Genetic variability in quantitative traits of field pea (*Pisum sativum* L.) genotypes at Bekoji District, 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 in 2020 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, except pod per plant, pod length and seed per pod. The genotypes variations for grain yield in the range between 412 to 4498 kg ha^{-1}. A total of four genotypes had higher grain yield than high yielding check variety, Bursa (3714.0 kg ha^{-1}) of which EH 010011-3, EH 05048-5 and EK 08017-3 had 21.11, 1.13 and 1.19% yield advantages, respectively, over higher yielding check variety. The mean performance of genotype EH010011-3 was highest with mean grain yield 4498 kg/ha .The genotypic coefficient of variation ranged from 2.20% for days to maturity to 24.31% for thousand seed weight, whereas the phenotypic coefficient of variation ranged from 2.33% for days to maturity to 29.40 % for thousand seed weight. The estimated broad sense heritability ranged from 63.85% for harvest index to 89.21% for days to maturity. Genetic advance as percent of mean ranged from 4.28% for days to maturity to 42.16% 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: Genetic advance; Heritability; *Pisum sativum;* Traits; Variability

1. INTRODUCTION

Field pea (*Pisum sativum* L.) is self-pollinated an annual herbaceous legume crop that belongs to family Leguminosae and genus *Pisum* **[15]** and better adapted to cool moist climate. Field pea is grown predominantly as a dry seed, but can also be harvested immature as a green vegetable. In Ethiopia field pea is used in the form of split, milled seeds **[3]**. It is a good source of dietary protein which is practically cheaper than animal protein thereby supplementing and complementing the cereal based sector of the farming community and the low income urban population Extensive areas of the central and northern highlands of Ethiopia are cultivated with field pea.

It is a diploid species (2n=2x=14 chromosomes) and has determinate (bush or dwarf) or indeterminate (climbing) growth habit (majority of pea plants) **[39]**. The center of origin for field pea is considered the Mediterranean to central Asia as well as the highlands of Ethiopia **[12]**. In Ethiopia field pea is cultivated since ancient time in Ethiopia **[13]** 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 **[20]**. Field pea grow around the world for its fresh green seeds, tender green pods, dried seeds, and soil restorative purposes **[26]**.

In Ethiopia, *Pisum sativum* is grown in high altitude area (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 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 **[11].**

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 **[3]**. 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 **[29]** though pea protein is deficient in sulphur- containing amino acids (Cysteine and methionine) **[26]**.

A Field pea has a dual advantage in fixing atmospheric nitrogen and serves as a “break crop” [**16]**.

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. This fungus spread locally with air currents, whereas rain controls the disease by washing off spores and making them burst instead of germinating **[20]**. The most preferable management measure against the pathogen is developing resistant varieties **[30]**. 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 **[38]** and other centers of diversity, including Central Asia and Ethiopia **[36]**.

The existence of wide range of field pea germplasm in Ethiopia makes the country the secondary center of genetic diversity **[17]**. This indicates that has Ethiopia the potential for improving field pea for desired traits either through selection and/or hybridization breeding programs.

Genetic variability is the key factor for the success of any breeding program. In field pea, studies showed that the landraces and accessions in the breeding programs are focused on selection and evaluation from the existing diversity **[32]**. That indicates the great potential for the breeding program. Even selection among a diverse population provide a certain amount of success in the breeding program, crossing will be essential to combine to different contrasting genotypes to produce a hybrid that combine the trait of interest and produce heterosis **[1], [28],[31]; 37]; [9]**.

Therefore, this study was conducted in the field pea populations of the breeding program with the following specific objectives.

❖ Objectives:

- Estimate the genetic variability among the field pea genotypes for yield & yield related traits.
- 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 research site of Kulumsa Agricultural Research Center during 2020 main cropping season. Bekoji is located 39°14’46’’E longitude and 07^{o}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 nitisols with a good drainage system. It contains 5.5% organic matter, 0.25% nitrogen and its PH is 5.35 (KARC, 2000). (Kulumsa Agricultural Research Center meteorology station unpublished paper).

2.2. Experimental Materials and Design

Forty-nine field pea genotypes obtained from Kulumsa Agricultural Research Centers was used for this study. The list and description of the materials used for the study are presented in (Table1). A plot size of 4m x 0.8m (3.2m^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 1m and 1.5m, respectively. The experiment was laid out in 7 x 7 simple lattice designs at each genotype was assigned randomly in blocks of each replication.

Table 1: Description of Field pea accetions

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 AND DISCUSSION

3.1. Analysis of Variance

Analysis of variance (ANOVA) was computed for 8 traits of 49 field pea genotypes for Bekoji and results 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 number of pod per plant, pod length and number of seed per pod.

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 **[22]; [25]; [18]; [27]; [35]**. **[2]** And **[7]** 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. The analysis of variance table for the eleven characters tested at Bekoji as 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

The 49 field pea genotypes had days to flowering and days to maturity in the range between 72 and 82 and 144 and 156 days respectively. The four genotypes (GIZ-02019-2 and PDFPTp-313-015) showed early flowering (72 days), but these genotypes had non-significant difference with PDFPTp-313-062. The genotype, EH 010009-1 showed delayed flowering (82 days), but had non-significant difference with GIZ-02019-1, PDFPTp-313-028 and PDFPTp-313-065. The three genotypes (PDFPTp-313-015, GIZ-02019-1, GIZ-02019-2 and PDFPTp-313-062) took 144 days after sowing to attain maturing while EH 08027-1, EH 08041-4 and EH 08042-4 took 156 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 70 to 82 days. Ten genotypes had 64 to 69 days of grain filling period with non-significant difference while 35 genotypes had 71 to 75 days of GFP with non-significant difference.

It was observed significant variation among field pea genotypes, and the difference between early and delayed flowering and maturity was 10 and 12 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, **[35]** and **[27]** observed significant differences among field pea genotypes for days to flowering and days to maturity. **[18]** Also observed significant variation among field pea genotypes for grain filling period.

The plant height of genotypes was in the range between 75 cm (PPTp-313-015) and 182 cm (EH 08041-1). Among the tested genotypes the twenty eight genotypes had shorter plant height (75 to 150 cm) but most of the genotypes had tall plant height in the range between 152 to 182 cm. The presence of highly significant variation among field pea genotypes on plant height was reported by **[23]** and **[5]**. Similar result also reported in field pea by **[33]**. 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 (shriviled). Therefor the twenty eight genotypes with the 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

The tested genotypes showed the performance differences for thousand seed weight in the range between 151g (EH 08027-2) and 263g (EH 010009-1). The two check varieties, Burkitu and Bursa had 196 and 185g thousand seed weight, respectively. A total of 33 and 23 genotypes had higher thousand seed weight than Burkitu and Bursa, respectively. 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, **[5]**: **[25]** and **[34]** observed significant differences among field pea genotypes for thousand seed weight.

The four genotypes, EH 010011-3, EK 08017-3, EH 05048-5 and EH 010009-1 had significantly higher grain yield of 4498, 3758, 3756 and 3735 kg ha^{-1}, respectively. The two check varieties, Burkitu and Bursa had 3348 and 3714 kg ha^{-1}, respectively. The lowest grain yield of 412 kg ha^{-1} was registered for GIZ-02019-1. 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. **[5]** And **[34]** also reported significant differences among field pea genotypes for grain yield.

The genotype, EH 08042-4 had the highest biomass yield of 5449g ha^{-1}. In contrast, GIZ-02019-1 had the lowest biomass yield of 784g ha^{-1}. The high yield Bursa variety also had the third higher biomass yield of 5050 g ha$^{-1,}$ while Burkitu variety had 3903g ha^{-1} biomass yield. The lowest biomass yield of 784 g ha^{-1} was measured for GIZ-02019-1. On the other hand, the harvest index of genotypes ranged from GIZ-02019-1(17 g ha^{-1}) to EH 08023-5 (32.0 g ha^{-1}).The two check varieties, Burkitu and Bursa had 25.0g ha^{-1} and 28.0g ha^{-1} harvest index , respectively. A total of 2 and 15 genotypes had harvest index higher than Burkitu and Bursa varieties, respectively.

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 guarantee the genotypes to have higher harvest index. In support of this suggestion, **[25]** and **[5]** 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. **[4]** And [**34]** similarly observed significant differences among field pea genotypes for biomass yield and harvest index.

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 estimated phenotypic (PCV) and genotypic (GCV) coefficient of variations for eight traits of 49 field pea genotypes evaluated at Bekoji in 2020 main cropping season. The phenotypic and genotypic coefficients of variation ranged from 2.33% to 29.40% and 2.20 to 24.31%, respectively. The lowest and highest GCV and PCV estimated for days to maturity and thousand seed weight g/ha, respectively.

According to **[14]** 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, harvest index and total biomass g ha^{-1}, while high PCV was estimated for thousand seed weight (g/plot) and grain yield kg ha^{-1}. **[18]** Reported higher genotypic and phenotypic coefficient of variation for grain yield and number of seed per plant.

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 **[27]; [25]; [5]**.

3.3.2. Heritability and Genetic Advance

Broad sense heritability (H^2) estimated for eight traits of 49 field pea genotypes at Bekoji site was in the range between 63.85 (Harvest index) and 89.21% (days to maturity), while genetic advance as percentage of mean (GAM) ranged from 4.28 (Days to maturity) to 42.16% (grain yield). **[21]** 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, 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. The high estimate of genetic advance for these traits showed the possibility of improving the populations through selection.

[18] 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. **[6]** Reported high broad sense heritability in days to flowering, days to maturity and 100-seed weight. **[34]** Also observed high heritability in days to flowering, maturity, 1000-seed weight and grain yield in field pea genotypes. **[18]** 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 grain filling period, 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 **[21]**. Thus selection based on performances of field pea genotypes is possible for the traits that high H^2 and GAM were estimated.

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**	**σg^2**	**σph^2**	**σe^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

σg^2 = Genotypic variance , σgl^2 = Variance for genotype x location interaction, σe^2 = Error variance, σph^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 ($p \leq 0.01$) except number of pod per plant, pod length and number of seed per pod. The highest yielding genotypes obtained at Bekoji was recorded by EH 010011-3 (4498 kg/ha), 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, harvest index and total biomass. 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. In similar fashion the traits with high heritability provide high genetic advance as percent of mean in this study. Similarly biomass, plant height and harvest index those highly related to grain yield provide high genetic advance that can support 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. In order to have more concrete result and conclusion the study should be done by including more genotypes and tested across locations.

This result being from one location, it is recommended for further testing in diverse environments to identify favorable environments for genotypes. It needs further studies on field pea to identify and select genotypes that have important agronomic properties and use them in direct hybridization. It should be worthwhile to study more available germplasm over years and locations to identify more accessions as well as to confirm the importance of the traits identified as predictors of yield.

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