	71.85 ^{a-j}	208.25 ^{a-b}
EH 08041-3	69.67 ^{h-k}	144.24 ^{a-d}	74.69 ^{a-d}	188.75 ^{a-f}
EH 07005-1	72.22 ^{e-g}	140.76 ^{f-j}	68.60 ^{g-m}	152.00 ^{f-h}
EH 010011-3	71.21 ^{f-i}	142.93 ^{a-h}	71.68 ^{a-j}	194.75 ^{a-e}
EH 07002-1	69.13 ^{i-l}	142.52 ^{a-i}	73.47 ^{a-c}	201.50 ^{a-d}
EH 08021-4	68.82 ^{j-m}	143.20 ^{a-h}	74.40 ^{a-d}	179.50 ^{a-g}
EH 010004-1	69.87 ^{g-k}	143.72 ^{a-h}	73.81 ^{a-e}	182.00 ^{a-g}
EH 07006-5	70.33 ^{f-j}	143.97 ^{a-g}	73.55 ^{a-e}	159.25 ^{c-h}
EH 010009-1	69.10 ^{i-l}	140.69 ^{g-j}	71.63 ^{a-j}	197.50 ^{a-d}
EH 08042-2	69.12 ^{j-i}	143.97 ^{a-g}	74.81 ^{a-c}	209.50 ^a
EH 07007-5	71.96 ^{f-h}	142.71 ^{a-j}	70.73 ^{b-l}	173.25 ^{a-g}
EH 08041-4	74.39 ^{c-e}	144.72 ^{a-b}	70.27 ^{d-l}	184.00 ^{a-g}
EH 08042-4	76.27 ^{a-c}	143.94 ^{a-g}	67.64 ^{j-m}	190.50 ^{a-e}
EH 08041-1	72.64 ^{d-f}	143.47 ^{a-h}	70.77 ^{a-l}	201.25 ^{a-d}
EH 010009-2	68.63 ^{j-m}	143.70 ^{a-h}	75.12 ^{a-b}	189.50 ^{a-c}
EH 08003-1	69.63 ^{h-k}	144.20 ^{a-e}	74.62 ^{a-d}	191.75 ^{a-e}
EK 08023-5	68.52 ^{j-m}	140.94 ^{e-j}	72.39 ^{a-h}	168.25 ^{c-g}
EH 08016-2	67.65 ^{k-m}	140.75 ^{f-j}	73.07 ^{a-g}	172.75 ^{a-g}
EH 08027-1	71.92 ^{f-h}	145.09 ^a	73.17 ^{a-f}	203.75 ^{a-c}
EH 08027-3	75.65 ^{a-c}	144.50 ^{a-c}	68.82 ^{f-m}	178.50 ^{a-g}
EK 08017-5	69.37 ^{i-l}	144.01 ^{a-f}	74.59 ^{a-d}	192.00 ^{a-e}
EK 08016-4	68.01 ^{j-m}	142.75 ^{a-i}	74.62 ^{a-d}	188.50 ^{a-f}

Table 3. Continued.

Genotype	Days to flowering	Days to maturity	Grain filling period	Plant height (cm)
EH 08003-7	76.87 ^{a-b}	144.01 ^{a-f}	67.09 ^{k-m}	194.75 ^{a-e}
EK 08024-4	67.13 ^{l-m}	142.04 ^{a-i}	74.74 ^{a-d}	176.00 ^{a-g}
EK 08017-3	68.40 ^{j-m}	141.31 ^{c-j}	72.87 ^{a-g}	202.00 ^{a-d}
PDFPTp-313-050	68.47 ^{j-m}	143.79 ^{a-h}	75.28 ^a	176.75 ^{a-g}
PDFPTp-313-015	64.37 ^{n-o}	136.58 ^k	72.17 ^{a-i}	94.75 ^{i-j}
PDFPTp-313-017	69.15 ^{i-l}	143.31 ^{a-h}	74.12 ^{a-e}	177.50 ^{a-g}
PDFPTp-313-26	69.13 ^{j-i}	143.38 ^{a-h}	74.33 ^{a-d}	174.00 ^{a-g}
PDFPTp-313-020	69.47 ^{j-i}	140.54 ^{h-j}	71.03 ^{a-k}	150.75 ^{g-h}
PDFPTp-313-052	68.15 ^{j-m}	141.31 ^{c-j}	73.12 ^{a-g}	166.75 ^{d-g}
PDFPTp-313-062	64.68 ^{n-o}	138.02 ^{j-k}	73.42 ^{a-e}	183.75 ^{a-g}
PDFPTp-313-098	66.71 ^{m-n}	141.26 ^{c-j}	74.65 ^{a-d}	177.00 ^{a-g}
PDFPTp-313-022	68.69 ^{j-m}	142.29 ^{a-i}	73.57 ^{a-c}	176.50 ^{a-g}
GIZ-02019-1	68.23 ^{j-m}	136.55 ^k	68.33 ^{h-m}	113.75 ^j
GIZ-02019-2	63.94 ^o	136.54 ^k	72.57 ^{a-h}	88.75 ^j
PDFPTp-313-028	69.00 ^{j-m}	143.78 ^{i-m}	74.78 ^{a-d}	151.00 ^{g-h}
PDFPTp-313-065	69.98 ^{g-k}	139.60 ^{g-k}	69.74 ^{c-l}	128.00 ^{h-i}

Mean values followed by similar letter(s) in each column had non-significant difference each other at P<0.05 using Duncan's Multiple Range Test (DMRT).

3.2.2. Yield Components and Grain Yield

The tested genotypes showed the performance differences for thousand seed weight in the range between 145.28 (EH 08027-2) and 243.95 g (EH 08016-2). The genotype, EH 010009-1 with 228.2 g and other four genotypes with 152 to 161 g thousand seed weight had non-significant difference with EH 08016-2 and EH 08027-2, respectively. The two check varieties, Burkitu and Bursa had 179.73 and 181.48 g thousand seed weight, respectively. A total of 30 and 29 genotypes had higher thousand seed weight than Burkitu and Bursa, respectively (Table 4). 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. In agreement our research results, [3], [19] and [25] observed significant differences among field pea genotypes for thousand seed weight.

The three genotypes, EH 010011-3, EH 05048-5 and EK

08017-3 had significantly higher grain yield of 5148.3, 4338.08 and 4325.9 kg ha⁻¹, respectively. The two check varieties, Burkitu and Bursa had 3919.23 and 3848.14 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 442.41 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 give 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. [3] and [25] also reported significant differences among field pea genotypes for grain yield.

Table 4. Mean performance of 49 field pea genotypes for yield components and grain yield evaluated across two locations (Bekoji and Asasa) in 2019.

Genotype	Thousand seed weight (g)	Yield kg ha ⁻¹	Biomass g/plot	Harvest index (%)
Bursa	181.48 ^{m-t}	3919.23 ^{b-g}	5358.93 ^{a-b}	23.98 ^{k-s}
Burkitu	179.73 ^{m-u}	3848.14 ^{b-h}	4400.67 ^{b-l}	28.77 ^{b-g}
EH 05048-5	205.18 ^{c-h}	4338.08 ^{a-b}	5108.93 ^{a-c}	27.42 ^{c-k}
EH 08034-2	165.63 ^{s-x}	3240.51 ^{d-k}	4324.86 ^{b-l}	24.30 ^{j-q}
EH 010006-2	164.58 ^{t-x}	3198.37 ^{d-l}	4414.83 ^{a-l}	23.90 ^{k-t}
EH 08021-1	181.10 ^{m-u}	2334.53 ^{l-m}	3017.95 ^{n-o}	24.95 ^{h-p}
EH 09021-5	165.88 ^{r-x}	3225.94 ^{d-l}	3700.67 ⁱ⁻ⁿ	28.10 ^{b-i}
EH 08003-2	194.85 ^{f-n}	3761.90 ^{b-i}	4956.25 ^{a-d}	24.10 ^{j-r}
EH 08036-4	178.30 ^{n-v}	3344.33 ^{c-k}	4778.83 ^{a-h}	22.80 ^{m-u}
EH 010005-2	188.38 ^{h-p}	3482.27 ^{b-j}	5122.99 ^{a-c}	22.00 ^{o-v}
EH 08027-2	145.28 ^y	3364.84 ^{c-k}	5297.18 ^{a-b}	20.72 ^{r-w}
EH 08036-1	185.58 ^{j-p}	3070.15 ^{f-l}	4787.15 ^{a-h}	20.55 ^{s-w}
EH 08041-3	192.58 ^{g-n}	2897.67 ^{i-m}	4506.08 ^{a-k}	21.17 ^{q-v}
EH 07005-1	214.25 ^{b-d}	3577.62 ^{b-j}	4837.15 ^{a-e}	24.00 ^{k-s}
EH 010011-3	211.20 ^{b-f}	5148.30 ^a	5288.20 ^{a-b}	31.42 ^{ab}
EH 07002-1	204.27 ^{c-i}	3242.93 ^{g-l}	4357.36 ^{b-l}	22.20 ^{n-v}
EH 08021-4	179.63 ^{m-u}	3847.01 ^{b-h}	4365.45 ^{b-l}	28.42 ^{b-h}
EH 010004-1	201.77 ^{c-j}	4031.98 ^{b-e}	4971.52 ^{a-d}	26.12 ^{e-m}
EH 07006-5	192.40 ^{g-o}	2920.42 ^{i-m}	4174.64 ^{c-m}	22.35 ^{n-v}
EH 010009-1	228.20 ^{a-b}	4080.44 ^{b-d}	4915.62 ^{a-e}	26.62 ^{c-l}
EH 08042-2	206.80 ^{c-g}	2973.76 ^{h-m}	4421.52 ^{a-l}	21.77 ^{p-v}
EH 07007-5	212.40 ^{b-e}	3921.41 ^{b-g}	4797.89 ^{a-g}	25.50 ^{g-o}
EH 08041-4	187.50 ^{i-p}	3080.38 ^{g-l}	4865.98 ^{a-e}	19.92 ^{u-w}
EH 08042-4	178.20 ^{n-v}	3328.85 ^{c-k}	5204.54 ^{a-c}	20.50 ^{s-w}
EH 08041-1	163.83 ^{u-x}	3982.15 ^{b-f}	5315.98 ^{a-b}	23.32 ^{l-u}
EH 010009-2	209.85 ^{c-g}	3314.91 ^{c-k}	4231.79 ^{c-l}	25.52 ^{f-o}
EH 08003-1	196.50 ^{e-m}	3164.41 ^{d-l}	4981.79 ^{a-d}	20.37 ^{o-w}
EK 08023-5	178.75 ^{n-u}	4035.20 ^{b-e}	3879.54 ^{e-n}	33.07 ^a
EH 08016-2	243.95 ^a	4176.66 ^{b-c}	4428.82 ^{b-l}	30.05 ^{a-c}
EH 08027-1	167.42 ^{q-x}	2964.40 ^{h-m}	4720.55 ^{a-i}	19.95 ^{u-w}
EH 08027-3	154.50 ^{w-y}	2931.01 ^{h-m}	5453.82 ^a	17.52 ^w
EK 08017-5	194.23 ^{f-n}	3165.18 ^{d-l}	4528.65 ^{a-k}	22.95 ^{m-u}
EK 08016-4	217.27 ^{b-c}	2939.31 ^{h-m}	4051.39 ^{d-n}	23.67 ^{l-v}

Table 4. Continued.

Genotype	Thousand seed weight (g)	Yield kg ha ⁻¹	Biomass g/plot	Harvest index (%)
EH 08003-7	200.38 ^{c-k}	2569.30 ^{j-m}	4003.65 ^{d-n}	21.05 ^{q-w}
EK 08024-4	199.83 ^{d-l}	3327.96 ^{c-k}	3737.84 ^{h-n}	28.45 ^{b-h}
EK 08017-3	186.88 ^{i-p}	4325.90 ^{a-b}	4695.72 ^{a-j}	29.72 ^{a-d}
PDFFTp-313-050	166.77 ^{f-x}	3079.87 ^{f-l}	3752.37 ^{g-n}	26.17 ^{e-m}
PDFFTp-313-015	183.20 ^{k-r}	2087.56 ^m	2560.70 ^o	26.20 ^{d-m}
PDFFTp-313-017	152.00 ^{x-y}	3670.22 ^{b-i}	4795.72 ^{a-f}	24.35 ^{i-q}
PDFFTp-313-26	154.20 ^{w-y}	2502.40 ^{k-m}	3146.53 ^{m-o}	25.57 ^{e-n}
PDFFTp-313-020	171.35 ^{p-w}	3237.14 ^{d-l}	3777.37 ^{f-n}	27.57 ^{e-j}
PDFFTp-313-052	186.90 ^{i-p}	4026.15 ^{b-e}	4870.72 ^{a-e}	26.52 ^{e-l}
PDFFTp-313-062	184.97 ^{j-q}	2855.96 ^{i-m}	3669.46 ^{j-n}	24.40 ^{f-q}
PDFFTp-313-098	174.87 ^{o-v}	3190.14 ^{d-l}	3444.63 ^{l-o}	29.25 ^{b-e}
PDFFTp-313-022	182.65 ^{l-s}	3130.47 ^{e-l}	4003.66 ^{d-n}	24.77 ^{f-p}
GIZ-02019-1	200.95 ^{c-j}	442.41 ⁿ	825.54 ^p	18.90 ^{v-w}
GIZ-02019-2	187.72 ^{h-p}	3351.50 ^{c-k}	3628.66 ^{k-n}	29.07 ^{b-f}
PDFFTp-313-028	192.62 ^{g-n}	3306.25 ^{c-k}	4385.56 ^{b-l}	24.30 ^{f-q}
PDFFTp-313-065	161.00 ^{v-y}	3224.58 ^{d-l}	3511.37 ^{k-o}	28.70 ^{b-g}

Mean values followed by similar letter(s) in each column had non-significant difference each other at $P \leq 0.05$ using Duncan's Multiple Range Test (DMRT).

The genotype, EH 08027-3 had the highest biomass yield of 5453.82 g/plot, 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 825.54 g/plot (Table 4). The high yield Bursa variety also had the second higher biomass yield of 5358.93 g/plot while Burkutu variety had 4400.67 g/plot biomass yield and 24 genotypes had biomass yield higher than the biomass yield of this variety. The lowest biomass yield of 825.54 g/plot was measured for GIZ-02019-1. On the other hand, the harvest index of genotypes ranged from EH 08027-3 (17.52 g/plot) to EK 08023-5 (33.07 g/plot). The two check varieties, Burkutu and Bursa had 28.77 g/plot and 23.98 g/plot harvest index, respectively. A total of 6 and 29 genotypes had harvest index higher than Burkutu 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 contributed 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 guaranteed the genotypes to have higher harvest index. In support of this suggestion, [19] and [3] 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. [5] and [25] 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 over locations (pooled data) are presented in Table 5.

It was estimated the lowest and highest GCV of 1.09 and 17.25%, respectively, while 1.23 and 21.67% of lowest and highest PCV, respectively, over two locations. 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).

According to [11] 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 grain filling period) and moderate values for both PCV and GCV were recorded for plant height, thousand seed weight, biomass g/plot and harvest index in table 5. [13] reported higher genotypic and phenotypic coefficient of variation for grain yield and number of seed per plant.

The estimates of PCV and GCV being low and moderate for all traits except high PCV was estimated for grain yield for pooled data and near to similar trends were observed for estimates of PCV and GCV for most of traits at both locations 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 [21]; [19]; [3].

3.3.2. Heritability and Genetic Advance

Heritability (H^2) in broad sense and genetic advance as percent of mean (GAM) ranged between 63 (grain yield) to 94 (days to flowering) and 1.99 (Days to maturity) to 28.89% (total biomass), respectively for combined data (Table 5). The combined ANOVA result showed that high estimate of

heritability were observed for days to 50% flowering, days to maturity, grain filling period, plant height, thousand seed weight, harvesting index and total biomass.

Johnson, Robinson and Comstock [16] 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 from combined analysis variance over locations showed that both H^2 and GAM estimates were high for plant height, total biomass, harvesting index and grain yield. The estimates of H^2 and GAM were high and moderate for thousand seed weight respectively (Table 5). The high estimate of genetic advance for these traits showed the possibility of improving the populations through selection.

Habtamu and Million [13] reported lower estimates of heritability for grain yield, hundred seed weight, number of pods per plant, plant height, number of seed per plant and days to 50% flowering. [4] Reported high broad sense heritability in days to flowering, days to maturity and 100-seed weight. [25]

Also observed high heritability in days to flowering, maturity, 1000-seed weigh and grain yield in field pea genotypes.

Habtamu and Million [13] reported lower estimates of genetic advance for number of pod per plant, number of seed per plant, number of seed per pod, plant height and days to 50% flowering.

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 can 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 [16]. 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 was observed for plant height, grain yield, total biomass and harvesting index at both locations (Table 5).

Table 5. Estimates of variability components, heritability and genetic advance for eight traits of 49 Field pea genotypes evaluated over two locations in 2019.

Trait	Mean	Range	σ_g^2	σ_{gl}^2	σ_e^2	σ_{ph}^2	GCV (%)	PCV (%)	(H^2) (%)	GA (5%)	GAM (5%)
DTF	70	64-78	9.09	4.16	1.21	9.69	4.3	4.44	94	6.01	8.57
DTM	142	137 – 145	2.41	7.95	1.35	3.09	1.09	1.23	78	2.83	1.99
GFP	72	65 – 75	3.77	14.49	2.85	5.2	2.69	3.16	73	3.41	4.73
PLH	176	89 – 209	425.68	960	262.9	557.13	11.71	13.4	76	37.2	21.9
TSW	187	145 – 244	358.1	213.72	203.9	460.1	10.12	11.47	78	34.4	18.4
GY	3326	442 -5148	325087	614939.1	376728	513451	17.25	21.67	63	934.6	28.27
TBM	4334	826 -5454	502038	853020.8	360582	682329	16.35	19.06	74	1252	28.89
HI	25	18-33	48.15	8.86	6.54	12.13	12.63	14.48	76	5.62	22.71

σ_g^2 = Genotypic variance, σ_{gl}^2 = Variance for genotype x location interaction, σ_e^2 = Error variance,

σ_{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.

4. Summary and Conclusions

This study was conducted to assess the extent of genetic variability for grain yield and yield related traits in field pea. Analysis of variances ANOVA for each character showed the existence of highly significant difference among genotypes ($p \leq 0.01$) at over location. The highest yielding genotypes obtained at both locations was recorded by EH 010011-3 (4498 kg/ha at Bekoji, 5605 kg/ha at Asasa and 5148 kgha⁻¹ at over location) that showed the potential of this variety to be released in the future. In addition, the study also showed the existence of high genetic variability among the tested field pea genotypes that can be exploited in the breeding program.

The highest heritability was obtained for days to 50% flowering, days to maturity, 1000 seed weight, plant height, grain filling period, grain yield and harvest index at both the

locations. This indicates the repeatability of the performance of the genotypes in the next generation and makes the selection program more efficient. Therefore, selection of genotypes based on character with high heritability would be more satisfactory than any other characters for breeding program. The high heritability obtained for grain yield at both locations showed direct selection for grain yield can be used to improve productivity of the field pea genotypes in this study. In similar fashion the traits with high heritability provide high genetic advance as per cent of mean in this study. At both the locations grain yield, provide the highest genetic advance as per cent of mean that can be exploited in selection. Similarly biomass, plant height and harvest index those highly related to grain yield provide high genetic advance that can support positive correlated response.

The genetic parameter estimated in this study should be used to design the breeding program of field pea in the country. In order to have more concrete result and conclusion the study should be

done by including more genotypes and tested across locations.

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