



ISSN: 2230-9926

Available online at <http://www.journalijdr.com>

# IJDR

International Journal of Development Research

Vol. 14, Issue, 08, pp. 66446-66451, August, 2024

<https://doi.org/10.37118/ijdr.28554.08.2024>



RESEARCH ARTICLE

OPEN ACCESS

## GENOTYPIC AND PHENOTYPIC CORRELATION AND PATH COEFFICIENT ANALYSIS IN FIELD PEA (*PISUM SATIVUM* L.) GENOTYPES AT ASASA, ETHIOPIA

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### ARTICLE INFO

#### Article History:

Received 11<sup>th</sup> May, 2024  
Received in revised form  
14<sup>th</sup> June, 2024  
Accepted 09<sup>th</sup> July, 2024  
Published online 30<sup>th</sup> August, 2024

#### Key Words:

Genotypic correlation, Phenotypic correlation, direct effect, Path Coefficient, (*Pisum sativum*).

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### ABSTRACT

In Ethiopia, field pea (*Pisum sativum* L.) is the main source of protein for resource poor growers. The improvement of varieties for yield and disease resistance is one of the important activities to support farmers and improve the productivity of the crop. Consequently, this study was showed to evaluate the genotypic correlations, phenotypic correlations and path coefficient analysis between the field pea genotypes for yield and yield associated traits. Forty-nine field pea genotypes were evaluated in simple lattice design at Asasa in 2019 cropping season. Data collected for morpho-agronomic traits were subjected for analysis of variance. The analysis of genotypic correlations, phenotypic correlations and path coefficient showed significant differences among genotypes for most of the traits. Grain yield per plot had positive and highly significant genotypic association with plant height, while highly significant phenotypic correlation observed between grain yield and harvest index and biomass yield. Days to flowering had positive and highly significant genotypic association with days to 90% physiological maturity, plant height and biological yield, while negative and highly significant genotypic association with harvest index. Days to 90% physiological maturity had positive and highly significant genotypic association with plant height and total biomass, while negative and highly significant genotypic association with harvest index. Path coefficient analysis at genotypic levels showed that harvest index and total biomass per plot had strong positive direct effect on grain yield per plot. Residual effect in genotypic path analyses at Asasa was 0.1996 (Table 4), showing that 80.04% of the variability in seed yield was explained by the component factors at genotypic levels. The remaining 19.96 % variation could be explained by other explanatory variable not control in this research; while at phenotypic level residual effect was 0.1017 at Asasa indicating that 89.83% of variability was explained by component factors (Table 5). The study showed the existence of reasonable genetic variability among the field pea genotypes that could be exploited in breeding programs.

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Citation: Temesgen Abo and Wassu Mohamed. 2024. "Genotypic and Phenotypic Correlation and path Coefficient Analysis in field pea (*Pisum Sativum* L.) Genotypes at Asasa, Ethiopia". International Journal of Development Research, 14, (08), 66446-66451.

## INTRODUCTION

Field pea (*Pisum sativum* L.) is self-pollinated an annual herbaceous legume crop that belongs to family Leguminosae and genus *Pisum* (Duke, 1981). It is a diploid species ( $2n=2x=14$  chromosomes) and has determinate (bush or dwarf) or indeterminate (climbing) growth habit (majority of pea plants) (Zohary and Hopf, 2002). The center of origin for field pea is considered the Mediterranean to central Asia as well as the highlands of Ethiopia (Davies, 1976). Extensive areas of the central and northern highlands of Ethiopia are cultivated with field pea Temesgen (2022). In Ethiopia field pea is cultivated since ancient time in Ethiopia (Dawit *et al.*, 1994) and its wild and primitive forms of the species was concealed in the highlands of Ethiopia. Due to this fact Ethiopia considered as one of the centers of diversity for field pea Temesgen (2021). Field pea grow around the world for its fresh green seeds, tender green pods, dried seeds, and soil restorative purposes (McPhee, 2003). Field pea ranked as fourth largest in the world in volume of production in 2014 with 17.4 and 11.2 million tons of green and dry peas respectively, after soybean, groundnut and common bean (William *et al.*, 2017).

In Ethiopia, *Pisum sativum var. sativum* is grown in high altitude area (1800-3200) m.a.s.l (Haddis Yirga *et al.*, 2013). Among the highland pulse crops Field pea is the third most important staple food legume crop in Ethiopia next to faba bean and common bean, among the highland pulses. Field pea covers about 216,786.33 hectares of arable lands with a total production of 3,608,112.40 quintals with average yield of 1.664 t ha<sup>-1</sup>. It constitutes 12.73% of the total area covered by pulses (CSA, 2019). In Ethiopia, field pea is mainly used to prepare "shiro wet", a stew eaten with local bread made of teff, i.e. "Injera". The crop is commonly grown in association with faba bean (*Vicia faba*), and is important food, cash and "hunger break" crop in highlands of the country Temesgen, (2021). Field pea supplies 344 calories, 20.1 g protein and 64.8 g carbohydrates/100g edible portion (Asfaw *et al.*, 1994). It is known as poor man's meat in the developing world since it provides valuable cheap protein. In combination with wheat, rice and other cereals it provides a balanced diet (Santalla *et al.*, 2001) though pea protein is deficient in sulphur-containing amino acids (Cysteine and methionine) (McPhee, 2003). A Field pea has a dual advantage in fixing atmospheric nitrogen and serves as a "break crop" (Gemetchu *et al.*, 2016). Despite the importance of field pea in Ethiopia, the major yield-limiting

constraints in field pea production in Ethiopia are aphids, low yielding local varieties, lodging, diseases (ascochyta blight, powdery mildew), and pod shattering (Gebeyew *et al.*, 2022). This fungus spread locally with air currents, whereas rain controls the disease by washing off spores and making them burst instead of germinating (Hagedorn, 1991). The most preferable management measure against the pathogen is developing resistant varieties (Sharma, 1995). The high diversity of the field pea accession associated with the robust representation of its center of domestication, that is, the Near East and Mediterranean (Warkentin *et al.*, 2015) and other centers of diversity, including Central Asia and Ethiopia (Van der Maesen *et al.*, 1988). The existence of wide range of field pea germplasm in Ethiopia makes the country the secondary center of genetic diversity (Gemechu *et al.*, 2012). Some scholars also considered the high elevation of Ethiopia within the range of the center of origin of the crop (Temesgen, 2021). This indicates that has Ethiopia the potential for improving field pea for desired traits either through selection and/or hybridization breeding programs. Genetic variability is the key factor for the success of any breeding program. In field pea, studies showed that the landraces and accessions in the breeding programs are focused on selection and evaluation from the existing diversity (Smykal *et al.*, 2011). That indicates the great potential for the breeding program. Even selection among a diverse population provide a certain amount of success in the breeding program, crossing will be essential to combine to different contrasting genotypes to produce a hybrid that combine the trait of interest and produce heterosis (Arunachalam and Bandyopadhyay, 1984; Reddy, 1988; Singh, 1990; Wallace and Yan 1998; Chahal and Gosal, 2002).

the target trait (like yield) will be important. Yield it is highly affected by different yield component traits that required a clear understanding how these traits affect yield and designing a selection procedure. This indicate sometimes direct selection for the target trait (grain yield) which is a polygenic trait may not be effective in a unless yield contributing traits are considered during selection (Srivastava *et al.*, 2017). So, to have a successful breeding program, the breeder should study the genetic variability of the base population, understand the nature of inheritance of the traits and understand the interrelationship among traits of interest to design the breeding strategy. Despite the large number of filed pea accessions held in the gene bank of Ethiopia, Limited information available on the magnitude and pattern of genetic variability for these materials. Therefore, this study was conducted in the field pea populations of the breeding program with the following specific objectives. The objectives of this study were to examine the phenotypic and genotypic correlations in a set of diverse pea genotypes using morphological and agronomic characters of field pea genotypes.

## MATERIALS AND METHODS

**Description of the Study Area:** The experiments were conducted at Asasa research site of Kulumsa Agricultural Research Center during 2019 main cropping season. Asasa is located at 07°06'12"N latitude and 38°11'32"E longitude with an altitude of 2340 m.a.s.l. The site receives an average annual rainfall of 620 mm with the average annual minimum and maximum temperatures of 5.8°C and 23.6°C,

**Table 1. Discription of Fieldpea 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 and Holeta Agricultural Research Centers

The crossing among the highly divergent parents can produce varieties with broad genetic base (Russell, 1978; Chandel and Joshi, 1983; Singh, 1990) (Gemechu *et al.*, 1997) and raises the yield ceilings imposed by a narrow genetic base (Chandel and Joshi, 1983). The national field pea program conducted research activities and released about 46 varieties, still now these varieties did not address the production constraints of field pea in the country (MOANR, 2016). So, to design appropriate breeding strategy assessing the genetic variability and estimating the genetic parameters (heritability of traits) in the base population will be prerequisite since it is the base to get high yielding; biotic and abiotic stress tolerant varieties. In addition, assessing the genotype x environment interaction will be crucial since most of the traits are governed through polygenic inheritance that affected mostly by the environment (Legesse, 2015; Benti and Yohannis, 2017). Besides to plan appropriate selection method understanding the association among traits and its effect on

respectively. The soil type of Asasa is gleysol and its pH is 6.25 light sandy soil with low water holding capacity (Kulumsa Agricultural Research Center meteorology station unpublished paper).

**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

**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.

**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.

**Thousand Seed weight (TSW) (g):** the weight in gram of 1000 seeds randomly taken from the each plot.

**Grain Yield (g/plot):** the net plot grain yield in gram per plot Gy(g/plot).

**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.

**Grain Filling Period (GFP):** The number of days from days to 50% flowering to days to 90% physiological maturity.

**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.

**Harvest index (HI):** ratio of grain yield which is oven dried over total biomass of oven dried.

This was calculated by the following formula:

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

#### Data Collected on plant basis

**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).

**Experimental Materials and Design:** Forty-nine field pea genotypes obtained from Kulumsa and Holeta Agricultural Research Centers was used for this study. The list and description of the materials used for the study are presented in (Table 1). A plot size of 4m x 0.8m (3.2m<sup>2</sup>) 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 location and each genotype was assigned randomly in blocks of each replication. All agronomic management practices were applied equally and properly as per the recommendations of Kulumsa Agricultural Research Center for each location.

**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.

**Number of pods per plant (PPP):** Average number of mature pods, counted at harvest on five randomly taken plants.

**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.

#### Data Analysis

**Estimation of phenotypic and genotypic correlations:** Phenotypic and genotypic correlation coefficients were estimated using the formulae of Weber and Moorthy (1952).

$$r_g(xy) = \frac{Gcov(x,y)}{\sqrt{\sigma_{gx}^2 \times \sigma_{gy}^2}}$$

Where  $r_g$  = genotype correlation coefficient,  $Gcov(x,y)$  = genotype co-variance between Variable x and y,  $\sigma_{gx}^2$  = genotype

variance for variable x,  $\sigma_{gy}^2$  = genotype variance for variable y. The phenotypic correlation was calculated as follow:

$$r_{p(xy)} = \frac{Pcov(x,y)}{\sqrt{\sigma_{px}^2 \cdot \sigma_{py}^2}}$$

Where  $r_p$  =phenotype correlation coefficient,  $Pcov(x,y)$  = phenotype co-variance between variable x and y,  $\sigma_{px}^2$ = phenotype variance for variable x,  $\sigma_{py}^2$ = phenotype variance for variable y.

**Path coefficient analysis:** In path coefficient analysis, yield per plot was taken as a dependent variable while the rest of the characters were considered as independent variables. The direct and indirect effects of the independent traits on field pea yield per plot were estimated by the simultaneous solution of the following general formula suggested by (Dewy and Lu, 1959).

$$r_{ij} = p_{ij} + \sum r_{ik} p_{jk}$$

Where,  $r_{ij}$  = mutual association between independent variable (i) and dependent variable (j) as measured by phenotypic and genotypic correlation coefficient,  $p_{ij}$  = component of direct effect of independent variable (i) as measured by the phenotypic and genotypic path coefficient,  $\sum r_{ik} p_{jk}$  = summation of components of indirect effect of a given independent variable (i) on a given dependent variable (j) via all other independent characters (k). The path analysis based on the genotypic and phenotypic correlation coefficients were estimated using the "path analysis" function of the bio-tools package of R (da Silva, 2017). From the analysis the  $R^2$  that indicate the proportion of the variance accounted by the independent variables and U, the residuals not explained by the model also estimated.

## RESULTS AND DISCUSSION

#### Genotypic and Phenotypic Correlation Coefficients among Yield

**Related Traits:** Phenotypic correlation coefficient for all possible combinations of the eight traits is presented in Table 2 and 3. At Asasa, a correlation among other traits indicated with harvest index has significant positive correlation with grain filling period, but negatively correlated with days to flowering and, days to maturity. This showed the complex nature of association among traits in field pea. The negative correlation was observed between thousand seed weight and days to 50% flowering (-0.1) that showed the increase in one trait may reduce the performance in other traits. This association also explained with the positive association of plant height and days to maturity (Table 3). The result of present study is similar to the results reported by Temesgen *et al.* (2023) that indicated the positive and highly significant correlation between seed yield and plant height. Also Barkat *et al.* (2019) reported positive and highly significant correlation seed yield between plant heights. At Asasa, harvest index also has negative and significant correlation with biomass yield and grain filling period but has negative correlation with days to flowering and days to maturity. Similar results were reported by Temesgen *et al.* (2023) for days to flowering and days to maturity. 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. In addition the negative correlation of days to flowering and grain filling period indicated the impact of the terminal stress at Asasa late flowering accessions.

#### 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 (Dewy and Lu, 1959). The results of genotypic path coefficient analysis of grain yield with other traits are presented in Table 4 at Asasa.

**Table 1. Genotypic correlation coefficients among seven traits at Asasa in 2019**

Trait	DTF	DTM	PHT	GFP	HI	GY	TSW	TBM
DTF	1	0.51***	0.40**	-0.24	-0.61***	-0.03 <sup>ns</sup>	-0.1 <sup>ns</sup>	0.43**
DTM		1	0.74***	-0.96	-0.69***	0.13 <sup>ns</sup>	-0.09 <sup>ns</sup>	0.69***
PHT			1	-0.17	-0.18 <sup>ns</sup>	0.41**	0.1 <sup>ns</sup>	0.57***
GFP				1	0.42**	0.05	0.07	-0.25
HI					1	0.48***	0.17 <sup>ns</sup>	-0.31*
GY						1	0.23 <sup>ns</sup>	0.69***
TSW							1	0.01 <sup>ns</sup>
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 2. Phenotypic correlation coefficients among eight traits at Asasa in 2019**

Trait	DTF	DTM	PHT	GFP	HI	GY	TSW	TBM
DTF	1	0.4**	0.36**	-0.92***	-0.52***	-0.04 <sup>ns</sup>	-0.1 <sup>ns</sup>	0.38**
DTM		1	0.58***	-0.02 <sup>ns</sup>	-0.40**	0.14 <sup>ns</sup>	-0.06 <sup>ns</sup>	0.52***
PHT			1	-0.13 <sup>ns</sup>	-0.13 <sup>ns</sup>	0.26 <sup>ns</sup>	0.11 <sup>ns</sup>	0.41**
GFP				1	0.39**	0.07 <sup>ns</sup>	0.09 <sup>ns</sup>	-0.21 <sup>ns</sup>
HI					1	0.53***	0.19 <sup>ns</sup>	-0.2 <sup>ns</sup>
GY						1	0.2 <sup>ns</sup>	0.71***
TSW							1	0.02 <sup>ns</sup>
TBM								1

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 3. Genotypic direct (bold face and at the diagonal) and indirect effects (off the diagonal) of seven characters on grain yield per plot at Asasa**

Trait	DTM	DTF	PHT	GF	HI	TSW	TBM	$r_{G(GY,x)}$
DTM	0.057	0.021	0.013	0.001	-0.52	-0.008	0.56	-0.03 <sup>ns</sup>
DTF	0.029	0.041	0.007	0.005	-0.459	-0.009	0.353	0.13 <sup>ns</sup>
PHT	0.042	0.016	0.018	0.001	-0.136	0.009	0.463	0.41**
GFP	-0.04	-0.025	-0.003	-0.005	0.314	0.006	-0.204	0.48**
HI	-0.04	-0.025	-0.003	-0.002	0.754	0.015	-0.254	0.48**
TSW	-0.005	-0.004	0.002	-0.001	0.129	0.089	0.011	0.23 <sup>ns</sup>
TBM	0.039	0.018	0.01	0.001	-0.235	0.001	0.815	0.69**

R-squared: 0.9601497

Residual effect: 0.1996254

K-value (for collinearity): 0.05

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 4. Phenotypic direct (bold face and at the diagonal) and indirect effects (off the diagonal) of seven characters on grain yield per plot at Asasa**

Trait	DTM	DTF	PHT	GF	HI	TSW	TBM	$r_{P(GY,x)}$
DTM	0.018	-0.068	0.011	0.004	-0.27	-0.003	0.445	-0.04 <sup>ns</sup>
DTF	0.007	-0.173	0.007	0.16	-0.355	-0.006	0.324	0.14 <sup>ns</sup>
PHT	0.01	-0.062	0.019	0.023	-0.091	0.007	0.356	0.26 <sup>ns</sup>
GFP	0	0.159	-0.003	-0.173	0.264	0.005	-0.184	0.07 <sup>ns</sup>
HI	-0.007	0.09	-0.003	-0.067	0.681	0.011	-0.174	0.53***
TSW	-0.001	0.019	0.002	-0.016	0.127	0.058	0.014	0.2 <sup>ns</sup>
TBM	0.009	-0.065	0.008	0.037	-0.138	0.001	0.861	0.71 <sup>ns</sup>

R-squared: 0.9896496

Residual effect: 0.1017371

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.

While, phenotypic path coefficient analysis of grain yield with other traits are presented in Table 5 at Asasa. Days to physiological maturity, Plant height, harvest index, thousand seed 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 at Asasa (Table 5). Asfakun *et al.* (2013) reported appositive direct effect of days to 50% flowering, number of pods per plant and hundred seed weight on grain yield. Temesgen *et al.* (2023) reported a positive direct effect of days to 50% flowering, plant height, pods per plant, pod length, seed per pod, hundred seed weight, harvesting index and total biomass 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, (2021). According, plant height, harvest index and total biomass have significant and positive association with grain yield at genotypic level.

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. The path analysis is the partitioning of the total correlation into direct and indirect effects of independent variable(s) on dependent variable. 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 at Asasa. At Asasa, days to 50% flowering had negative direct effect where as it had a positive indirect effect on grain yield with total biomass, days to maturity, plant height and grain filling period. Also thousand seed weight had positive direct effect at phenotypic level on grain yield but had a negative indirect effect through days to maturity and grain filling period. Grain filling period had negative direct effect on grain yield but it had a positive indirect

effect on grain yield with days to maturity, plant height and biomass yield. And also harvest index have a positive direct effect at genotypic level where as it had a negative indirect effect on grain yield through total biomass, days to maturity, days to flowering, plant height and grain filling period Temesgen *et al*, (2023).

## SUMMARY AND CONCLUSIONS

This study was conducted to assess the extent of genotypic correlation and phenotypic correlation for grain yield and yield related traits in field pea. Genotypic correlation and phenotypic correlation for each character showed the existence of highly significant difference among genotypes ( $p \leq 0.01$ ) at Asasa sub research station. The genotypic correlation of grain yield per plot was positively and highly significantly correlated with plant height, harvest index and total biomass per plot. At Asasa the path analysis for grain yield at genotypic level showed that harvest index, thousand seed weight, plant height, days to flowering and days to maturity and total biomass yield exerted positive direct effect on grain yield per plot. Total biomass yield, grain filling period, plant height and harvest index showed positive significant correlation with grain yield that indicate these two traits can be used as indirect selection criteria to improve grain yield per plot. The strong positive direct effect was exerted at phenotypic level by total biomass, thousand seed weight, plant height, days to maturity and harvest index. Harvest index also have positive correlation with grain yield per plot that makes these traits more preferable for direct selection to improve grain yield per plot in field pea. The genetic parameter estimated in this study should be used to design the breeding program of field pea in the country. In order to have more concrete result and conclusion the study should be done by including more genotypes and tested across locations. It needs further studies on field pea to identify and select genotypes that have important agronomic properties and use them in direct hybridization. It should be worthwhile to study more available germplasm over years and locations to identify more accessions as well as to confirm the importance of the traits identified as predictors of yield.

**Acknowledgements:** The author would like to thank breeding and genetics research division staffs of Kulumsa Agricultural Research Center who managed the field experiments. The financial support provided from government fund by Ethiopian Institute of Agricultural Research (EIAR) is also duly acknowledged.

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