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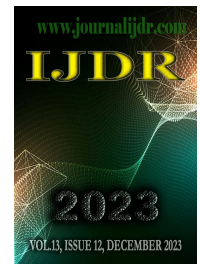
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GENOTYPIC AND PHENOTYPIC CORRELATION AND PATH COEFFICIENT ANALYSIS IN FIELD PEA (*PISUMSATIVUML.*) GENOTYPES AT BEKOJI, ETHIOPIA

Temesgen Abo^{1,*}, Wassu Mohamed², Tesfahun Alemu³

¹Kulumsa Agricultural Research Center (EIAR), Asella, Ethiopia

²School of Plant Sciences, Haramaya University, Haramaya, Ethiopia

³Holeta Agricultural Research Center (EIAR), Addis Ababa, Ethiopia

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*Corresponding author: *Temesgen Abo*

ABSTRACT

For resource-poor Ethiopian farmers, field pea (*Pisumsativum L.*) is the main source of protein. To increase the productivity of the crop and support farmers, the development of yield and disease-resistant varieties is an important activity. Thus, the purpose of this study was to examine genotypic and phenotypic correlation and path coefficient analysis and associated agronomic traits among field pea genotypes. Forty-nine field pea genotypes were evaluated in simple lattice design. A study was conducted during June- October 2020 cropping season at Bekoji sub research center. Data collected for morpho-agronomic traits were subjected for analysis of variance. Grain yield per plot had positive and highly significant genotypic association with plant height while highly significant phenotypic correlation observed between grain yield and plant height and biomass yield. In addition, grain yield had positive and highly significant phenotypic correlations with days to maturity, and grain filling period. The presence of highly significant and positive correlation of these traits with grain yield at genotypic and phenotypic levels indicated prime importance of these traits in selection program to identify field pea genotypes with high grain yield. Path coefficient analysis at genotypic levels showed that days to flowering and total biomass per plot had strong positive direct effect on grain yield per plot. The study showed the existence of reasonable associations among the yield and yield related traits that could be exploited in breeding programs.

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INTRODUCTION

Field pea is a self-pollinated and annual herbaceous legume belonging to the family Leguminosae and genus *Pisum* Duke, (1981) that prefers a cool, moist climate. It is thought to be originated in the Ethiopia, part of Europe and Asia Kumari *et al.*, (2022). Generally, field peas are grown as dry seeds, but they can also be harvested as green vegetables when immature. Field peas are used in Ethiopia in the form of split, milled seeds (Asfaw *et al.*, 1994). In addition to providing dietary protein to the farming community, it is also cost-effective compared to animal protein, thus complementing and supplying the cereal-based sector of the urban poor. Extensive areas of the central and northern highlands of Ethiopia are cultivated with field pea Temesgen, (2022). Historically, field pea has been grown in the Mediterranean and central Asian regions, as well as in the Ethiopian highlands. Field peas have been cultivated in Ethiopia since ancient times Kumari *et al.*, (2022) and their wild and primitive forms have been hidden in the highlands. The fact that Ethiopia has a variety of field peas makes it one of the centers of field pea diversity Hagedorn, (1991).

Globally, field peas are grown for their fresh green seeds, tender green pods, dried seeds, and soil restorative properties McPhee, (2003). "It contributes significantly to soil fertility restoration and is an inexpensive and valuable protein source (Gemechu, *et al.*, 2013). According to Alekseyeva, (2022) buckwheat can fix atmospheric nitrogen and solubilize native soil phosphorus and potassium (Das *et al.*, 2023). Peas grown in high-altitude areas (1800-3200) m.a.s.l" (Haddis and Dargie, 2013). "Among the highland pulse crops, Field pea is the third most important staple food legume crop in Ethiopia after faba bean and common bean. An average yield of 1.664 t ha⁻¹ is obtained from about 216,786.33 hectares of arable lands, covering 3,608,112.40 quintals of production. The area covered by pulses is 12.73 percent" Anonymous, (2019). "In Traditionally, Ethiopians eat field pea as part of their "Shiro wet", which is a stew served with local bread made of tef, or "Injera". Food, cash, and hunger relief crops are grown with faba beans (*Vicia faba*) in the highlands of the country (Gebeyew *et al.*, 2022). There are 344 calories, 20.1 grams of protein, and 64.8 grams of carbohydrates in 100 grams of edible field peas. As a cheap source of protein, it is often referred to as poor man's meat in developing countries. Although pea protein is deficient in sulfur-containing amino acids (Cysteine and methionine), it can still provide a balanced diet in combination with wheat, rice, and other

cereals” (Santalla *et al.*, 2001). “A Field pea has a dual advantage in fixing atmospheric nitrogen and serves as a break crop” Gemechu and Seid, (2016). “Field peas are an important crop in Ethiopia, but they are severely constrained by aphids, low-yielding local varieties, lodging, diseases (ascochyta blight, powdery mildew), and pod shattering (Gebeyew *et al.*, 2022). The fungus spreads via air currents, while rain controls the disease by washing away spores and preventing them from germinating” Sharma, (1995). The development of resistant varieties is the most effective management strategy against pathogens (Warkentin and Smýkal, 2015).

Experimental Materials and Design: Forty-nine field pea genotypes obtained from Kulumsa Agricultural Research Center 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 (3.2m²) 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 accretions

Acc.code	Genotype name	Seed Source	Acc.code	Genotype name	Seed Source
G-1	Bursa	Breeder seed	G-26	EH 010009-2	PVT 2018
G-2	Burkitu	Breeder seed	G-27	EH 08003-1	NVT 2018
G-3	EH 05048-5	NVT 2018	G-28	EK 08023-5	NVT 2018
G-4	EH 08034-2	NVT 2018	G-29	EH 08016-2	NVT 2018
G-5	EH 010006-2	PVT 2018	G-30	EH 08027-1	NVT 2018
G-6	EH 08021-1	NVT 2018	G-31	EH 08027-3	NVT 2018
G-7	EH 09021-5	NVT 2018	G-32	EK 08017-5	NVT 2018
G-8	EH 08003-2	NVT 2018	G-33	EK 08016-4	NVT 2018
G-9	EH 08036-4	NVT 2018	G-34	EH 08003-7	NVT 2018
G-10	EH 010005-2	PVT 2018	G-35	EK 08024-4	NVT 2018
G-11	EH 08027-2	NVT 2018	G-36	EK 08017-3	NVT 2018
G-12	EH 08036-1	NVT 2018	G-37	PDFPT p-313-050	ICARDA
G-13	EH 08041-3	NVT 2018	G-38	PDFPT p-313-015	ICARDA
G-14	EH 07005-1	NVT 2018	G-39	PDFPT p-313-017	ICARDA
G-15	EH 010011-3	PVT 2018	G-40	PDFPT p-313-26	ICARDA
G-16	EH 07002-1	NVT 2018	G-41	PDFPT p-313-020	ICARDA
G-17	EH 08021-4	NVT 2018	G-42	PDFPT p-313-052	ICARDA
G-18	EH 010004-1	PVT 2018	G-43	PDFPT p-313-062	ICARDA
G-19	EH 07006-5	NVT 2018	G-44	PDFPT p-313-098	ICARDA
G-20	EH 010009-1	PVT 2018	G-45	PDFPT p-313-022	ICARDA
G-21	EH 08042-2	NVT 2018	G-46	GIZ 02019 – 1	GERMANY
G-22	EH 07007-5	NVT 2018	G-47	GIZ 02019 – 2	GERMANY
G-23	EH 08041-4	NVT 2018	G-48	PDFPT p-313-028	ICARDA
G-24	EH 08042-4	NVT 2018	G-49	PDFPT p-313-065	ICARDA
G-25	EH 08041-1	NVT 2018			

Seed Source: Kulumsa Agricultural Research Center

“The high diversity of field pea accessions can be attributed to the strong representation of its centers of domestication, the Near East and Mediterranean (Van der *et al.*, 1988), as well as other centers of diversity, including Central Asia and Ethiopia”. Ethiopia is a secondary center of genetic diversity for field peas due to the diversity of its germplasm (Smýkal *et al.*, 2011). Through selection and/or hybridization breeding programs, Ethiopia has the potential to improve field pea for desired traits (Temesgen *et al.*, 2021). In order for a breeding program to be successful, genetic variability must be taken into account. In field pea breeding programs, landraces and accessions are selected and evaluated based on the existing diversity Temesgen, (2021). This indicates a great deal of potential for the breeding program. Selection among a diverse population can provide a certain level of success in breeding, but crossings are necessary to combine different contrasting genotypes to create a hybrid that combines the traits of interest and produces heterosis (Gosal, 2002). As a result, this study was conducted using field pea populations from the breeding program with the following specific objectives. Therefore, the objective of this study was to assess associations among yield and yield related traits of field pea genotypes.

MATERIALS AND METHODS

Description of the Study Area: The experiments were conducted at Bekoji research site of Kulumsa Agricultural Research Center during June-October 2020 main cropping season. Bekoji is located 39°14'46"E longitude and 07°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 eutricnitolsols 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).

All agronomic management practices were applied equally and properly as per the recommendations of Kulumsa Agricultural Research Center for Bekoji sub center.

Data Collection: Data on agronomic and morphological traits were collected on plot and individual plant basis. In this experiment the following data was recorded in plot and average plant basis.

Data Collected on Plot Basis

- 1) **Days to 50% flowering (DTF):** The number of days from the date of sowing to the date at which about 50% of the plants in a plot showed blooming on about 50% of their flower buds.
- 2) **Days to 90% maturity (DTM):** The number of days from the date of sowing to a stage when 90% of plants have reached their physiological maturity was assessed by yellowish foliage color and shedding start on the lower stem, pods and seeds hardened.
- 3) **Thousand Seed weight (TSW) (g):** the weight in gram of 1000 seeds randomly taken from the each plot.
- 4) **Grain Yield (g/plot):** the net plot grain yield in gram per plot Gy(g/plot).
- 5) **Grain Yield per Hectare (kg/ha):** The net plot grain yield adjusted at 10.0% moisture content was converted in to yield per hectare in a kilogram.
- 6) **Grain Filling Period (GFP):** The number of days from days to 50% flowering to days to 90% physiological maturity.
- 7) **Above Ground Total Biomass per Plot (TBPP):** The mean weight of above ground parts sun dried and weighted to get the biological yield per plot in grams.
- 8) **Harvest index (HI):** ratio of grain yield which is oven dried over total biomass of oven dried.

This was calculated by the following formula:

$$\text{Harvest index (HI)\%} = \frac{\text{Seed yield per plot(g)}}{\text{Biomass per plot(g)}} 100$$

Data Collected on Plant Basis

- 1) Plant Height (PH): Average height of five randomly selected plants in each plot measured (cm) from the ground surface to the top of the main stem at physiological maturity (where the color of their pods changed from green to lemon yellow).
- 2) Pod length (PL): Average length of 25 fully matured pods randomly taken from each five sample plants per each test genotype was measured from the pod apex to the peduncle in centimeters.
- 3) Number of pods per plant (PPP): Average number of mature pods, counted at harvest on five randomly taken plants.
- 4) Number of Seeds Per Pod (SPP): Average number of seeds per pod, counted at harvest on five randomly taken plants, in five randomly taken pods per plant.

Association among Yield and Yield Components

Genotypic and Phenotypic Correlation of Grain Yield with Other Traits: The results of genotypic correlation analysis are presented in Table 2. Grain yield had positive and highly significant correlations with plant height, harvest index and total biomass at genotypic levels (Table 2) Devi *et al.*, (2022) also reported a positive and significant correlation between seed yield and plant height, pods plant-1. In addition, grain yield had positive and highly significant genotypic correlations with days to maturity and grain filling period (Table 2). (Asfakun *et al.*, 2013) Reported a positive and highly significant genotypic correlation of grain yield with day to maturity and pod length. Grain yield had positive and highly significant correlations with harvest index and total biomass at phenotypic levels (Table 2). In addition, grain yield had positive and highly significant phenotypic correlations with days to maturity, plant height and grain filling period at Bekoji (Table 2).

yield traits at genotypic levels at Bekoji. Days to flowering and thousand seed weight have non-significant correlations with grain yield at genotypic level (Table 2). The presence of non-significant correlations of the traits with grain yield indicated that the two traits are independent of each other.

Genotypic and Phenotypic Correlation Coefficients Among Yield Related Traits: Phenotypic correlation coefficient for all possible combinations of the eight traits is presented in Table 3. The correlation among the yield related traits showed that days to maturity has positive and significant correlation with plant height and biomass yield (Table 3) Similar results were reported by (Gizachew *et al.*, 2022). Similarly, biomass yield correlated positively with days to maturity, plant height. However, no significant negative correlation was observed among the measured traits. The result of present study is similar to the results reported by (Barkat *et al.*, 2019) that indicated the positive and highly significant correlation between seed yield and plant height. The phenotypic correlation among other traits was observed in this study like total biomass yield was positively and highly significantly correlated with days to maturity and plant height. Similar results were reported by (Alemu *et al.* 2017) for thousand seed weight, plant height, biomass yield, harvest index and days to physiological maturity (Table 3). This showed the longer the grain filling period the higher the grain yield through availability of more time for the transfer of sink to the seed.

Path Coefficient Analysis

Genotypic and Phenotypic Path Analyses of Yield and Other Traits: Only characters that had significant relationship with grain yield were included in the path analysis (K.M, *et al.*, 2018). The results of genotypic path coefficient analysis of grain yield with other traits are presented in Table 4. While, phenotypic path coefficient analysis of grain yield with other traits are presented in Table 5. Days to physiological maturity, Plant height, harvest index, thousand seed

Table 2. Genotypic correlation coefficients among eight traits at Bekoji in 2020

Trait	DTF	DTM	PHT	GFP	HI	GY	TSW	TBM
DTF	1	0.51 ^{ns}	0.46 ^{ns}	-0.40 ^{ns}	-0.52 ^{ns}	0.07 ^{ns}	-0.33 ^{ns}	0.52 ^{ns}
DTM		1	0.54 ^{***}	0.59 ^{***}	-0.25 ^{ns}	0.43 ^{***}	-0.12 ^{ns}	0.71 ^{***}
PHT			1	0.14 ^{ns}	-0.27 ^{ns}	0.33 [*]	-0.08 ^{ns}	0.58 ^{***}
GFP				1	0.22 ^{ns}	0.38 [*]	0.19 ^{ns}	0.27 ^{ns}
HI					1	0.55 ^{***}	0.13 ^{ns}	-0.06 ^{ns}
GY						1	0.26 ^{ns}	0.79 ^{***}
TSW							1	0.13 ^{ns}
TBM								1

DTF = Date to flowering, DTM = Date to maturity, PHT = plant height, GFP = Grain filling period, HI = Harvest index, GY = Grain yield, TSW = Thousand seed weight, TBM = Total Biomass.

Table 3. Phenotypic correlation coefficients among eight traits at Bekoji

Trait	DTF	DTM	PHT	GFP	HI	GY	TSW	TBM
DTF	1	0.48 ^{ns}	0.42 ^{ns}	-0.43 ^{ns}	-0.47 ^{ns}	0.07 ^{ns}	-0.28 ^{ns}	0.47 ^{ns}
DTM		1	0.50 ^{***}	0.59 ^{ns}	-0.23 ^{ns}	0.38 ^{**}	-0.12 ^{ns}	0.66 ^{***}
PHT			1	0.12 ^{ns}	-0.25 ^{ns}	0.32 [*]	-0.04 ^{ns}	0.55 ^{***}
GFP				1	0.19 ^{ns}	0.33 [†]	0.14 ^{ns}	0.25 ^{ns}
HI					1	0.56 ^{***}	0.06 ^{ns}	-0.03 ^{ns}
GY						1	0.16 ^{ns}	0.79 ^{***}
TSW							1	0.09 ^{ns}
TBM								1

DTF = Date to flowering, DTM = Date to maturity, PHT = plant height, GFP = Grain filling period, HI = Harvest index, GY = Grain yield, TSW = Thousand seed weight, TBM = Total Biomass.

These results agree with (Alemu *et al.*, 2017) reported grain yield/plot positively and significantly correlated with harvest index and biomass yield/plot. The presence of highly significant and positive correlation of these traits with grain yield at genotypic and phenotypic levels indicated prime importance of these traits in selection program to identify field pea genotypes with high grain yield (Temesgen *et al.*, 2023). Direct selection only for higher yield could be misleading because many factors interact to determine crop yield. Similar results were reported by (Alemu *et al.*, 2017) for thousand seed weight, plant height, biomass yield, harvest index and days to physiological maturity. Grain yield had not any negative associations with grain

weight and total biomass have positive and highly significant direct effect while, days to flowering and grain filling period had showed negative and highly significant direct effect at phenotypic level (Table 4). (Asfakun, *et al.*, 2013) reported a positive direct effect of days to 50% flowering, number of pods per plant and hundred seed weight on grain yield. The trait which has positive correlation with grain yield and has large and positive direct effect the trait is considered as an important component of yield (Temesgen *et al.*, 2023). Plant height, harvest index and total biomass have significant and positive association with grain yield at genotypic level (Temesgen *et al.*, 2021).

Table 4. Genotypic direct (bold face and at the diagonal) and indirect effects (off the diagonal) of seven characters on grain yield per plot at Bekoji

Trait	DTF	DTM	PHT	GFP	HI	TSW	TBM	$r_{p(GY,x)}$
DTF	0.992	-0.602	0.021	-0.443	-0.302	-0.019	0.423	0.07
DTM	0.506	-1.180	0.024	0.654	-0.145	-0.007	0.578	0.43
PHT	0.456	-0.637	0.045	0.155	-0.157	-0.005	0.472	0.329**
GFP	-0.397	-0.696	0.006	1.109	0.128	0.011	0.220	0.381***
HI	-0.516	0.295	-0.012	0.244	0.581	0.007	-0.049	0.55
TSW	-0.327	0.142	-0.004	0.211	0.075	0.057	0.106	0.26
TBM	0.516	-0.838	0.026	0.299	-0.035	0.007	0.814	0.789***

R-squared: 0.9753179

Residual effect: 0.1571054

k-value (for collinearity): 0

Note: DTF = Days to flowering, DTM = Days to maturity, PHT = plant height, GFP = Grain filling period, HI = Harvest index, GY = Grain yield, TSW = Thousand seed weight, TBM = Total Biomass.

Table 5. Phenotypic direct (bold and diagonal) and indirect effects (off the diagonal) of seven characters on grain yield per plot at Bekoji in 2019

Trait	DTF	DTM	PHT	GFP	HI	TSW	TBM	$r_{p(GY,x)}$
DTF	0.202	0.016	0.185	-0.264	-0.011	0.386	0.032	0.070
DTM	-0.213	0.420	0.019	-0.254	-0.129	-0.005	0.542	0.380**
PHT	-0.186	0.210	0.038	-0.052	-0.140	-0.002	0.452	0.320
GFP	0.191	0.248	0.005	-0.431	0.107	0.006	0.205	0.330
HI	0.208	-0.097	-0.010	-0.082	0.562	0.002	-0.025	0.560***
TSW	0.124	-0.050	-0.002	-0.060	0.034	0.040	0.074	0.160
TBM	-0.208	0.277	0.021	-0.108	-0.017	0.004	0.821	0.790***

R-squared: 0.968388

Residual effect: 0.177797

k-value (for collinearity): 0

DTF = Days to flowering, DTM = Days to maturity, PHT = plant height, GFP = Grain filling period, HI = Harvest index, GY = Grain yield, TSW = Thousand seed weight, TBM = Total Biomass

These indicate that those traits had true association with grain yield and their importance in determining these complex traits. Therefore, important consideration should be given while practicing selection aimed at the improvement of grain yield. According to Wright, (1921) path coefficient analysis provides a better knowledge of direct and indirect causes of associations. Days taken to maturity and days to 50% flowering have a negative direct effect at genotypic and phenotypic level; whereas positive indirect effects with plant height, grain filling period and total biomass at Bekoji (Temesgen *et al.*, 2021). Plant height had also positive direct effect at phenotypic level where as it had negative indirect effect on grain yield with days to flowering, harvest index and thousand seed weight. Plant height had positive direct effect on grain yield, but had a negative indirect effect on grain yield through days to 50% flowering, harvest index and thousand seed weight. Also total biomass had positive direct effect and had a negative indirect effect with harvest index, days to flowering and days to maturity at genotypic level (Temesgen *et al.*, 2023). Legesse, (2015) reported higher positive direct effects of days to maturity, biological yield, harvest index and hundred seed weight on seed yield, indicating that selection of superior field pea genotypes for seed yield on the basis of these characters would be effective (Thakur *et al.*, 2019) reported that path coefficients for seed yield per plant recorded the highest positive direct effect contributing to seed yield plant⁻¹ is, harvest index followed by biological yield, pods plant⁻¹, primary branches plant⁻¹ plant height, days to 50 % flowering. Whereas, negative direct effects on seed yield per plant were observed due to days to maturity and 100 seed weight. (Temesgen *et al.*, 2021) reported a positive direct effect of plant height (0.419), day to maturity (0.189), day to flower initiation (0.066) and number of seed per pod (0.087) has positively direct effect on seed yield. Residual effect in genotypic path analyses was 0.1571 (Table 4), showing that 84.29% of the variability in seed yield was explained by the component factors at genotypic levels respectively. The remaining 15.71 % variation could be explained by other explanatory variable not control in this research; while at phenotypic level residual effect was 0.1778, indicating that 82.22% of variability was explained by component factors (Table 4) (Temesgen *et al.*, 2021).

CONCLUSION

This study was conducted to assess the extent of genetic variability for grain yield and yield related traits in field pea. At Bekoji the positive highly significant correlation was observed between grain yield per plot with days to maturity, seed per pod, pod per plant, harvest index and total biomass/plot. The genotypic path analysis, days to 50% flowering, plant height, grain filling period, thousand seed weight, harvest index and total biomass showed strong positive direct effect on grain yield per plot. Total biomass, grain filling period and plant height showed strong significant positive correlation with grain yield per plot that indicate these trait can be used as indirect selection criteria to improve grain yield.

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