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Genetic Variability, Heritability and Genetic Advance for Agronomic Traits in Field Pea (*Pisum sativum* L.) Gene Pools

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ABSTRACT

A total of 49 field pea genotypes were grown in 7 x 7 simple lattice design at two environments in south-eastern highlands of Ethiopia during 2018/19 main cropping season to study genetic variability, heritability and genetic advance for grain yield and yield-related traits. The combined / pooled/ analysis of variance revealed that there was a significant difference ($p< 0.001$) among the 49 field pea genotypes for all the characters studied, except for number of seeds per pod, which was non-significant. High phenotypic coefficient of variation and genotypic coefficient of variation were recorded for grain yield, and moderate values for 1000-seed weight and plant height was observed across locations. Estimates of heritability ranged from 23.66 % for ascocayta blight to 90.73 % for days to flowering, while grain yield showed 63.18 % heritability. High genotypic coefficient of variation along with high heritability coupled with genetic advance as percent over mean was observed for grain yield per ha and moderate genotypic coefficient of variation along with high heritability coupled with moderate or relatively high value of genetic advance as percent over mean in plant height and seed size was observed across locations; indicating the importance of this trait in yield improvement of field pea.

Key words: Genetic advance, genotype, Heritability, *Pisum sativum*, Variability

Abbreviations: GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; GA: Genetic Advance; GAM: Genetic Advance in Percent of Mean, h^2 (b): Broad sense heritability

INTRODUCTION

Pulses are the second most important crops in Ethiopia both in terms of area coverage and in terms of total production after cereals. Field pea is the fourth most important legume crop in Ethiopia after faba bean, haricot bean and chick pea in terms of both area and total amount of production (CSA, 2018). It is grown on 220,508.39 hectares of land with total production of 3,685,190.65 quintals and productivity of 16.71 qt ha^{-1}; which accounts for 13.79 % of the total area covered by pulses and 12.37 % of the total pulses production in the country (CSA, 2018). The species *P. sativum* is known to dominate the production system, though wild and primitive forms are also known to exist in the high elevations of the country (Musa *et al*., 2006).

Ethiopia, Western and Central Asia and the Mediterranean region are proposed as possible centers of origin for field pea because of the high pea genetic diversity sampled in these regions (Messiaen *et al*., 2006). Field pea is grown by small-scale farmers on marginal lands with minimum management practices as compared to cereals. It has a great economic merit in the livelihood of the farming communities of Ethiopia (Tamene, 2017). It serves as a source of food and feed with valuable and cheap sources of protein as a complement to cereals for the majority of the poor population mainly for those who cannot afford to use proteins from an animal source. It is also a good source of cash to the farmers (Girma, 2003). Due to its pertinent atmospheric nitrogen fixing capacity (up to 60 kg ha^{-1} $year^{-1}$); field pea is a suitable rotational crop in areas

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where cereal monocropping is abundant and also contributes a substantial role in soil fertility restoration (Angaw and Asakew, 1994).

Despite its huge importance in the country, the national average productivity of field pea is low (1.67 t ha^{-1}) as compared to a number of cereals, and relative to many other countries of the world (Kelley *et al*., 2000). This is primarily due to inherent low yielding potential of the indigenous cultivars, biotic (diseases like powdery mildew and Ascochyta blight) and abiotic (frost) factors, instability of cultivars, poor adaptation and poor crop management (Sahile *et al*., 2008; Ateet *et al*.,2015; Teshome and Tegegn,2017; Adisu and Ermiyas,2017). To alleviate some of these problems, the national high land pulse research program released 17 field pea varieties in the country (MoALR, 2017).

However, further development of desirable genotypes with high yield potential is essential for the improvement and sustainability of production and productivity of the crop. These depend upon the extent of genetic variability in the base population (Singh, 2001). The existence of high genetic diversity among Ethiopian field pea landraces accessions were reported; which are collected from various geographical regions of Ethiopia (Gemechu *et al*., 2005). Breeders need continuous evaluation of genotypes to identify germplasms with desirable traits for selecting superior genotypes for genetic improvement of the crop when there are new introducing germplasms, many gene pools and segregating breeding populations (Saddika *et al*., 2013).

The development of an intensive breeding program needs detailed biological information and knowledge on the existence of genetic variability, heritability and expected genetic advance for yield and related traits of the genotypes rather than direct selection by their yield (Carl *et al*., 2014).

Therefore, the present study was conducted to estimate the extent of genotypic variability, heritability and the expected genetic advance of important morpho-agronomic traits for efficient design of field pea breeding schemes.

Materials and Methods

Experimental sites and materials

Field experiments were carried out during the main cropping season (June to November) of the year 2018/19 at Bekoji and Koffale, which are situated in the south-eastern highlands of Ethiopia.

Weather data for the two study locations are shown in Table 1. Forty-nine field pea materials, including twenty-one introduced field pea materials, nineteen single plants selected from bulked gene pool materials, and nine released varieties, were evaluated (Table 2).

Table 1: Description of the test environments (Tamene, 2017).

Locations	Locations	Locations
Latitude	Bekoji (07°31′22″N)	Koffale (07°04′27″N)
Longitude	39°14′46″E	38°46′45″E
Altitude (m.a.s.l.)	2780	2660
Mean annual rainfall (mm)	1010	1211
Minimum temperature (°C)	7.9	7.1
Maximum temperature (°C)	16.6	18
Agro-ecologies	CHMH	CHMH

CHMH: Cool Humid Mid Highland

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Table 2: Description of field pea genotypes used in the Study.

No	Genotype	Source	Pedigree /Origin
1	GPHA-05	HARC	SPS
2	GPHA-013	HARC	SPS
3	GPHA-03	HARC	SPS
4	GPHA-019	HARC	SPS
5	GPHA-02	HARC	SPS
6	GPHA-010	HARC	SPS
7	GPHA-07	HARC	SPS
8	GPHA-08	HARC	SPS
9	GPHA-06	HARC	SPS
10	GPHA-012	HARC	SPS
11	GPHA-04	HARC	SPS
12	GPHA-016	HARC	SPS
13	GPHA-09	HARC	SPS
14	GPHA-01	HARC	SPS
15	GPHA-018	HARC	SPS
16	GPHA-017	HARC	SPS
17	GPHA-014	HARC	SPS
18	GPHA-011	HARC	SPS
19	GPHA-015	HARC	SPS
20	P-313-010	ICARDA	Australia

ISSN: 2208-2719

Table 2: contin.

22	**P-313-045**	**ICARDA**	**Australia**
22	P-313-086	ICARDA	Australia
23	P-313-082	ICARDA	Australia
24	P-313-042	ICARDA	Australia
25	P-313-071	ICARDA	Australia
26	PDFPT-BEK	ICARDA	Australia
27	G 227 63-2C	HARC	G22763-2c
28	P-313-053	ICARDA	Australia
29	P-313-070	ICARDA	Australia
30	P-313-027	ICARDA	Australia
31	P-313-065	ICARDA	Australia
32	P-313-026	ICARDA	Australia
33	P-313-090	ICARDA	Australia
34	P-313-046	ICARDA	Australia
35	MILKEY	HARC	NEP634 X1801/Holeta
36	P-313-098	ICARDA	Australia
37	HASAB	HARC	JI No 116
38	E	HARC	
39	HOLETA	HARC	Holeta local-90
40	WALMERA	HARC	FpExDz X 305PS2108-22-1
40	P-313-059	ICARDA	Australia
41	P-313-061	ICARDA	Australia
42	P-313-068	ICARDA	Australia
43	P-313-089	ICARDA	Australia
44	p-313-067	ICARDA	Australia
45	p-313-003	ICARDA	Australia
46	ADI	HARC	G22763-2C X 305PS210813-2
47	BURKITU	HARC	EH-92004-02
48	BILALO	KARC	
49	BURSA	KARC	

Where KARC = Kulumsa Agricultural Research Center, HARC = Holeta Agricultural Research Center, ICARDA = International Center of Agricultural Research for Dry Areas, SPS = Single plant selection from bulked gene pool

Experimental design and treatments

The experiment was laid out in a 7 x 7 simple lattice design. Each plot consisted of two rows of 4-m length, with spacing of 20 cm between rows and 5 cm between plants. Each genotype was planted in a plot size of 1.6 m^2. The space between plots within block was 1 m and between blocks was 1.5 m. Each row was sown with 80 seeds, and each plot contained a total of 160 seeds. 100 kg ha^{-1} DAP fertilizer was applied during planting. Weeding and all other recommended agronomic practices were followed for both locations. For statistical analysis, yield from a net plot area of 1.6 m^2 was harvested and converted into kg ha^{-1} base at 10% standard grain moisture content.

Data collection and analysis

Data on days to 50% flowering, days to 95% physiological maturity, 1000-seed weight (g), grain yield (kg ha^{-1}), ascocayta blight (1-9), and powdery mildew (1-9) were assessed on plot bases, while plant height (cm), number of pods $plant^{-1}$, and number of seeds pod^{-1} were recorded on five random samples of plants selected from the central rows of each plot. Mean values of the five random samples of plants $plot^{-1}$ were then used for the analysis of data collected on an individual plant basis.

Data for all traits were subjected to analysis of variance using the General Linear Model (PROC GLM) of the SAS version 9.0 software (SAS, 2002). The significance of variance effects was considered at $P \leq 0.05$, $P \leq 0.01$, and $P \leq 0.001$, respectively.

Homogeneity of error mean square between the two locations was tested by the F-max test method of Hartley (1950) and combined analyses were performed for all parameters whose error mean squares were homogenous. Mean comparisons among genotypes were carried out using a Duncan Multiple range test (DMRT) as mentioned by (Duncan, 1955).

Genetic parameters, such as phenotypic and genotypic variance, heritability, phenotypic and genotypic coefficient of variations, genetic advance and genetic advance as percentage of mean were calculated by adopting the following equations suggested by biometricians. The phenotypic and genotypic variances were estimated according to the method suggested by Singh and Chaudhary (1985) as follows.

Genotypic Variance ($\sigma^2 g$) = (MSg - MSe) / r (for individual location)
Environmental variance ($\sigma^2 e$) =MSe (error mean square)
Phenotypic variance ($\sigma^2 p$) =$\sigma^2 g$ + ($\sigma^2 e$ /r) (for individual location)
Genotypic Variance ($\sigma^2 g$) = (MSg - MSg*l) / rl (for combined location)
genotypes X location Variance ($\sigma^2 g*l$) = (MSg*l - MSe) /r (for combined over locations)
Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g$ + ($\sigma^2 e$ /rl) + ($\sigma^2 g*l$ /l) (for combined over locations)
Where, MSg = mean square due to genotypes, MSe = error mean square, r = number of replication , MSg*l = mean square due to genotypes X location, l = number of location
Genotypic and phenotypic coefficients of variability were estimated according to the (Burton and Devane,1953) by using the following formulae.

$$PCV = \sqrt{\frac{\sigma^2 p}{\bar{x}}} * 100 \qquad GCV = \frac{\sqrt{\sigma\ 2g}}{\bar{x}} * 100$$

Where, PCV = Phenotypic Coefficient of variation, GCV = Genotypic Coefficient of variation $\sigma^2 p$= Phenotypic variance , $\sigma^2 g$ = Genotypic Variance, $\bar{x}$ = mean value of the trait

Deshmukh et al. (1986) classified the PCV and GCV estimates as follows:
Low, <10%, Moderate, 10-20% , High, >20%

Broad sense heritability values for all parameters (h^2(b)) were estimated based on the formula given by (Falconer and Mackay, 1996) as follows:

$$h^2 (b) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

According to Johnson et al. (1955) the heritability (h^2 (b)) was categorized as:
Low, 0-30%, Medium, 31-60%, High, >60%

Genetic advance (GA) was estimated as per formula given by (Allard, 1960)

$$GA = K \times \sqrt{\sigma^2 p} \times h2\ (b)$$

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Where; K = Selection differential at 5 per cent selection intensity which accounts to a constant value 2.06, σ^2p = Phenotypic variance, h2 (b) = Broad sense heritability

Genetic advance over mean (GAM) was calculated using the following formula and was expressed in percentage.

$$GAM = \frac{GA*100}{\bar{x}}$$

According to Johnson et al. (1955), the GAM can be placed in the following categories.
Low, <10%, Moderate, 10-20% , High, >20%

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Results and Discussion

The combined/pooled/ analysis of variance revealed highly significant (*P≤0.01*) to significant *(P≤0.05)* main effect differences for genotypes observed for the traits under study except for number of seeds pod $^{-1}$ (Table 3). The significant differences obtained in the present experiment indicated the presence of considerable variation in the genetic materials studied (Table 3).

The finding in this study was in agreement with Yasin and Mathewos (2014), who reported highly significant to significant differences between 24 field pea genotypes for plant height, harvest index, biological yield, 1000-seed weight and grain yield; except for seed per plant and pod per plant. Rafiul et al. (2017) also observed highly significant variations among 46 pea genotypes for all the characters studied *viz.*, days to 50% flowering, grain filling period, days to 90% maturity, plant height ,number of pods per plant, seeds per pod, seeds per plant, ascocayta blight, powdery mildew, thousand seed weight and grain yield (kg ha^{-1}).

Test locations exerted highly significant to significant effects on stand count, days to flowering, days to maturity, plant height, seeds per pod, 1000-seed weight, ascocayta blight and powdery mildew indicating the phenotypic expression of these traits were different at both locations. Non-significant location effects were observed for number of pods per plant and grain yield (kg ha^{-1}), (Table 3). Similar results were reported by (Legesse, 2015) where, days to flowering, days to maturity, biological yield, seed per plant, seed per pod, 100-seed weight, plant height and harvest index exhibited highly significant location effects among 36 field pea genotypes evaluated. The interaction effects of locations and genotypes showed highly significant to significant effects for all traits studied except days to 50% flowering, days to 95% maturity and plant height (Table 3). Significant to highly significant of genotype (G) x location (L) interaction was observed in this study, indicating the differential response of genotypes for those traits at each location. Yasin and Mathewos (2014) observed highly significant difference of genotype x location interaction for biological yield, seeds per plant, 100-seed weight, number of pods per plant, grain yield (kg ha^{-1}) and harvest index. Tamene (2017) also reported highly significant to significant genotype by location interaction effect on grain yield, powdery mildew and number of pods per plant and non-significant on plant height.

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Table 3: Mean squares from a combined analysis of variance for ten traits of 49 field pea genotypes tested across two locations.

Traits	LOC (df=1)	REP/LOC (df=2)	BLOCK/REP*LOC (df=24)	GENOTYPE (df=48)	LOC*GENOTYPE (df=48)	Error (df=72)	CV(%)
Stand count	2809***	827.59	101.28	148.53***	55.86*	30.79	6.62
Days to 50% flowering	43.2***	0.27	1.59	15.13***	1.40^{ns}	1.21	1.42
Days to 95% maturity	16512.3***	26.58	78.41	12.16***	2.93^{ns}	2.34	1.07
Plant height (cm)	53724.6***	1849.23	156.56	666.32***	144.67^{ns}	100.87	9.06
Number of pods plant^{-1}	1.8^{ns}	15.94	1.99	2.72***	1.70*	1.04	12.23
Number of seeds pod^{-1}	4.6***	0.30	0.63	0.79^{ns}	0.49**	0.37	12.09
1000-seed weight (g)	130011.8***	186.94	82.62	1608.34***	288.44***	75.71	4.61
Grain yield (kg ha^{-1})	1294980.8^{ns}	7249826.90	511565.80	4592338.60***	1690687.40***	402246.60	16.68
Ascocayta blight (1-9)	246.9***	0.41	0.41	0.79**	0.60*	0.37	14.13
Powdery mildew (1-9)	490.3***	0.53	0.45	0.56***	0.42*	0.24	18

*, **,*** and ns were significant at P≤0.05, highly significant at P≤0.01,very highly significant at P≤0.001 and non-significant at p>0.05 respectively. CV= coefficient of variation, df = degree of freedom. SCAH =Stand count at harvest (%), DF = Days to 50% flowering (days), DM = Days to maturity (days), PH =Plant heigh (cm),PPP= Pods per plant (number), SPP =Seeds per pod (number), TSW =Thousand seed weight (grm,), GYKGH= Grain yield (Kg/ha),AB =Ascochyta blight (1-9 scale) , PM= Powdery mildew (1-9 scale).

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Phenotypic and Genotypic Variations

Variance components, phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) for the characters studied are presented in Table 4. The estimates of phenotypic and genotypic variances were the highest for grain yield, 1000-grain weight and plant height; and the lowest for powdery mildew, ascocayta blight and number of pods per plant.

The PCV was ranged from 1.22 % for days to maturity to 28.18 % for grain yield (Table 4). In addition to the latter, moderate or relatively high PCV values were noted for powdery mildew (13.84 %) , plant height (11.65 %), seed weight (10.63 %), ascocayta blight (10.34 %) and number of pods plant^{-1} (9.90 %) (Table 4).

Estimates of GCV ranged from 1.07 % for days to maturity to 22.40 % for grain yield (Table 4). Moderate value or relatively high value of GCV was observed for plant height and seed size. Powdery mildew, number of pods plant^{-1}, stand count, number of seeds per pod, ascocayta blight showed low or relatively moderate GCV values. Days to 50 % flowering and days to maturity had very low estimates of PCV and GCV.

In general, PCV values were greater than GCV values, although the differences were small. The small differences indicated that the environmental effect was small for the expression of most characters.

Among all characters, high PCV and GCV values (> 20 %) were observed for grain yield (28.18 %, 22.40 %) and moderate PCV and GCV values (10-20 %) and for 1000-seed weight (10.63 %, 9.63 %) and plant height (11.65 %, 10.30 %) in over all locations, respectively.

PCV and GCV with higher values specified that the genotypes show evidence of much variation among themselves with respect to these characters. This indicated that selection may be effective based on these characters and their phenotypic expression would be a good indication of genotypic potential. The estimates are consistent with the findings of Tamene (2017), where high level of genetic variation was observed for grain yield and relatively high variation for seed size; moreover Ofga and Petros (2017) reported moderate PCV and GCV for 1000-seed weight.

Significantly higher PCV than GCV values (observed for number of pods per plant, stand count, powdery mildew and ascocayta blight incidence) suggests the significant contribution of environment and genotype x environment effect on the expression of these traits. This was in agreement with results reported by Saxesena *et al*. (2014). Because the magnitude of genetic variation is better assessed from GCV than PCV, breeders commonly focus on traits with high GCV estimates as reported by Kebebew *et al*. (2015).

Higher and relatively higher GCV was obtained in grain yield and 1000-seed weight, and plant height, respectively, indicating the existence of wide genetic variation for these traits among the genotypes; and there could be much potential for improving these traits through hybridization and/or direct selection. Insignificant differences between PCV and GCV values were observed for days to flowering, days to maturity, plant height, 1000-seed weight, and grain yield indicating that the observed variations were owing to genetic factors; hence, the environmental effect played only a small role in the expression of these traits.

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Table 4: Genotypic variance ($\sigma^2 g$), environmental variance ($\sigma^2 e$), GxL variance ($\sigma 2g*l$), phenotypic variance ($\sigma^2 p$), genotypic (GCV) and phenotypic (PCV) coefficient of variation, heritability in the broad sense (Hb2), and genetic advance and genetic advance in percent of the mean (GAM) of ten traits of 49 field pea genotypes from combined ANOVA over two locations, Bekoji and Kofele.

Traits	Range	Mean	$\sigma^2 g$	$\sigma^2 g*l$	$\sigma^2 e$	$\sigma^2 p$	PCV %	GCV %	ECV %	H2	GA	GAM %
Stand (%)	**56 – 94**	83.77	23.17	12.53	30.79	37.13	7.27	5.75	6.62	62.39	7.84	9.36
Days to 50% flowering	**74 -83**	77.71	3.43	0.10	1.21	3.78	2.50	2.38	1.42	90.73	3.64	4.68
Days to 95% maturity	**139 -147**	142.62	2.31	0.29	2.34	3.04	1.22	1.07	1.07	75.93	2.73	1.92
Plant height (cm)	**85 -141**	110.83	130.41	21.90	100.87	166.58	11.65	10.30	9.06	78.29	20.85	18.81
Number of pods plant^{-1}	**7 -11**	8.33	0.26	0.33	1.04	0.68	9.90	6.07	12.23	37.59	0.64	7.68
Number of seeds pod^{-1}	**3.9 - 5.9**	5.00	0.07	0.06	0.37	0.20	8.86	5.40	12.09	37.13	0.34	6.79
1000-seed weight (g)	**153 -259**	188.69	329.98	106.36	75.71	402.09	10.63	9.63	4.61	82.07	33.95	17.99
Grain yield (kg ha^{-1})	**1955- 6084**	3803	725412.80	644220.40	402246.60	1148084.65	28.18	22.40	16.68	63.18	1396.68	36.73
Ascocayta blight (1-9)	**2.9 -5**	4.29	0.05	0.12	0.37	0.20	10.34	5.03	14.13	23.66	0.22	5.05
Powdery mildew (1-9)	1.8 -3.6	2.70	0.03	0.09	0.24	0.14	13.84	6.83	18.00	24.36	0.19	6.96

Similarly, small differences between PCV and GCV values in most of the traits studied were reported by Singh (2014). The two values differ only slightly, indicting lesser influence of the environmental factors. Similar values of GCV and PCV indicate that the major part of variation is shared by genetic components for the characters studied. High genotypic coefficient of variation indicates availability of high variation.

Powdery mildew, number of pods plant^{-1}, stand count, number of seed per pod, ascochyta blight, all showed low or relatively moderate PCV and GCV values. The low value of this variation indicates that selection is not effective for this character, because of the narrow genetic variability and the significant contribution of environment and genotype by environment effect on the expression of these traits.

Days to 50 % flowering and days to maturity observed very low estimate of PCV and GCV. The low value of this variation also indicates that the selection is not effective for this character, because of the narrow genetic variability even though it showed less influence of environment effect on the expression of these traits. The present result agrees with the results of Brijendra *et al.* (2013) and Legesse (2015) who also reported low estimates of PCV and GCV for days to 50 % flowering and days to maturity in field pea.

Estimates of Heritability (H2) in a Broad Sense

Estimates of broad sense heritability (Hb2) are presented in Table 4. In the present work, heritability estimate for the 10 characters studied indicated that, Hb2 values varied from low to high depending on the traits under study. It ranged from 23.66 % for ascocayta blight to 90.73 % for days to flowering (Table 4). High estimates of Hb2 were as follows: for days to flowering (90.73 %), seed size (82.07 %), plant height (78.29 %), days to maturity (75.93 %), grain yield (63.18 %) and stand (62.39 %) (Table 4). Natalia et al. (2016) reported high heritability for 1000-seed weight (95%) and seed yield (61%). The present result was also in agreement with the report of Ofga and Petros (2017) who have shown that field peas have high broad sense heritability in days to flowering, days to maturity and 100-seed weight. Tamene (2017) also observed high heritability in days to flowering, maturity, 1000-seed weigh and grain yield in field pea genotypes.

Low Hb2 estimate was noted for ascocayta blight (23.66 %) and powdery mildew (24.36 %). These findings were in line with the reports of Habtamu and Million (2013) who have observed low broad sense heritability for ascocayta blight and powdery mildew in field pea. Moderate Hb2 estimates were observed for number of pods per plant and number of seeds pod^{-1}; such moderate values indicted the limited scope for crop improvement of these characters. Hafiz *et al*. (2014) observed highest heritability value for number of seeds per plant (98) that is contrary to the present result (37.13) as indicated in Table 4. Most of the characters studied show high heritability estimates. This indicates less influence of the environment, and so there is a good scope for the improvement of these traits through selection.

Estimates of Expected Genetic Advance (GA)

The estimated genetic advance and expected genetic advance as percent of the mean for the characters are presented in table 4. The genetic gain expected from selection of the superior 5 %

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of the genotypes varied from a low of 1.92 % to a high of 36.73 % (Table 4). The lowest and highest GAM estimates were obtained for days to maturity and grain yield, respectively. Moderate or relatively high values of GAM in plant height and seed size were observed. Comparatively, value of genetic advance as a percent of mean for stand, number of pods per plant, number of seeds per pod, ascocayta blight and powdery mildew incidence were relatively moderate. The present findings are partially similar with (Rafiul *et al*., 2017). A low value of GAM for days to 50 % flowering and days to 95 % maturity was recorded.

Since high heritability does not always indicate a high genetic gain, heritability with genetic advance, considered together, should be used in predicting the ultimate effect of selecting superior varieties (Ali *et al*., 2002). The effectiveness of selection depends upon genetic advance of the character selected along with heritability (Menju *et al*., 2002). The GCV, along with heritability estimates, provides reliable estimates of the amount of GA to be expected through phenotypic selection. High GCV, along with high heritability and high GAM, provides better information than single parameters alone (Baye *et al*., 2005).

In the current study, values for Hb2 and GAM ranged from 23.66 % to 90.73 %, and 1.92 to 36.73 %, respectively (Table 4). These values are lower in Hb2 and higher in GAM compared to the values reported by Tamene (2017). This is because both variation in additive and non-additive genetic factors and the environmental variance are population specific (Visscher *et al*., 2008); heritability in one population does not necessarily predict the heritability of the same traits in another population. On the other hand, this large difference in Hb2 values of similar traits of field pea genotypes could be explained by the difference in data used from two locations in the current study compared to four location used in the other study. Differences in Hb2 of traits in this study may have resulted either due to some traits being inherently less variable than the others, or there are differences in the magnitude of environmental influence on phenotypic performances of the genotypes.

Higher heritability (H2), coupled with high GAM, was observed for grain yield per ha and higher heritability (H2) coupled with moderate or relatively high value of GAM in plant height and seed size; indicating that the phenotype of an individual in the current population is a good indicator of the genotypes, or it may mean that most of the variation in this trait observed in the present population is caused by variation in genotypes. This suggests the predominance of additive gene action in the expression of this trait (Elangovan *et al*., 2014), making it easily transferred from parent to offspring. Hence, based on this, traits selection will be effective. The result of this finding is in agreement with Aybegun *et al*. (2018) who have observed higher heritability (H2) coupled with moderate or relatively high value of GAM in plant height and seed size. Moreover, high genetic advance as percent of mean along with high heritability for 1000-seed weight, seed yield and plant height was reported by Natalia *et al*. (2016). High Hb2 value for plant height was also reported by Kumar *et al*. (2013).

High estimates of Hb2 and relatively moderate estimates of GAM were observed for stand count. In such cases, the coexistence of additive and non-additive gene action would be responsible for the expression of this trait (Elangovan *et al*., 2014). Days to flowering and days to maturity possessed high Hb2 with low GAM, and this is in line with the findings of Saxesena *et al*. (2014), suggesting the predominance of non-additive gene action. On the other hand, the high

Hb2 of these characters could be as a result of the favorable environmental condition rather than genotypic effect; thus, simple selection procedure in early segregating generations will not be effective for screening of these traits. High heritability might not necessarily lead to increased genetic gain, unless sufficient genetic variability existed in the germplasm. Therefore, there must be sufficient existing genetic variability (either through reintroduction from landraces and elite germplasms from other breeding programs, or introgression of novel alleles from wild relatives) in order to obtain increased genetic gain in days to flowering and days to maturity of field pea. The low Hb2 values were coupled with low GAM for ascocayta blight, powdery mildew, number of pods plant^{-1} and number of seeds pod^{-1}.These conditions suggested less scope for selection as they were more influenced by environment and accounted for non-additive gene effects. The reason for the low heritability is a result of some variances constituting the environmental variance. This low estimate of genetic advance as a percent of mean arises from a low estimate of phenotypic variance and heritability. In this case, one could expect slow progress of improvement in these traits through direct selection due to a quantitative mode of inheritance. Similarly, low Hb2 and GAM values for number of seeds pod^{-1} was reported (Legesse, 2015; Aybegun *et al*., 2018); but in contrast to this result, high Hb2 values was reported for this trait.

Conclusions

Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. The present study indicated that: all traits showed significant variations among the genotypes except number of seeds per pod. The PCV values were greater than GCV values, although the differences were small. The small differences indicated that the environmental effect was small for the expression of most of characters. Among all characters, high PCV and GCV values (> 20 %) were observed for grain yield (28.18 %, 22.40 %) and moderate PCV and GCV values (10-20 %) for 1000-seed weight (10.63 %, 9.63 %) and plant height (11.65 %, 10.30 %). Estimates of heritability ranged from 23.66 % for ascocayta blight to 90.73 % for days to flowering; while grain yield showed 63.18% heritability. Whereas, high GAM for grain yield (36.73) and moderate GAM for plant height (18.81) and 1000-seed weight (17.99) were recorded.

Higher heritability (H2), coupled with high GAM, was observed for grain yield per ha, and Higher heritability (H2) coupled with Moderate value of GAM in plant height and seed size, indicated that the phenotype of an individual in the current population is a good indicator of the genotypes. Or it means that most of the variation in this traits observed in the present population is caused by variation in genotypes. It indicates the importance of this trait in yield improvement of field pea. Thus, there is enormous opportunity in the improvement program of the field pea genotypes. Furthermore, these field pea materials need to be tested in similar agroecologies for their stability.

Recommendations

As a result of this study, being from two locations within a year, it is recommended for further testing in diverse environments to identify favorable environments for genotypes and for their stability.

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 in this study.

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Future work

It should be noted that plant breeders need to continue their efforts to explore genetic diversity in different traits of agronomic importance through an in-depth study of morphological, physiological, agronomic, and molecular basis of genotypic differences with a larger number of field pea accessions using modern molecular tools (Molecular breeding like QTL mapping, DNA marker-assisted selection, etc.) and scientific techniques.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests

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