

Genetic variability in quantitative traits of field pea (*Pisumsativum*L.) genotypes at Bekoji District, Ethiopia

ABSTRACT:

*For resource-poor Ethiopian farmers, field pea (*Pisumsativum* L.) is the main source of protein. To increase the productivity of the crop and support farmers, the development of yield and disease-resistant varieties is an important activity. Thus, the purpose of this study was to examine genetic variability and associated agronomic traits among field pea genotypes. A total of 49 field pea genotypes were evaluated at Bekoji in 2020 using a simple lattice design. Analyses of variance were performed on the morpho-agronomic data collected. Most traits were significantly different among genotypes, except pod per plant, pod length, and seed per pod. Variations in genotypes for grain yield ranged from 412 to 4498 kg ha⁻¹. EH 010011-3, EH 05048-5, and EK 08017-3 were the genotypes with the most yield advantage over Bursa (3714.0 kg ha⁻¹), with yield advantages of 21.11, 1.13, and 1.19%, respectively, over the highest yielding check variety. Genotype EH 010011-3 showed the highest mean grain yield of 4498 kg/ha. Phenotypic coefficients of variation ranged from 2.33% for days to maturity to 29.40% for thousand seed weights, whereas genotypic coefficients of variation ranged from 2.20% to 24.31% for days to maturity. In general, the estimated broad sense heritability ranged from 63.85% for harvest index to 89.21% for days to maturity. The genetic advance as a percentage of mean ranged from 4.28% for days to maturity to 42.16% for grain yield. The study showed that field pea genotypes exhibit reasonable genetic variation, which could be used to develop breeding programs.*

Keywords: Genetic advance; Heritability; *Pisumsativum*; Traits; Variability

1. INTRODUCTION

Field pea is a self-pollinated and annual herbaceous legume belonging to the family Leguminosae and genus *Pisum* [15] that prefers a cool, moist climate. Generally, field peas are grown as dry seeds, but they can also be harvested as green vegetables when immature. Field peas are used in Ethiopia in the form of split, milled seeds [3]. In addition to providing dietary protein to the farming community, it is also cost-effective compared to animal protein, thus complementing and supplying the cereal-based sector of the urban poor. Extensive areas of the central and northern highlands of Ethiopia are cultivated with field pea.

The Pea plant has two pairs of chromosomes ($2n=2x=14$) and can grow in a bush or dwarf form or a climbing form (the majority of peas) [40]. Historically, field pea has been grown in the Mediterranean and central Asian regions, as well as in the Ethiopian highlands. Field peas have been cultivated in Ethiopia since ancient times [13], and their wild and primitive forms have been hidden in the highlands. The fact that Ethiopia has a variety of field peas makes it one of the centers of field pea diversity [20]. Globally, field peas are grown for their fresh green seeds, tender green pods, dried seeds, and soil restorative properties [26]. It contributes significantly to soil fertility restoration and is an inexpensive and valuable protein source. Peas grown in high-altitude areas (1800-3200) m.a.s.l. [19]. Among the highland pulse crops, Field pea is the third most important staple food legume crop in Ethiopia after faba bean and common bean. An average yield of 1.664 t ha⁻¹ is obtained from about 216,786.33 hectares of arable lands, covering 3,608,112.40 quintals of production. The area covered by pulses is 12.73 percent [11].

In Traditionally, Ethiopians eat field pea as part of their "Shiro wet", which is a stew served with local bread made of teff, or "Injera". Food, cash, and hunger relief crops are grown with fava beans (*Vicia faba*) in the highlands of the country. There are 344 calories, 20.1 grams of protein, and 64.8 grams of carbohydrates in 100 grams of edible field peas. As a cheap source of protein, it is often referred to as poor man's meat in developing countries. Although pea protein is deficient in sulfur-containing amino acids (Cysteine and methionine), it can still provide a balanced diet in combination with wheat, rice, and other cereals [29]. A Field pea has a dual advantage in fixing atmospheric nitrogen and serves as a "break crop" [16].

Field peas are an important crop in Ethiopia, but they are severely constrained by aphids, low-yielding local varieties, lodging, diseases (ascochyta blight, powdery mildew), and pod shattering. The fungus spreads via air currents, while rain controls the disease by washing away spores and preventing them from germinating [20]. The development of resistant varieties is the most effective management strategy against pathogens [30]. The high diversity of field pea accessions can be attributed to the strong representation of its centers of domestication, the Near East and Mediterranean [39], as well as other centers of diversity, including Central Asia and Ethiopia [37].

Ethiopia is a secondary center of genetic diversity for field peas due to the diversity of its germplasm [17]. Through selection and/or hybridization breeding programs, Ethiopia has the potential to improve field pea for desired traits.

In order for a breeding program to be successful, genetic variability must be taken into account. In field pea breeding programs, landraces and accessions are selected and evaluated based on the existing diversity [33]. This indicates a great deal of potential for the breeding program. Selection among a diverse population can provide a certain level of success in breeding, but crossings are necessary to combine different contrasting genotypes to create a hybrid that combines the traits of interest and produces heterosis [1], [28],[32];38]; [9].

As a result, this study was conducted using field pea populations from the breeding program with the following specific objectives.

❖ **Objectives:**

- ❖ Estimate the genetic variability in yield and yield-related traits among field pea genotypes.
- ❖ Determine the degree of association between agronomic characteristics of field pea genotypes.

2. MATERIALS AND METHODS

2.1. Description of the Study Area

During the 2020 main cropping season, the experiments were carried out at the Kulumsa Agricultural Research Center's Bekoji research site. 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 nitisols with a good drainage system. It has a PH of 5.35 [31], 5.5% organic matter, and 0.25% nitrogen.

2.2. Experimental Materials and Design

This study used 49 field pea genotypes obtained from Kulumsa Agricultural Research Centers. The materials used for the research are listed and described in (Table1). This study used a plot size of 4m x 0.8m (3.2m²), with each plot consisting 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 distances between plots and blocks were 1m and 1.5m, respectively. The experiment was set up in 7 x 7 simple lattice designs, with each genotype randomly assigned in blocks of each replication.

Table 1: Description of Fieldpea Genotype

Acc.code	Genotype name	Acc.code	Genotype name
G-1	Bursa	G-26	EH 010009-2

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

Seed Source: Kulumsa Agricultural Research Centers

3.RESULTS ANDDISCUSSION

3.1. Analysis of Variance

The results of an analysis of variance (ANOVA) for eight traits of 49 field pea genotypes for Bekoji are presented in Table 2. 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 grain yield at Bekoji; and the results showed the presence of significant differences among field pea genotypes for all traits, except the number of pod per plant, pod length and the number of seed per pod.

Observed variations in morpho-agronomic traits among the field pea genotypes indicate the potential for exploiting those variations in field pea improvement programs. Several other Ethiopian researchers reported significant differences between field pea genotypes for days to flowering, days to maturity, plant height, 1000 seed weight, and seed yield per plant [22]; [25]; [18]; [27]; [36]. [2] [7].

Table 2. Analysis of variance for eleven traits tested at Bekoji in a simple lattice design

Trait	Rep (1)	Block (rep)(12)	Genotype (48)	Error (36)	CV (%)
Days to flowering	0.83	1.29	16.72**	1.34	1.53
Days to maturity	0.04	0.79	20.94**	1.35	0.72
Grain filling period	1.24	1.61	19.88**	2.47	1.9
Plant height (cm)	1528.26	80.07	979.43**	123.87	7.3
Number of pods per plant	2.24	0.095	0.175ns	0.175	14.03
Pod length (cm)	0.02	0.15	0.28ns.	0.18	7.5
Number of seeds per pod	3.31	0.33	0.51ns	0.44	16.35
Thousand seed weight (g)	25.21	327.16	936.1**	228.36	8.1
Biomass g/plot	2420000	329561	1597645**	222924	12.8
Yield kg ha ⁻¹	1334978	198642	945853**	197041	16.5
Harvest index (%)	5.88	1.53	22.72**	2.97	6.9

3.2. Mean Performances of Genotypes

3.2.1. Phenology and Growth Traits

Depending on the cultivar, flowering time ranged from 72 to 82 days, and maturing time ranged from 144 to 156 days. There was no significant difference between GIZ-02019-2 and PDFPTp-313-015, but these genotypes had an early flowering period (72 days). Despite being a late flowerer (82 days), EH 010009-1 showed no significant difference from GIZ-02019-1, PDFPTp-313-028, and PDFPTp-313-065. A PDFPTp-313-015, GIZ-02019-1, GIZ-02019-2, and PDFPTp-313-062 genotype reached maturity within 144 days after sowing. A PDFPTp-313-015, GIZ-02019-1, GIZ-02019-2, and PDFPTp-313-062 genotype reached maturity within 156 days.

In terms of days to flowering and days to maturity, most genotypes had non-significant differences. Grain filling periods ranged from 70 to 82 days for genotypes. Ten genotypes had grain filling periods of 64 to 69 days with no significant difference while 35 genotypes had grain filling periods of 71 to 75 days. It was observed significant differences in flowering and maturity timing between field pea genotypes, with an early flowering date being 10 days earlier than a delayed maturity date. Comparatively, there was a 10-day difference between the short and long grain filling periods. Based on the breeding objective, these differences among field pea genotypes could be exploited in improvement programs. This research result is supported by the results of [36] and [27], which observed significant differences among pea genotypes in the number of days to flowering and days to maturity. [18] There was also a significant variation in grain filling period between field pea genotypes.

Depending on the genotype, the plants could reach heights between 75 cm (EH 08041-01) and 182 cm (PPTP-313-015). The twenty-eight genotypes tested had shorter plant heights (75 to 150 cm), but most genotypes had taller plant heights between 152 and 182 cm. There is a highly significant

difference in plant height between field pea genotypes, as reported in [23] and [5]. There was a similar result reported by [34] for field peas as well. Due to the fact that tall plant height is associated with high lodging, which in turn results in low productivity and poor grain quality (shriveled), field pea varieties were developed with medium to short plant heights. Therefore the twenty-eight genotypes with a plant height less than 150 cm 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

For thousand seed weights of 151g (EH 08027-2) to 263g (EH 010009-1), genotypes showed differences in performance. In the two check varieties, Burkitu and Bursa, the thousand seed weight was 196 and 185 grams, respectively. Compared to Burkitu and Bursa, 33 genotypes had higher thousand seed weights. It is more likely to identify genotypes with heavy seeds and develop improved varieties based on the wide range of variation observed among genotypes for thousand seed weight. We observed significant differences in thousand seed weights between field pea genotypes in studies [5]: [25] and [35].

The grain yields of the four genotypes, EH 010011-3, EK 08017-3, EH 05048-5, and EH 010009-1, were significantly higher, at 4498, 3758, 3756, and 3735 kg ha⁻¹, respectively. Burkitu and Bursa, the two control varieties, had 3348 and 3714 kg ha⁻¹, respectively. GIZ-02019-1 produced the lowest grain yield of 412 kg ha⁻¹. The study found a significant difference in grain yield between genotypes, allowing for genotype selection for higher yield than improved varieties. Furthermore, eight genotypes with higher grain yield than the superior Bursa variety also had higher thousand seed weight than this variety and Burkitu.

EH 080424 had the highest biomass yield of 5449g ha¹. GIZ020191 had the lowest biomass yield of 784g ha¹. The high yielding Bursa variety also had the third highest biomass yield of 5050 g ha¹, while the Burkitu variety had 3903g ha¹ biomass yield. GIZ020191 had the lowest biomass yield (784 g ha¹). The harvest index of genotypes, on the other hand, ranged from GIZ020191(17 g ha¹) to EH 080235. (32.0 g ha¹). Burkitu and Bursa had harvest indexes of 25.0g ha¹ and 28.0g ha¹, respectively. Harvest indexes were higher in 2 and 15 genotypes than in Burkitu and Bursa varieties, respectively.

Genotypes with a large photosynthetic area may have a better chance of converting light and nutrients from the soil to dry biomass. This may have also contributed to the genotypes' higher grain yield. For example, 8 of 10 genotypes that had yield advantages over the higher yielding Bursa variety also had higher biomass yield, though the difference was not statistically significant. However, higher biomass and grain yield may not guarantee that the genotypes will have a higher harvest index. [25, 5] provided evidence that genotypes with higher biomass have a greater potential to convert light and soil nutrients to grain yield than genotypes with lower biomass. [4] And [35]

Table 3. The mean values of the studied 49 genotypes of field pea for the eight characters at Bekoji 2020 cropping season.

Genotype	DTF	DTM	GFP	PHT	TSW(g)	GY g/ha	TBM g/ha	HI (%)
Bursa	74	153	79	171	196	3714	5050	25
Burkitu	73	150	77	158	185	3348	3903	28
EH 05048-5	74	154	80	139	205	3756	4660	28
EH 08034-2	80	155	75	173	174	2772	4151	23
EH 010006-2	75	150	76	143	172	2642	3466	25
EH 08021-1	76	155	80	139	190	3049	3833	27
EH 09021-5	73	148	75	146	180	2667	3364	26
EH 08003-2	79	149	70	130	200	2384	3462	23
EH 08036-4	81	155	74	169	201	2684	4504	21
EH 010005-2	79	153	74	168	191	2713	4455	21
EH 08027-2	82	152	70	150	151	3300	4779	23
EH 08036-1	78	154	77	172	187	2031	3630	19
EH 08041-3	75	154	80	160	198	2432	3931	21
EH 07005-1	76	150	75	131	217	2522	3464	24
EH 010011-3	76	154	78	177	202	4498	5260	29
EH 07002-1	73	151	78	147	210	2070	3792	18
EH 08021-4	73	154	81	129	182	3330	4627	24
EH 010004-1	75	155	80	135	211	3406	4979	23
EH 07006-5	74	155	81	126	200	2553	3530	24
EH 010009-1	73	150	77	161	263	3735	5098	25
EH 08042-2	74	155	82	156	223	2402	3894	21
EH 07007-5	78	155	77	147	219	2881	4227	23
EH 08041-4	81	156	75	170	189	2029	4640	17
EH 08042-4	81	156	75	145	181	2861	5449	18
EH 08041-1	79	155	76	182	167	2752	4484	21
EH 010009-2	73	154	81	162	216	3387	4859	23
EH 08003-1	74	154	81	170	201	2585	4221	20
EK 08023-5	73	150	77	148	177	3044	3022	32
EH 08016-2	73	150	78	142	251	3163	3755	28
EH 08027-1	75	156	81	156	169	2141	3769	19
EH 08027-3	79	154	76	152	168	2437	4526	19
EK 08017-5	74	154	80	166	206	2764	3886	23
EK 08016-4	73	154	81	153	219	2547	3701	23

Table 3 continue

Genotype	DTF	DTM	GF	PHT	TSW(g)	GY g/ha	TBM g/ha	HI (%)
EK 08024-4	73	151	79	137	195	2944	3394	28
EK 08017-3	74	151	77	170	205	3758	4497	28
PDFPTp-313-050	73	154	81	132	193	2178	2870	24
PDFPTp-313-015	72	144	73	75	180	1602	2199	25
PDFPTp-313-017	74	154	80	162	198	2848	4074	24
PDFPTp-313-26	74	154	81	135	154	1830	2466	25
PDFPTp-313-020	73	151	78	103	160	2524	3098	26
PDFPTp-313-052	73	152	79	139	181	3046	3827	26
PDFPTp-313-062	72	144	72	145	192	1455	2097	22
PDFPTp-313-098	72	150	78	136	198	2386	2840	27
PDFPTp-313-022	74	154	80	117	190	2452	3555	23
GIZ-02019-1	73	144	72	134	198	412	784	17
GIZ-02019-2	72	144	73	85	211	2414	3103	26
PDFPTp-313-028	74	155	81	116	200	3084	3983	26
PDFPTp-313-065	74	148	75	129	211	2023	2544	26
Mean	75	152	77	145	195	2699	3827	24
LSD (5%)	2.35	2.36	3.19	22.57	30.65	900.25	957.56	3.56

3.3. Estimates of Variability

3.3.1. Genotypic and Phenotypic Variations

The predicted PCV and GCV coefficients of variation for eight variables among 49 field pea genotypes assessed in Bekoji during the main cropping season of 2020. The genotypic and phenotypic coefficients of variation fell within the respective ranges of 2.20 to 24.31% and 2.33% to 29.40%. For days to maturity and thousand seed weight g/ha, respectively, the lowest and greatest GCV and PCV estimates were made.

According to [14], PCV and GCV can be classified as low (less than 10%), moderate (10-20%), or high (greater than 20%). Low PCV and GCV values were calculated for phenology traits (days to flowering, days to maturity, and plant height), moderate PCV and GCV values were calculated for grain filling period, harvest index, and total biomass g ha⁻¹, and high PCV was calculated for thousand seed weight (g/plot) and grain yield kg ha⁻¹. [18] Grain yield and number of seeds per plant had higher genotypic and phenotypic coefficients of variation.

Breeders can use direct selection for traits with high estimates of these genetic parameters, whereas traits with low and moderate estimates of these genetic parameters indicate that the breeder should use alternative methods to create variability, such as crossing. Similar results have been reported for field pea genotypes tested in different locations [27], [25], and [5].

3.3.2. Heritability and Genetic Advance

Broad sense heritability (H^2) was estimated to be between 63.85 (Harvest index) and 89.21% (days to maturity) for eight traits of 49 field pea genotypes at the Bekoji site, while genetic advance as percentage of mean (GAM) ranged from 4.28 (Days to maturity) to 42.16% (grain yield). [21] Heritability values are suggested to be low (30%), moderate (30-60%), and high (>60%), and genetic advance as a percentage of mean is classified as low (1%), moderate (10-20%), and high (> 20%). Both H^2 and GAM estimates were high for days to 50% flowering, days to maturity, plant height, grain filling period, harvesting index, thousand seed weight, grain yield, and total biomass based on this delineation.

The high estimate of genetic progress for these traits indicated the possibility of improving the populations through selection. [18] Lower heritability estimates for grain yield, hundred seed weight, number of pods per plant, plant height, number of seeds per plant, and days to 50% flowering were reported. [6] Broad sense heritability was reported to be high in days to flowering, days to maturity, and 100-seed weight. [35] Field pea genotypes also showed high heritability in terms of days to flowering, maturity, 1000-seed weight, and grain yield. Lower genetic advance estimates for number of pods per plant, number of seeds per plant, number of seeds per pod, plant height, and days to 50% flowering were reported [18].

Our findings revealed that high heritability value was associated with high genetic advance as a percentage of mean for grain filling period, grain yield, thousand seed weight, and total biomass. This means that if these traits produce a strong positive correlation with the target trait, they can be improved through direct selection or used as indirect selection criteria to improve seed yield or other traits. The importance of considering both genetic advance and heritability of traits in determining how much progress can be made through selection has been suggested [21]. Thus, selection based on field pea genotype performance is possible for traits with high H^2 and GAM estimates.

Table 4. Estimates of mean, Range, Variance components, Coefficient of Variability, heritability and Genetic advance of the eight characters studied at Bekoji in 2020

Trait	Mean	Range	σ_g^2	σ_{ph}^2	σ_e^2	GCV (%)	PCV (%)	H^2 (%)	GA (5%)	GAM (5%)
DTF	75	72-82	8.77	10.11	1.32	3.95	4.24	86.74	5.681	7.57
DTM	152	144-156	11.17	12.52	1.18	2.20	2.33	89.21	6.502	4.28
PLHT	145	75-182	9.92	12.39	112.54	4.09	4.57	80.07	5.807	7.54
GFP	77	70-82	487.67	611.54	2.23	15.23	17.05	79.74	40.62	28.02

HI (%)	23	17-32	403.41	631.77	2.61	10.30	12.89	63.85	33.06	16.96
GY	2687	412-4498	783590.97	1006514.9	197255	23.20	26.29	77.85	1608.9	42.16
TSW	195	151-263	426822.84	623863.8	248.5	24.31	29.40	68.42	1113.19	41.43
TBM	3816	784-5449	11.26	14.23	239663	14.59	16.40	79.12	6.148	26.73

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

The purpose of this study was to determine the degree of genetic variability in field pea grain yield and yield-related traits. Except for the number of pods per plant, pod length, and number of seeds per pod, the analysis of variance revealed highly significant variations ($p < 0.01$). The highest yielding genotype (EH 010011-3) was obtained at Bekoji, indicating that this variety has the potential to be released in the future. Furthermore, the study revealed a high genetic variability among the tested field pea genotypes, which can be used in the breeding program.

Days to 50% flowering, days to maturity, 1000 seed weight, plant height, grain filling period, grain yield, harvest index, and total biomass had the highest heritability. This indicates that the genotypes' performance will be repeatable in the next generation, making the selection program more efficient. As a result, selecting genotypes based on heritability would be preferable to any other character for a breeding program. In this study, traits with high heritability provide high genetic advance as a percentage of mean. Similarly, biomass, plant height, and harvest indexes, which are highly related to grain yield, provide high genetic advance, which can support a positive correlated response. The study showed the presence of genetic variability among the genotypes that can be exploited in the breeding program. The genetic parameter estimated in this study should be used to design the breeding program of field pea in the country.

Because the results were only obtained from one location, more testing in different environments is required to identify the genotypes that perform the best. Furthermore, performing multiple field pea accessions in different environments may reveal the genotypes' genetic potential, making it easier to select the best traits for future field pea breeding programs.

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