

Genetic Variability and Associations of Yield and Yield Related Traits for Fieldpea (*Pisum stivum* L.) Genotypes in Arsi Zone, Southeastern Ethiopia

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To cite this article:

Gizachew Yilma Kebede, Gebeyaw Achenef Haile, Temesgen Abo. Genetic Variability and Associations of Yield and Yield Related Traits for Fieldpea (*Pisum stivum* L.) Genotypes in Arsi Zone, Southeastern Ethiopia. *International Journal of Genetics and Genomics*.

Vol. 9, No. 3, 2021, pp. 50-55. doi: 10.11648/j.ijgg.20210903.12

Received: July 16, 2021; Accepted: July 27, 2021; Published: August 4, 2021

Abstract: Field pea is an important pulse crops in Ethiopia, however the production is reduced due to many constraints including limited availability of improved variety and traditional farming systems. Twenty five advanced field pea genotypes were evaluate for ten traits at three locations during 2015/16 main cropping season using RCBD with two replications. Thus the objectives of this study were to estimate genetic variability of the genotypes and to assess the associations of yield and yield related traits. The ANOVA result showed that significant variation among genotypes. Mean square from genotype by environment interaction showed that highly significant variation among the genotypes for all traits. The genotypic and phenotypic coefficient of variation ranged from 2.4 to 12.9 and 2.9 to 22 respectively. Heritability estimates and genetic advance as present of mean also ranged from 20% to 90% and from 2.2% to 25.8% respectively. Higher estimate of heritability recorded from days to 50% flowering and thousand seed weight. Grain yield showed a significant and negative genotypic association with plant height and stand count. Stand count, days to 50% flowering, thousands seed weight and powdery mildew have a negative direct effects on grain yield while plant height has appositve direct effect on grain yield. The first two principal components explained about 58.36% of the total variation among the genotypes. The first components explained about 38.97% of the total variation and mostly explained by stand count, powdery mildew and days to 50% flowering. So the research gives as clear information about the 25 field pea genotypes for future breeding strategy.

Keywords: Correlation, Heritability, Path Analysis, Pulse Crops

1. Introduction

Field pea (*Pisum sativum* L.) is the most commonly grown pulse crops in Ethiopia and it ranks fourth in terms of total production and area coverage next to faba bean, haricot bean and chickpea [1]. Field pea belongs to the family leguminosae with $2n=14$ chromosome number. Ethiopia is the center of diversity for field pea and grown in an altitude of 1,800 – 3,000 masl with annual rainfall of 700 – 1,000 mm. According to the central statistics agency [1], it grown in 220,209 ha of land and it accounts 13.79% from total pulse production with a total of production 368,519,065 tones and its productivity is 1.67 t/ha.

There are wide ranges of field pea genotypes in Ethiopia

and makes the country the second center of genetic diversity [2]. In Ethiopia, field pea is mainly used as to prepare shiro wat as traditionally and cultivated in association with faba bean for standing base for the crop [3]. The presence of wide genetic variability in field pea crop is a pre request for effective breeding program.

Field pea plays important roles in economical and nutritional values for small scale farmers who produce the crops in traditional methods. It has good and cheap sources of proteins and improves soil fertility and helps as break crop to pest and diseases when it rotated with cereal crops [4]. Regardless of its economic and nutritional importance for the

farmers, the production and productivity of the crop is remain low (1.67 t/ha) as compared to other field pea producer country in the world.

Improvement of traits through selection or other breeding methods is the basic strategy for the increment of yield. In order to select elite breeding materials from the population it must have high genetic variability among the genotypes [5]. For efficient and optimum selection of elite genotypes knowledge of genetic variability, genetic advance, heritability and associations among traits is essential [6].

The major problem for the low production of field pea is lack of genotypes which perform consistently across different environments and seasons. In addition to this local cultivars coupled with traditional practices, biotic (powdery mildew, ascochyta blight) and abiotic factors (drought, soil salinity, frost etc) are the major production constraints of the crop. Therefore, developing high yielding and disease resistant

field pea genotypes is very important for farmers to sustain their production and to ensure the sustainability of food security in the target area. Here 25 elite genotypes of field pea including two standard checks were evaluated with the objectives of to estimate genetic variability of the genotype and assess associations among yield and yield related traits of field pea genotypes.

2. Materials and Methods

2.1. Experimental Sites and Materials

The experiments were carried out at three locations; Kulumsa, Bekoji and Asasa during 2015/16 main growing season. A total of twenty five advanced field pea genotypes including two standard checks which is released recently were used for the experiment. Descriptions of three study experimental sites were presented in Table 1.

Table 1. Description of the experimental sites.

Location	Latitude	Longitude	Altitude	Mean annual rainfall	Temperature		Soil type	Agro ecology
					Min	Max		
Kulumsa	0801'10"N	3909'11"E	2200	820	10.5	22.8	clay	Mid altitude
Bekoji	0732'37"N	3915'21"E	2780	1020	7.9	18.6	clay	Highland
Asasa	0707'09"N	3911'56"E	2340	620	5.8	23.6	clay loam	Mid altitude

Min = minimum temperature in degree Celsius, Max = maximum temperature in degree Celsius.

Table 2. List of field pea experimental materials.

ENTRY	Variety name	ENTRY	Variety name
1	Bilalo	14	EH 08033-1
2	EH 07002-1	15	EH 08034-2
3	EH 07005-1	16	EH 08036-1
4	EH 07006-5	17	EH 08036-4
5	EH 07007-3	18	EH 08041-1
6	EH 07014-2	19	EH 08041-3
7	EH 08003-1	20	EH 08041-4
8	EH 08003-2	21	EH 08042-1
9	EH 08005-1	22	EH 08042-2
10	EH 08027-1	23	EH 08042-4
11	EH 08027-2	24	EH 08042-3
12	EH 08029-3	25	Burkitu
13	EH 08031-1		

The experiment was carried out and arranged using randomized complete block designs with two replications. The plot size of the experiment was 4 m long and 0.4 m wide, i.e. 1.6 m² areas with spacing of 0.2 m and 5 cm between rows and plants respectively. Each plot had two rows and the spacing between treatments was 1 m to separate two genotypes. Planting was done on randomly allocated plots within each replication by hand drilling. 100 kg ha⁻¹ of DAP fertilizer was applied and all other agronomic practices were done throughout the growing season. The net grain yield harvested from 1.6 m² plot size was finally converted in to hectare and the moisture contents was adjusted to the standard units of field pea 10%.

2.2. Data Collected

Data collected from plot base were stand count (%), days to 50% flowering, days to maturity, thousand seed weight (g), grain yield (kg ha⁻¹), powdery mildew (1-9) scale and ascochyta blight (1-9) scale based on [16] 1-9 scale where, 1 for nil: No visible disease symptom (Immune), 3 for slight (resistant), 5 for medium (moderately resistant), 7 for severe (susceptible), 9 for very severe (highly susceptible), while plant height (cm), number of pods per plant and number of seed per pod were recorded from randomly selected five plants.

3. Result and Discussion

The analysis of variance showed that highly significant variation (0.01%) were observed among the tested genotypes for all traits except days to maturity, ascochyta blight, number of seed per pod and number of pods per plant (Table 3). This revealed that the presence of variability among the field pea genotypes evaluated. These results are similar with the findings of [7, 8] for grain yield, thousands seed weight, plant height, days to 50% flowering and days to maturity.

Highly significant (0.01%) genotype by environment interaction effect were recorded for stand count, thousand seed weight and grain yield. This significant genotype by environment interaction implies that different performance of genotype in each location for the traits. Mean square due to location also showed that highly significant variation for all traits and this indicates that there is different performance among genotypes across the tested environments.

Table 3. Mean squares from combined data analysis for ten traits.

Traits	Location (L)	R/L	Genotypes (G)	G*L	Error	CV (%)
	Df=2	Df=3	Df=24	Df=48	Df=72	
Number of Stand count	11243***	233***	117.3***	96***	38	8.1
Days to 50% flowering	1063***	44**	27.61***	8.7ns	8.5	3.9
Days to maturity	2787***	50ns	24.91ns	24.9ns	25.3	4.0
Plant height in cm	16742***	1166***	467.2***	197ns	152	8.8
Number of pods per plant	198***	24.6*	6.9ns	7.3ns	6.2	34.9
Number of seeds per pod	32***	0.2ns	1.3ns	1.6ns	1.2	23.4
Thousands seed weight in g	11778***	301ns	2884***	178*	115	6.5
Grain yield in kg/ha	13940205***	4981800***	1450570***	1150604**	608142	34.8
Powdery mildew (1-9) scale	262***	2.6**	0.93**	0.5ns	0.4	15.7
Ascochyta blight (1-9) scale	12.4***	0.7ns	0.5ns	0.4ns	0.5	18.9

G= genotype, L= location, G*L= genotype by environment interaction, R/L = replication with in location, CV= coefficient of variation, DF = degree of freedom, “****” = highly significant variation at 0.1% level of significant, “***” = highly significant variation at 1% level of significant, “**” = significant variation at 5% level of significant, “ns” = non-significant variation.

Table 4. Combined mean performance of 25 field pea genotypes for ten traits.

Entry	Genotypes	SC	FLD	MTD	PLH	PPL	SPP	TSW	GYH	AB	PM
1	Bilalo	81	71	125	142	7	5	183	3130	3.5	3.8
2	EH 07002-1	82	72	124	137	6	5	174	2423	3.5	4.5
3	EH 07005-1	69	71	125	138	9	4	198	1984	3.3	3.8
4	EH 07006-5	75	73	122	124	7	4	192	2556	3.5	4.2
5	EH 07007-3	69	77	127	132	8	5	191	3124	3.3	4.2
6	EH 07014-2	73	76	124	131	7	4	177	1739	3.8	3.7
7	EH 08003-1	75	74	124	139	6	4	192	2355	3.8	3.7
8	EH 08003-2	74	75	124	131	7	4	164	2338	3.7	4.0
9	EH 08005-1	80	77	124	141	7	4	149	1134	3.8	5.2
10	EH 08027-1	80	74	126	142	8	4	140	1735	3.3	4.7
11	EH 08027-2	78	78	124	128	5	4	122	1792	3.8	4.3
12	EH 08029-3	76	77	127	141	7	5	170	1880	4.0	4.0
13	EH 08031-1	86	78	129	161	6	4	204	1665	4.0	4.8
14	EH 08033-1	78	75	128	152	7	5	150	2297	4.2	4.8
15	EH 08034-2	78	76	127	143	9	5	136	2481	4.2	4.2
16	EH 08036-1	73	73	128	151	7	4	155	2887	4.2	4.7
17	EH 08036-4	76	75	128	144	8	5	133	2830	3.7	4.2
18	EH 08041-1	75	76	126	129	8	5	135	2275	3.8	4.0
19	EH 08041-3	74	76	127	146	7	4	156	2267	3.7	4.5
20	EH 08041-4	71	78	130	152	8	5	163	2293	4.2	4.3
21	EH 08042-1	76	75	128	144	9	5	172	1598	3.2	4.0
22	EH 08042-2	76	74	124	143	6	5	175	2263	3.7	3.8
23	EH 08042-4	81	77	127	149	7	5	158	2083	3.7	4.0
24	EH 08042-3	80	76	128	147	7	5	159	2039	3.7	3.8
25	Burkitu	68	72	123	132	9	5	161	2794	3.5	4.0
	Mean	76	75	126	141	7	5	164	2238	4	4
	CV (%)	8.1	3.9	4.0	8.8	34.9	23.4	6.5	34.8	18.9	15.7

SC= Number of stand count, FLD= days to 50% flowering, MTD= days to maturity, PLH= plant height in cm, PPL= number of pods per plant, SPP= number of seed per pod, TSW= Thousand seed weight in g, GYH= grain yield in kg/ha, AB= ascochyta blight (1-9) scale, PM= powdery mildew (1-9) scale.

Mean performance of the genotypes for 10 traits was presented in Table 5. The result showed that significant variation among genotypes for all traits. Days to maturity ranged from 122 days for EH 07006-5 to 130 days for EH 08041-4. Plant height ranged from 124 cm for EH 07006-5 to 152 cm for EH 08041-4. Number of pods per plant, grain yield and thousand seed weight showed significant variation and ranged from 5 to 9, 1,134 to 3,130 kg/ha⁻¹ and 122 g to 204 g respectively.

The mean grain yield performance of genotypes showed that there were significant differences across three locations. The lowest mean grain yields per hectare were

recorded from genotype EH 07014-2 (1,272 kg/ha⁻¹), EH 08027-1 (382 kg/ha⁻¹) and EH 08003-2 (888 kg/ha⁻¹) at Asasa, Kulumsa and Bekoji respectively. At Kulumsa, Bekoji and Asasa highest mean grain yield were recorded from Bilalo (3,950 kg/ha⁻¹), genotype EH 07007-3 (3,843 kg/ha⁻¹) and EH 07002-1 (3,908 kg/ha⁻¹) respectively. The combined mean performance of the genotypes showed that all candidate genotypes have no more yield advantage than standard check Bilalo (3,130 kg/ha⁻¹), but three candidate genotypes EH 08036-4 (2,820 kg/ha⁻¹), EH 08036-1 (2,887 kg/ha⁻¹) and EH 07007-3 (3,124 kg/ha⁻¹) have better mean grain yield than standard check Burkitu (2,794 kg/ha⁻¹).

Table 5. Mean performance of genotype at each location for grain yield and thousand seed weight.

No-	Genotype	Asasa		Kulumsa		Bekoji	
		GYH	TSW	GYH	TSW	GYH	TSW
1	Bilalo	2066	190	3950	164	3374	195
2	EH 07002-1	3908	198	1700	153	1662	172
3	EH 07005-1	2270	220	1765	171	1917	204
4	EH 07006-5	2224	206	2482	171	2964	199
5	EH 07007-3	3704	212	1826	166	3843	194
6	EH 07014-2	1272	189	1947	171	1999	173
7	EH 08003-1	2548	206	1910	172	2607	200
8	EH 08003-2	3053	173	3075	157	888	164
9	EH 08005-1	1455	167	1010	131	938	149
10	EH 08027-1	2779	142	382	134	2046	145
11	EH 08027-2	3011	131	916	118	1450	116
12	EH 08029-3	1776	205	619	125	3245	180
13	EH 08031-1	1823	220	585	176	2588	218
14	EH 08033-1	2775	160	1006	133	3110	158
15	EH 08034-2	2871	152	1852	116	2720	140
16	EH 08036-1	3563	167	1586	145	3511	155
17	EH 08036-4	3720	146	1603	116	3167	136
18	EH 08041-1	1972	144	2068	124	2786	138
19	EH 08041-3	2850	177	1311	142	2642	150
20	EH 08041-4	2530	180	1074	155	3275	154
21	EH 08042-1	1584	181	929	157	2282	177
22	EH 08042-2	2049	184	1903	167	2839	175
23	EH 08042-4	1823	178	999	141	3428	156
24	EH 08042-3	1713	165	1571	152	2832	160
25	Burkitu	2161	163	2833	144	3390	178
Mean		2460	178	1636	148	2620	167

GYH= grain yield in kg/ha, TSW= thousand seed weight in grams.

3.1. Estimation of Genetic Parameters

Estimation of genotypic (GCV) and phenotypic (PCV) coefficient of variance, heritability (H^2) and genetic advance (GA) are presented in table 6 below. Genotypic coefficient of variation ranged from 2.4% for days to 50% flowering to 12.9% for thousands seed weight. Lowest estimates of GCV recorded for all traits except grain yield and thousands seed weight. Higher estimate of GCV were reported for days to 50% flowering [9]. Lowest estimate of GCV were reported by [9, 10] for days to maturity. Higher genotypic coefficient of variation reported for grain yield and thousands seed weight [11]. Higher and medium phenotypic coefficient of variation recorded for grain yield and thousands seed weight respectively, but other traits recorded lower phenotypic coefficient of variation. High GCV and PCV were reported for number of pods per plant, powdery mildew, thousand seed weight and grain yield [14].

Higher heritability is essential for the improvement of traits through simple selection. Broad sense heritability were ranged from 20% for stand count to 90% for thousands seed weight. Thus, days to 50% flowering and thousands seed weight estimated higher broad sense heritability, but stand count, grain yield and powdery mildew observed lowest heritability. These results are in agreement with [10, 11] for days to 50% flowering and thousand seed weight. The lowest heritable traits are difficult or limited possible for improvements with simple selection. Higher genetic advance were recorded for grain yield and thousands seed weight. In agreement with this result [11] reported highest genetic advance for grain yield and thousand seed weight, while lower genetic advance was observed from stand count, days to 50% flowering and powdery mildew. Low genetic advance as percentage of mean were reported for plant height, seed yield and days to 50% flowering [9].

Table 6. Estimates of genetic parameters of six traits.

Traits	GV	PV	H^2	Mean	GA	GAM	GCV	PCV	CV	Error
SC	3.5	19.6	0.2	76.1	1.7	2.2	2.5	5.8	8.1	38.0
FLD	3.2	4.6	0.7	74.9	3.0	4.0	2.4	2.9	3.9	8.5
PLH	45.1	77.9	0.6	140.7	10.5	7.5	4.8	6.3	8.8	152.0
TSW	450.9	480.6	0.9	164.3	42.4	25.8	12.9	13.3	6.5	114.7
GYH	50,003	241,763	0.2	2,238.5	209.8	9.4	10.0	22.0	34.8	608,164
PM	0.1	0.2	0.4	4.2	0.4	8.3	6.2	9.4	15.7	0.4

GV= genotypic variance, PV= phenotypic variance, H^2 = broad sense heritability, GA = genetic advance, GAM = genetic advance as a percentage of mean, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, CV = coefficient of variation, SC= Number of stand count, FLD= days to 50% flowering, PLH= plant height in cm, TSW= Thousand seed weight in g, GYH= grain yield in kg/ha, PM= powdery mildew (1-9) scale.

3.2. Association of Traits

The genotypic and phenotypic associations were presented in Table 7. Grain yield showed that highly significant ($p < 0.01$) and negative genotypic association with stand count and plant height, but has no any significant association with other traits. Significant and positive genotypic correlation of grain yield with plant height, days to 50% flowering and number of pods per plant [9, 15]. Powdery mildew also showed positive and highly significant genotypic associations with stand count and days to 50% flowering. The phenotypic correlation coefficient showed that no any significant positive or negative associations between each traits. The significant genotypic correlation of grain yield with plant height and stand count showed that the possibility of improvement of grain yield by improving or selecting those traits.

Table 7. Genotypic correlation above diagonal and phenotypic correlation below diagonal for six traits.

Traits	SC	FLD	PLH	TSW	GYH	PM
SC	1.00	0.35	0.70	-0.13	-0.60**	0.72***
FLD	0.08	1.00	0.31	-0.39	-0.69	0.41*
PLH	0.15	0.11	1.00	0.06	-0.46*	0.68
TSW	-0.03	-0.20	0.03	1.00	0.07	-0.37
GYH	-0.19	-0.26	0.14	0.11	1.00	-0.71
PM	0.08	0.17	0.22	-0.18	0.02	1.00

SC= Number of stand count, FLD= days to 50% flowering, PLH= plant height in cm, TSW= Thousand seed weight in g, GYH= grain yield in kg/ha, PM= powdery mildew (1-9) scale.

3.3. Path Coefficient Analysis

Genotypic path coefficient analysis of the five traits on grain yield of 25 field pea genotypes were presented in Table 9. The result showed that only plant height has positive direct effect on grain yield, while it has a negative indirect effects on grain yield through stand count, days to 50% flowering, thousands seed weight and powdery mildew. Stand count, days to 50% flowering, thousands seed weight and powdery mildew have a negative direct effects on grain yield. Negative direct effect of days to 50% flowering, number of stand count, plant height, aschocytia blight, number of pods per plant and number of seeds per plant on grain yield were reported [7].

Table 8. Genotypic path coefficient.

Traits	SC	FLD	PLH	TSW	PM
SC	-0.147	-0.225	0.305	0.069	-0.603
FLD	-0.051	-0.646	0.137	0.205	-0.340
PLH	-0.103	-0.203	0.436	-0.030	-0.562
TSW	0.019	0.250	0.025	-0.530	0.309
PM	-0.106	-0.264	0.294	0.197	-0.832

SC=Number of stand count, FLD=days to 50% flowering, PLH=plant height in cm, TSW=Thousand seed weight in g, PM= powdery mildew (1-9) scale.

3.4. Principal Component Analysis

The principal component analysis showed that the first two principal components have Eigenvalues greater than 1 explained about 58.36% of the total variation among the 25

field pea genotypes evaluated for six quantitative traits. About 90% of the total variation was explained by the first three principal components [12]. The two principal components had eigenvalues 2.338 and 1.163 respectively. The first principal component accounts 38.97% of the total variation of genotypes. Days to 50% flowering, powdery mildew, stand count and grain yield had high contributions for the variation in the first principal components; those imply that they contribute significantly to the discrimination among the genotypes. 67% of the traits in the first principal components have a positive impact on the variation while two traits, thousand seed weight and grain yield has negative effects on the total variation.

The second principal component accounted about 19.39% of the total variation of the genotypes. Thousands seed weight, plant height and days to 50% flowering had high contributions for the total variation. In the second component only days to 50% flowering has a negative impact while all other traits have positive impact on the total variation. About 77.3% and 88.7% of the total variation explained by the first five and four components respectively [7, 10]. The first two principal components were explained about 77% of the total variation [13].

Table 9. First two principal components of six traits of 25 field pea genotypes.

Traits	Comp. 1	Comp. 2
SC	0.4646	0.3033
FLD	0.4293	-0.378
PLH	0.3846	0.5459
TSW	-0.2375	0.6653
GYH	-0.4278	0.1417
PM	0.4610	0.0652
Eigenvalues	2.3380	1.1630
Proportion (%)	0.3897	0.1939
Cumulative	0.3897	0.5836

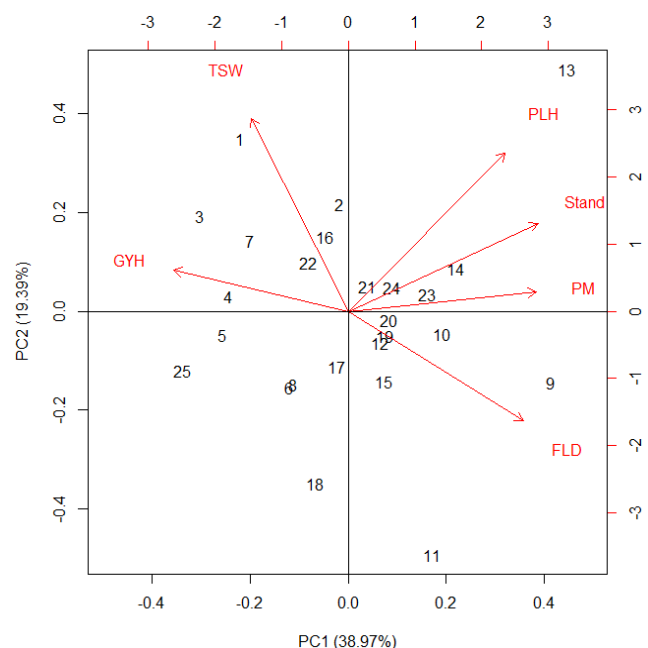


Figure 1. Plots of the first two principal components of six traits for 25 field pea genotypes.

4. Conclusion

The study showed the presence of high genetic variability among studied genotypes. Phenotypic variances were higher than genotypic variance, this indicates that the influence of environments on the performance of the traits. Low genotypic coefficients of variation were recorded for all traits except grain yield and 1000 seed weight. Highly heritable traits have good opportunity to select the better genotypes for breeding program. Accordingly, days to 50% flowering and 1000 seed weight showed high broad sense heritability. The genetic advance as percent of mean were ranged from 2.2% for stand count to 25.8% for 1000 seed weight. Grain yield showed highly significant and negatively correlated with stand count and plant height. High broad sense heritability along with high genetic advance as percent of mean was observed for 1000 seed weight. This indicates that the improvement of traits can be done with simple selection at phenotypic level.

Genotypic path coefficient analysis result showed that plant height has a positive direct effect on grain yield. The principal component analysis showed about 58.36% of the total variation was explained by the first two principal components. In this study the amounts of genetic variability were determined among grain yield and yield related traits. For future breeding program it is better to utilize the available genetic resources in order to develop better yielder variety.

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