

# Trait Associations in Prostrate and Semi-Leaf Less Type Field Pea (*Pisum sativum* L.) Gene Pools

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**Abstract:** The field experiment was conducted in 2019 main cropping season at two locations using simple lattice design to evaluate 49 field pea genotypes including nine released varieties for generating information on genotypic and phenotypic association among yield contributing traits and with grain yield, and to study their path analysis on grain yield. Positive and significant genotypic correlation observed between grain yield with plant height ( $r_g=0.67$ ), seeds per pod ( $r_g=0.45$ ), days to maturity ( $r_g=0.41$ ) and pods per plant ( $r_g=0.33$ ) for combined analysis. The association among most of traits demonstrated higher genotypic correlations than corresponding phenotypic correlations that; indicated the prevalence of genetic variation in expression of the traits. Genotypic path analysis also indicated that plant height (0.746) exerted the maximum positive direct effect on grain yield followed by stand count at harvest (0.443), 1000 seed weight (0.372), seeds per pod (0.214), pods per plant (0.213), and days to maturity (0.013). Therefore; selection for traits such as plant height, pods per plant, seeds per pod and days to maturity could improve grain yield in field pea.

**Keywords:** Genotypic, Phenotypic, Correlation, Direct Effect, Indirect Effect

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## 1. Introduction

Economically, Pulses are the second most important crops after cereals in the world's crop production. Field pea (*Pisum sativum* L.) is one of the most widely grown pulse crop in the world with annual production of 16205448 tonnes [8]. The major field pea-producing countries include Canada, Russian Federation, China, Ukraine, India, United States of America, France, Australia, Ethiopia and Germany [8].

In Ethiopia, field pea stands fourth next to faba bean, haricot bean and chickpea among pulse crops in total production and areas coverage [6]. It is grown on 220,508.39 hectares of land with total production of 368,519.065 tonnes and productivity of 1.671 t/ha; which accounts 13.79% from pulses total area coverage and 12.37% from total production in Ethiopia. [6]. It is widely cultivated in potential mid and high altitude areas of the country at elevations of 1800-3000 m with 700-1100 mm annual rainfall.

Field pea can be grouped in to two main types. The first is prostrate type that has normal leaves (vine lengths of 3 to 6 feet) and the second type is the semi leafless that has modified leaflets (shorter vine lengths of 2 to 4 feet) reduced

to tendrils [9].

Field pea has a great economic merit in the livelihood of the agricultural societies of the country. It contains high protein content, favorable amino acids composition and low trypsin inhibitor levels and there by supply the essential nutrients to various age groups [2] Due to its pertinent atmospheric nitrogen fixing capacity; field pea serves as a break crop suitable for rotation in areas where cereal monocropping is abundant.

Even though it has huge importance in the country, the national average production of field pea is low compared with the production of the crop in the advanced countries like India, USA, France [8]. This may be due to inherent low yielding potential of the landrace cultivars, biotic factors (diseases like powdery mildew (*Erysiphe polygoni*) and Ascochyta blight (*Mycosphaerella pinodes*)) and abiotic (frost) factors, inadequate land allocation, poor attention for the crop, instability of cultivars, poor adaptation and poor crop management [20, 16]. To increase the production of this crop there is a need to develop further desirable genotypes.

The improvement of field pea through phenotypic selection by their yield alone is not possible because grain

yield is a complex quantitative character affected by many environmental factors and genotype by environment interaction [18].

The association of heritable characters with yield attributing traits is useful for selection which can be determined by Correlation analysis [5]. Correlation studies determine the contribution of different characters, type, nature and degree of association among yield related traits and with grain yield [12]. The division of correlation coefficients can be partitioned into direct and indirect effects to give the importance to the causal factors through path coefficient analysis.

Moreover, Even if several research findings indicated the occurrence of strong association between grain yield and yield contributing traits in field pea; limited information is available in association between grain yield and yield contributing traits in Prostrate and Semi-Leaf Less Type Field Pea. Therefore; it is essential to understand the nature and magnitude of association among yield components and

with grain yield to select yield related traits indirectly for grain yield improvement. The current study was conducted to estimate the nature and degree of association among yield contributing traits and with grain yield, and to study their path analysis on grain yield.

## 2. Materials and Methods

### 2.1. Experimental Materials and Sites

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 at Bekoje (2780m altitude, 1010mm average annual rain fall with 7.9-16.6°C temperature) and Kofele (2660m altitude, 1211mm average annual rain fall with 7.1-18°C temperature) [19] in south-eastern highlands of Ethiopia during the main season of 2018/19 cropping season.

**Table 1.** List of field pea genotypes used in the Study.

No	Genotype	Source	Origin	Plant type
1	GPHA-05	HARC	SPS	P
2	GPHA-013	HARC	SPS	P
3	GPHA-03	HARC	SPS	P
4	GPHA-019	HARC	SPS	P
5	GPHA-02	HARC	SPS	P
6	GPHA-010	HARC	SPS	P
7	GPHA-07	HARC	SPS	P
8	GPHA-08	HARC	SPS	P
9	GPHA-06	HARC	SPS	P
10	GPHA-012	HARC	SPS	P
11	GPHA-04	HARC	SPS	P
12	GPHA-016	HARC	SPS	P
13	GPHA-09	HARC	SPS	P
14	GPHA-01	HARC	SPS	P
15	GPHA-018	HARC	SPS	P
16	GPHA-017	HARC	SPS	P
17	GPHA-014	HARC	SPS	P
18	GPHA-011	HARC	SPS	P
19	GPHA-015	HARC	SPS	P
20	P-313-010	ICARDA	Australia	S
21	P-313-045	ICARDA	Australia	S
22	P-313-086	ICARDA	Australia	S
23	P-313-082	ICARDA	Australia	S
24	P-313-042	ICARDA	Australia	S
25	P-313-071	ICARDA	Australia	S
26	PDFPTBEK	ICARDA	Australia	S
27	G227 63-2C	HARC	G22763-2c	P
28	P-313-053	ICARDA	Australia	S
29	P-313-070	ICARDA	Australia	S
30	P-313-027	ICARDA	Australia	S
31	P-313-065	ICARDA	Australia	S
32	P-313-026	ICARDA	Australia	S
33	P-313-090	ICARDA	Australia	S
34	P-313-046	ICARDA	Australia	S
35	MILKEY	HARC	NEP63 X180-1/ Holeta	P
36	P-313-098	ICARDA	Australia	S
37	HASABE	HARC	JI No 116	P
38	HOLETA	HARC	Hlocal-90/ holeta	P
39	WALMERA	HARC	FpExDz X 305PS2108	P
40	p-313-059	ICARDA	Australia	S
41	p-313-061	ICARDA	Australia	S
42	p-313-068	ICARDA	Australia	S

No	Genotype	Source	Origin	Plant type
43	p-313-089	ICARDA	Australia	S
44	p-313-067	ICARDA	Australia	S
45	p-313-003	ICARDA	Australia	S
46	ADI	HARC	G22763-2C X 305PS210813	P
47	BURKITU	HARC	EH-92004-02	P
48	BILALO	KARC		P
49	BURSA	KARC		P

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

P=Prostrate type, S=Semi leaf less type.

## 2.2. Experimental Design

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

## 2.3. Data Collection and Analysis

Data on days to 50% flowering, days to 95% physiological maturity, 1000 seed weight (g), grain yield (kg ha<sup>-1</sup>), ascochyta blight (1-9), and powdery mildew (1-9) were assessed on plot bases, while plant height (cm), pods plant<sup>-1</sup> and seeds pod<sup>-1</sup> 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<sup>-1</sup> were then used for the analysis of data collected on an individual plant basis.

Phenotypic and genotypic correlation coefficients of grain yield with other traits were estimated from combined over the two locations using the components of variance and covariance based on the standard procedure suggested by (Robinson *et al.*, 1951) by using the PROC CANDISC of SAS system [15] as follows:

$$r_p = \frac{Cov\ p(XY)}{\sqrt{var\ pX} \sqrt{var\ pY}}$$

$$r_g = \frac{Cov\ g(XY)}{\sqrt{var\ gX} \sqrt{var\ gY}}$$

Where  $r_p$  is phenotypic correlation coefficient between characters x and y;  $r_g$  is genotypic correlation coefficient between characters x and y;  $Cov\ p(XY)$  is phenotypic covariance between characters x and y;  $var\ pX$  is variance of character x;  $var\ pY$  is variance of character y;  $Cov\ g(XY)$  is genotypic covariance between characters x and y;  $var\ gX$  is genotypic variance of character x; and  $var\ gY$  is genotypic variance of character y.

Based on genotypic and phenotypic correlation, path coefficient which refers to the direct and indirect effects of

the yield components (independent characters) on grain yield (dependent character) was found out.

The direct and indirect effects of the independent characters (yield components) on dependent variable (yield) were estimated as described by [7] using the following formula.

$$r_{ij} = P_{ij} + \sum r_{ik}p_{kj}$$

where,  $r_{ij}$ =mutual association between the independent

character (i) and dependent character (j) as measured by the correlation coefficients,  $P_{ij}$ =direct effects of the independent character (i) on the dependent variable (j) as measured by the path coefficients, and  $\sum r_{ik}p_{kj}$ =summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent traits (k).

The residual effect, which determines how best the causal factors account for the variability of the dependent factor, yield, was obtained using the formula [17];

$l = p2R + \sum p_{ij}r_{ij}$ , where,  $p2R$  is the residual effect and  $\sum p_{ij}r_{ij}$  is summation of the product of direct effect of any variable and its correlation coefficient with yield.

## 3. Results and Discussion

### Phenotypic and Genotypic Correlation

The phenotypic and genotypic correlation among grain yield and yield components are indicated in Table 2.

The Grain yield showed highly significant ( $P \leq 0.01$ ) positive genotypic correlation with plant height ( $r_g = 0.67$ ), seeds pod<sup>-1</sup> ( $r_g = 0.45$ ), days to maturity ( $r_g = 0.41$ ) and significant positive genotypic correlation with pods per plant ( $r_g = 0.33$ ). It indicates the possibility of improving grain yield by improving any one / two or all of the traits.

[4] Reported highly significant positive genotypic correlation of seeds per pod and days to maturity with seed yield per plant supporting this finding. Similar result was also reported by [13] where, significant positive genotypic correlation of pods per plant with seed yield per plant. In contrast to this, this author reported negative significant genotypic correlation of days to maturity, plant height and negative non-significant genotypic correlation of seeds per pod. [3] Reported highly significant and positive genotypic correlation of pods per plant, plant height and seeds per pod with yield in garden pea, supported the present findings. Stand count at harvest, 100 seed weight and powdery mildew

disease demonstrated non-significant positive genotypic association with grain yield. Days to flowering and ascochyta blight disease showed non-significant negative genotypic association with grain yield.

Days to flowering demonstrated a significant and positive genotypic correlation with days to maturity. It implies that plants that early flower may mature earlier. Days to maturity showed a significant and positive genotypic correlation with number of pods per plant. Days to maturity and plant height showed a significant and positive genotypic correlation with number of seeds per pod. It indicates that tall plants supporting many leaves could increase total biomass production through increased carbon fixation that can be ultimately partitioned to reproduction organ and there by produce more number of seeds and increase seed yield in field pea, which has positive and significant correlation with crop improvement. Similar result was reported by [11].

Grain yield showed highly significant ( $P \leq 0.01$ ) positive phenotypic correlation with plant height ( $r_p = 0.57$ ), ( $r_g = 0.45$ ), days to maturity ( $r_g = 0.33$ ) and significant positive phenotypic correlation with pods per plant ( $r_p = 0.28$ ) and seeds per pod ( $r_p = 0.15$ ). This revealed that, improvement in any one or all of these positively related traits had contributed to selection of these characters for seed yield improvement.

The present finding was in line with [10] who observed highly significant positive phenotypic correlation of days to maturity, plant height and pods per plant with seed yield. This author also reported highly significant negative phenotypic correlation of seeds per pod with seed yield in contrast to this result. [11] Indicated the same results with the present findings. [4] Have reported highly significant positive phenotypic correlation of number of seeds per pod and significant positive phenotypic correlation of number of pods per plant and plant height with seed yield per plant. Similar result was also reported by [13] where; significant positive phenotypic correlation of number of pods per plant with seed

yield per plant was observed. In contrast to this, this author reported negative significant phenotypic correlation of days to maturity and positive non-significant phenotypic correlation of number of seeds per pod and plant height with seed yield.

[19] Also reported positive significant correlation of days to maturity with grain yield. In contrary to the present findings, he reported negative significant correlation of number of seeds per pod with grain yield.

Stand count at harvest, 1000 seed weight, Ascochyta blight and powdery mildew disease exhibited non-significant positive phenotypic correlation with grain yield. Days to flowering showed non-significant negative phenotypic correlation with grain yield.

Days to flowering observed significant and positive phenotypic correlation with days to maturity. It implies that plants with early flowering may mature earlier. Days to maturity and plant height exhibited significant and positive correlation with number of pods per plant. It indicates that tall plants may produce more number of pods per plant. Days to flowering, maturity and plant height demonstrated significant and positive phenotypic correlation with number of seeds per pod. It indicates that tall plants supporting many leaves could increase total biomass production through increased carbon fixation that can be ultimately partitioned to reproduction organs and there by produce more number of pods and seeds and increase seed yield in field pea, which have positive and significant correlation with crop production. Similar results were reported by [11]. Days to flowering, maturity, plant height, number of seeds per pod, Ascochyta blight and powdery mildew indicated significant negative phenotypic correlation with thousand seed weight. Ascochyta blight showed significant positive phenotypic association with powdery mildew. Stand count, days to flowering, maturity and plant height exhibited significant negative phenotypic association with Ascochyta blight and powdery mildew disease.

**Table 2.** Genotypic ( $r_g$ ) (above the diagonal) and phenotypic ( $r_p$ ) (below the diagonal) correlation among different characters in 49 field pea genotypes tested combined over the two locations.

Trait	SCAH	FD	MD	PH	PPP	SPP	TSW	GYKGH	AB	PM
SCAH	1.00	-0.19 <sup>ns</sup>	0.05 <sup>ns</sup>	0.56 <sup>**</sup>	0.08 <sup>ns</sup>	-0.08 <sup>ns</sup>	0.44 <sup>**</sup>	0.15 <sup>ns</sup>	0.28 <sup>*</sup>	0.02 <sup>ns</sup>
FD	-0.20 <sup>**</sup>	1.00	0.35 <sup>*</sup>	-0.03 <sup>ns</sup>	0.15 <sup>ns</sup>	0.24 <sup>ns</sup>	-0.09 <sup>ns</sup>	-0.13 <sup>ns</sup>	-0.03 <sup>ns</sup>	0.04 <sup>ns</sup>
MD	-0.34 <sup>**</sup>	0.26 <sup>**</sup>	1.00	0.45 <sup>**</sup>	0.31 <sup>*</sup>	0.46 <sup>**</sup>	-0.22 <sup>ns</sup>	0.41 <sup>**</sup>	-0.24 <sup>ns</sup>	0.36 <sup>*</sup>
PH	-0.01 <sup>ns</sup>	0.11 <sup>ns</sup>	0.72 <sup>**</sup>	1.00	0.24 <sup>ns</sup>	0.24 <sup>*</sup>	0.21 <sup>ns</sup>	0.67 <sup>**</sup>	0.22 <sup>ns</sup>	0.06 <sup>ns</sup>
PPP	0.01 <sup>ns</sup>	0.09 <sup>ns</sup>	0.13 <sup>*</sup>	0.19 <sup>**</sup>	1.00	0.23 <sup>ns</sup>	-0.11 <sup>ns</sup>	0.33 <sup>*</sup>	0.01 <sup>ns</sup>	0.00 <sup>ns</sup>
SPP	-0.09 <sup>ns</sup>	0.18 <sup>*</sup>	0.25 <sup>**</sup>	0.23 <sup>**</sup>	0.04 <sup>ns</sup>	1.00	0.04 <sup>ns</sup>	0.45 <sup>**</sup>	-0.17 <sup>ns</sup>	-0.08 <sup>ns</sup>
TSW	0.46 <sup>**</sup>	-0.21 <sup>**</sup>	-0.73 <sup>**</sup>	-0.40 <sup>**</sup>	-0.06 <sup>ns</sup>	-0.16 <sup>*</sup>	1.00	0.26 <sup>ns</sup>	0.25 <sup>ns</sup>	-0.28 <sup>*</sup>
GYKGH	0.08 <sup>ns</sup>	-0.05 <sup>ns</sup>	0.33 <sup>**</sup>	0.57 <sup>**</sup>	0.28 <sup>*</sup>	0.15 <sup>*</sup>	0.11 <sup>ns</sup>	1.00	-0.04 <sup>ns</sup>	0.06 <sup>ns</sup>
AB	-0.24 <sup>**</sup>	0.18 <sup>**</sup>	0.76 <sup>**</sup>	0.59 <sup>**</sup>	0.04 <sup>ns</sup>	0.12 <sup>ns</sup>	-0.54 <sup>**</sup>	0.03 <sup>ns</sup>	1.00	0.01 <sup>ns</sup>
PM	-0.35 <sup>**</sup>	0.20 <sup>**</sup>	0.92 <sup>**</sup>	0.63 <sup>**</sup>	0.05 <sup>ns</sup>	0.21 <sup>**</sup>	-0.70 <sup>**</sup>	0.07 <sup>ns</sup>	0.75 <sup>**</sup>	1.00

Where: - \*\*, \*, and ns=highly significant, significant and non-significant at 1%, 5% and  $P > 0.05$  respectively. SCAH=Stand count at harvest (%), DF=Days to 50% flowering (days), DM=Days to maturity (days), PH=Plant height (cm), PPP=Pods per plant (number), SPP=Seeds per pod (number), TSW=Thousand seed weight (g/m<sup>2</sup>), GYKGH=Grain yield (Kg/ha), AB=Ascochyta blight (1-9 scale), PM=Powdery mildew (1-9 scale).

Direct and indirect effect of different characters on grain yield of field pea genotypes at genotypic level is presented in Table 3.

Plant height exhibited the first maximum positive direct

effect on grain yield at genotypic level which led to positive and significant correlation of this trait with grain yield. This finding was in conformity with that of [4].

The second higher positive direct effect was observed by

number of pods per plant and number of seeds per pod on grain yield at genotypic level which led to positive and significant correlation of this trait with grain yield. [3] reported maximum direct effect of pods per plant and seeds per pod on yield, supported this findings.

Low positive direct effect was exhibited by days to mature and contributed indirectly to grain yield via plant height, seeds per pod, and pods per plant, powdery mildew and Ascochyta blight for its significant positive correlation with grain yield.

Stand count, thousand seed weight and powdery mildew also showed higher positive direct effect on grain yield which contributed for its non-significant positive correlation with grain yield.

Days to flowering showed the highest negative direct effect on grain yield which contributed for its non-significant negative correlation with grain yield.

The maximum positive indirect effect on grain yield was

exhibited by stand count and days to maturity through plant height while the next maximum positive indirect effects were exerted by pods per plant and seeds per pod through plant height. That means, these traits influenced grain yield via their positive indirect effects on plant height.

The maximum negative indirect effect on grain yield was demonstrated by plant height through stand count while thousand seed weight and Ascochyta blight exerted maximum negative indirect effects through stand count. That means, that these traits influenced grain yield via their negative indirect effects on stand count.

The magnitude of residual effect (0.49) implied that traits included in path analysis described about 51% of the variation in grain yield at genotypic level. However, the remaining variation in grain yield (49%) can be attained by incorporating other yield related components in the path analysis.

**Table 3.** Direct (bold face) and indirect effect (off diagonal) at genotypic level of nine traits on grain yield of 49 field pea genotypes at combined locations, Bekoje and Kofele.

Traits	SCAH	FD	MD	PH	PPP	SPP	TSW	AB	PM	$r_{ge}$
SCAH	0.443781	0.048872	0.000698	0.417945	0.0171	-0.01714	0.163742	-0.04048	0.003043	0.15
FD	0.084318	-0.25722	0.004886	-0.02239	0.032062	0.051417	-0.03349	0.004337	0.006086	-0.13
MD	-0.02219	-0.09003	0.01396	0.335849	0.066261	0.098549	-0.08187	0.034698	0.054772	0.41**
PH	-0.24852	0.007717	0.006282	0.746331	0.051299	0.051417	0.07815	-0.03181	0.009129	0.67**
PPP	-0.0355	-0.03858	0.004328	0.179119	0.213746	0.049275	-0.04094	-0.00145	0	0.33*
SPP	0.035502	-0.06173	0.006421	0.179119	0.049162	0.214237	0.014886	0.024578	-0.01217	0.45**
TSW	-0.19526	0.02315	-0.00307	0.15673	-0.02351	0.00857	0.372141	-0.03614	-0.0426	0.26
AB	-0.12426	0.007717	-0.00335	0.164193	0.002138	-0.03642	0.093035	-0.14458	0.001521	-0.04
PM	-0.00888	-0.01029	0.005026	0.04478	0	-0.01714	-0.1042	-0.00145	0.152144	0.06

Residual=0.49  $R^2=0.75$  Where: - \*\*, \*, and ns=highly significant, significant and non-significant at 1%, 5% and  $P>0.05$  respectively.. SCAH=Stand count at harvest (%), DF=Days to 50% flowering (days), DM=Days to maturity (days), PH=Plant height (cm), PPP=Pods per plant (number), SPP=Seeds per pod (number), TSW=Thousand seed weight (g/m<sup>2</sup>), GYKGH=Grain yield (Kg/ha), AB=Ascochyta blight (1-9 scale), PM=Powdery mildew (1-9 scale).

Direct and indirect effect of different characters on grain yield of field pea genotypes at phenotypic level is presented in Table 4.

Days to maturity demonstrated the highest positive direct effect on grain yield at phenotypic level which led to positive and significant correlation of this trait with grain yield. Similar result was reported by [10] who observed highest positive direct effect of days to maturity on grain yield. The second maximum positive direct effect was exerted by plant height relatively on grain yield and contributed indirectly to the grain yield via days to mature. It leads to positive and significant correlation of this trait with grain yield. Low positive direct effect was exhibited by number of pods per plant and contributed indirectly to the grain yield via days to maturity and plant height for its significant positive correlation with grain yield. In contrast to this finding, [1] reported high positive direct effect of pods per plant and seeds per pod on seed yield. 1000 seed weight and stand count exerted maximum positive direct effect on grain yield which contributed for its non-significant positive correlation with grain yield. Powdery mildew showed the highest negative direct effect on grain yield which contributed to its non-significant negative correlation with grain yield. The

next maximum negative direct effect was exerted by Ascochyta blight and days to flower. Low negative direct effect was exhibited by seeds per pod on grain yield. This negative direct effect was counterbalanced by the positive indirect influence via days to mature and plant height for its significant positive correlation with grain yield.

The maximum positive indirect effect on grain yield was exhibited by powdery mildew, Ascochyta blight and plant height through days to maturity while the next maximum positive indirect effects were exerted by 1000 seed weight through powdery mildew and days to flower and number of seeds per pod through days to maturity.

The maximum negative indirect effects on grain yield was exhibited by 1000 seed weight through days to maturity while the next maximum negative indirect effects were exerted by Ascochyta blight and plant height through powdery mildew and stand count through days to maturity.

The magnitude of residual effect (0.34) indicated that traits included in path analysis explained about 66% of the variation in grain yield at phenotypic level. However, the remaining variation in grain yield (34%) can be attained by incorporating other yield related traits in the phenotypic path analysis.

**Table 4.** Estimates of direct (bold face) and indirect effect (off diagonal) at phenotypic level of nine traits on grain yield in 49 field pea genotypes of combined of the two locations, Bekoje and Kofele.

Traits	SCAH	FD	MD	PH	PPP	SPP	TSW	AB	PM	$r_{ph}$
SCAH	0.130143	0.033515	-0.62131	-0.00515	0.000749	0.00084	0.276329	0.106708	0.418459	0.08
FD	0.026029	-0.16758	0.475117	0.056669	0.006743	-0.00168	-0.12615	-0.08003	-0.23912	-0.05
MD	0.044249	-0.04357	1.827372	0.370924	0.00974	-0.00233	-0.43852	-0.33791	-1.09995	0.33**
PH	0.001301	-0.01843	1.315708	0.515173	0.014235	-0.00215	-0.24029	-0.26232	-0.75323	0.57**
PPP	-0.0013	-0.01508	0.237558	0.097883	0.074923	-0.00037	-0.03604	-0.01779	-0.05978	0.28*
SPP	0.011713	-0.03016	0.456843	0.11849	0.002997	-0.00934	-0.09611	-0.05335	-0.25108	0.15*
TSW	-0.05987	0.035191	-1.33398	-0.20607	-0.0045	0.001494	0.600715	0.240093	0.836919	0.11
AB	0.031234	-0.03016	1.388803	0.303952	0.002997	-0.00112	-0.32439	-0.44462	-0.8967	0.03
PM	0.04555	-0.03352	1.681182	0.324559	0.003746	-0.00196	-0.4205	-0.33346	-1.1956	0.07

Residual=0.34,  $R^2=0.88$  Where: - \*\*, \*, and ns=highly significant, significant and non-significant at 1%, 5% and  $P>0.05$  respectively. SCAH=Stand count at harvest, DF=Days to 50% flowering, DM=Days to maturity (days), PH=Plant height (cm), PPP=Pods per plant, SPP=Seeds per pod, TSW=Thousand seed weight, AB=Ascochyta blight, PM=Powdery mildew.

## 4. Conclusion

The current study showed that plant height, days to maturity, pods per plant and seeds per pod exhibited highly significant genotypic and phenotypic correlation with grain yield for combined analysis. The association among most of traits demonstrated higher genotypic correlations than corresponding phenotypic correlations that; indicated the prevalence of genetic variation in expression of the traits. In some cases, however, the magnitudes of phenotypic correlation coefficients were higher than their corresponding genotypic correlation coefficients suggesting the importance of environmental effects. Genotypic path analysis indicated that plant height exerted the higher positive direct effect on grain yield followed by pods per plant, seeds per pod and days to maturity. Phenotypic path analysis also showed that days to maturity exerted maximum positive direct effect on grain yield followed by plant height and pods per plant. Therefore; selection for traits such as plant height, pods per plant, seeds per pod and days to maturity could improve grain yield in field pea.

## Conflict of Interests

The authors have not declared any conflict of interests.

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