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Genotypic and Phenotypic Correlation and Path Coefficient for Quantitative Traits in Field Pea (*Pisum sativum* L.) Genotypes at Arsi Highland of Ethiopia

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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 two locations Bekoji and Asasa in 2018/2019 cropping time of year. Grain yield per plot had positive and highly significant genotypic association through plant height whereas highly significant phenotypic correlation observed between grain yield and plant height and biomass yield. At Bekoji 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. At Asasa the path analysis for grain yield at genotypic level showed that harvest index, thousand seed weight, plant height, days to 50% flowering and days to 95% physiological maturity and total biomass yield exerted positive direct effect on grain yield per plot. Path coefficient analysis at genotypic levels of the combined data exhibited that days to 50% flowering and total biomass per plot had strong positive direct effect on grain yield per plot. The phenotypic path analysis of the combined data revealed total biomass yield, thousand seed weight, plant height and days to maturity has strong positive direct effect on grain yield per plot. The study showed the existence of reasonable genetic variability between the field pea genotypes that can be exploited in breeding programs.

Keywords: Correlation Analysis, Path Analyses, Direct Effect, *Pisum sativum* L.

1. Introduction

Field pea (*Pisum sativum* L.) is between the best essential legume crop of Ethiopia, belongs to family Leguminosae [9]. The center of origin for field pea is considered the Mediterranean to central Asia as well as the highlands of Ethiopia [6, 17]. In Ethiopia field pea is cultivated since antique time in Ethiopia [7] and its wild and primitive methods of the species was covered in the highlands of Ethiopia. Due to this fact Ethiopia considered as one of the centers of diversity for field pea [17]. Field pea grow around the world for its dried seeds, fresh green seeds, tender green pods, and soil fertility purposes [13].

In Ethiopia, *Pisum sativum var. sativum* is grown in high altitude

area (1800-3200) m.a.s.l [12]. Field pea is the third best essential chief food legume crop in Ethiopia next to Faba bean and common bean, amongst the highland pulse crops. Field pea covers about 223657.49 hectares of arable lands with a total production of 3,905,635.50 quintals with average yield of 1.75 t ha^{-1}. It constitutes 12.16% of the total area covered by pulses [5].

The Field pea is usually grown in association with faba bean (*Vicia faba*), and is important food, cash and "hunger break" crop in highlands of the Ethiopia [17]. Field pea supplies 344 calories, 20.1 g protein and 64.8 g carbohydrates/100 g edible portion [2, 17]. It is known as poor man's meat in the developing world since it provides

valuable cheap protein. In grouping with wheat, rice and other cereals it provides a balanced diet [15, 17] however pea protein is deficient in sulphur- containing amino acids (Cysteine and methionine) [13].

A Field pea has a double benefit in preservative atmospheric nitrogen and helps as a crop rotation [10, 17].

The existence of wide range of field pea germplasm in Ethiopia makes the country the secondary center of genetic diversity [11]. Some scholars also considered the high elevation of Ethiopia within the range of the center of origin of the crop [17]. This indicates that has Ethiopia the potential for improving field pea for desired traits either through selection and/or hybridization breeding programs.

Yield it is highly affected by different yield component traits that necessary a strong understanding how these traits affect yield and planning a selection technique [17]. This indicates sometimes direct selection for the target trait (grain yield) which is a polygenic trait may not be effective in unless yield contributing traits are considered during selection [16].

Therefore, this study was conducted in the field pea genotypes of the breeding program with the following specific objectives.

Therefore, the objective of this study was to assertion the genotypic and phenotypic correlations between the field pea genotypes for yield and yield related traits.

2. Materials and Methods

2.1. Description of the Study Area

The experiments were conducted at Bekoji and Asasa research sites of Kulumsa Agricultural Research Center during 2019 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 eutric nitisols with a good drainage system. It contains 5.5% organic matter, 0.25% nitrogen and its PH is 5.35 (KARC, 2000). 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, respectively. The soil type of Asasa is gleysol and its pH is 6.25 light sandy soils with low water holding capacity (Kulumsa Agricultural Research Center meteorology station unpublished paper).

2.2. 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 (Table 1). A plot size of 4 m x 0.8 m (3.2 m^2) 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 1 m and 1.5 m, 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.

Table 1. Description of Field pea accetions.

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

Seed Source: Kulumsa and Holeta Agricultural Research Centers.

2.3. 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.

2.3.1. 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.

2.3.2. 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).

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.

3. Results and Discussion

3.1. Association Among Yield and Yield Related Traits

3.1.1. Genotypic Correlation of Grain Yield with Other Traits

The results of genotypic correlation analysis are presented in Table 2 at over locations. Grain yield had positive and highly significant correlations with plant height and total biomass at genotypic levels at two locations. Asfakun *et al,* [1] reported a positive and highly significant genotypic correlation of grain yield with days to 95% physiological maturity.

The presence of highly significant and positive correlation of these traits with grain yield at genotypic and phenotypic levels indicated main importance of these traits in selection program to identify field pea genotypes with high grain yield. [14] Similarly indicated the positive and highly significant correlation between seed yield and plant height.

Grain yield had not any negative associations with grain yield traits at genotypic levels, but grain yield had a non-significant association with days to 50% flowering, Days to 95% physiological maturity, grain filling period and thousand seed weight at over locations (Table 2). The presence of non-significant correlations of the traits with grain yield showed that the two characters are independent of each other.

Table 2. Genotypic (above diagonal) correlation coefficients among seven traits for the combined analysis.

Trait	DTF	DTM	PHT	GFP	GY	TSW	TBM
Days to 50% flowering	1	0.58***	0.46***	-0.78***	0.03 ns	-0.23 ns	0.52 ns
Days to maturity		1	0.80***	0.06 ns	0.25 ns	-0.08 ns	0.68***
Plant height			1	0.06 ns	0.41**	0.06 ns	0.68***
Grain filling period				1	0.13 ns	0.21 ns	-0.12 ns
Grain yield					1	0.21 ns	0.72***
Thousand seed weight						1	0.04 ns
Total biomass							1

3.1.2. Phenotypic Correlation Coefficients Among Yield Related Traits

Phenotypic correlation coefficient for all possible combinations of the seven 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). Similarly, biomass yield correlated positively with days to maturity and plant height, plant height positively and highly correlated with days to 50% flowering and days to maturity. However, thousand seed weight had no significant and negative correlation with days to 50% flowering and days to maturity that showed the increase in one trait may reduce the performance in other traits. This exhibited the complex nature of association between traits in field pea [17].

The result of current study is similar to the results reported by Mussa *et al.* [14] that indicated the positive and highly significant correlation between seed yield and plant height. Also Barkat *et al,* [3] reported positive and highly significant correlation seed yield between plant heights.

Table 3. *Phenotypic (below diagonal) correlation coefficients among seven traits for the combined analysis.*

Trait	DTF	DTM	PHT	GFP	GY	TSW	TBM
Days to 50% flowering							
Days to maturity	0.55***						
Plant height	0.43***	0.73***					
Grain filling period	-0.76***	0.12 ns	0.06 ns				
Grain yield	0.03 ns	0.23 ns	0.34*	0.13 ns			
Thousand seed weight	-0.22 ns	-0.08 ns	0.07 ns	0.19 ns	0.18 ns		
Total biomass	0.49 ns	0.63***	0.59***	-0.11 ns	0.73***	0.03 ns	

3.2. Path Coefficient Analysis

3.2.1. Genotypic Path Analyses of Yield and Other Traits

Only characters that had significant association with grain yield were incorporated in the path analysis [8]. The results of genotypic path coefficient analysis of grain yield with other traits are presented in Table 4. Days to 50% flowering, Plant height, grain filling period, thousand seed weight and total biomass have positive and highly significant direct effect at genotypic level (Table 4), whereas days to physiological maturity have a negative direct effect at genotypic level. Asfakun *et al,* [1] reported a positive direct effect of days to 50% flowering, number of pods per plant and hundred seed weight on grain yield.

3.2.2. Phenotypic Path Analyses of Yield and Other Traits

The results of phenotypic path coefficient analysis of grain yield through other traits are presented in Table 5. Days to physiological maturity, plant height, thousand seed weight and total biomass have positive and highly significant direct effect at genotypic level (Table 5), whereas days to 50% flowering and grain filling period have a negative direct effect at phenotypic level (Table 5).

Residual effect in phenotypic path analyses was 0.5386

(Table 5). Showing that 288.979% of the variability in seed yield was explained by the component factors at phenotypic levels respectively. The remaining 53.86% variation could be explained by other explanatory variable not control in this research.

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. 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 [19], path coefficient analysis provides a better knowledge of direct and indirect causes of associations.

Thakur *et al,* [18] 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. Benti *et al,* [4] reported a positive direct effect of plant height (0.419), day to maturity (0.189), day to flowering (0.066) and number of seed per pod (0.087) has positively direct effect on seed yield.

Table 4. *Genotypic direct (bold face and at the diagonal) and indirect effects (off the diagonal) of six characters on grain yield per plot for the combined analysis.*

Trait	DTF	DTM	PHT	GF	TSW	TBM	rg(GY,x)
DTF	6.768	-2.844	0.02	-4.495	-0.029	0.613	0.033
DTM	3.95	-4.872	0.035	0.348	-0.01	0.794	0.245
PHT	3.082	-3.881	0.044	0.371	0.008	0.791	0.415
GFP	-5.251	-0.293	0.003	5.794	0.026	-0.146	0.133
TSW	-1.568	0.396	0.003	1.209	0.126	0.049	0.215
TBM	3.546	-3.309	0.03	-0.721	0.005	1.17	0.721

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

Table 5. *Phenotypic direct (bold face and at the diagonal) and indirect effects (off the diagonal) of six characters on grain yield per plot for the combined analysis.*

Trait	DTF	DTM	PHT	GF	TSW	TBM	rp(GY,x)
DTF	-1.181	0.144	0.045	0.539	-0.008	0.487	0.07
DTM	-0.648	0.262	0.077	-0.084	-0.003	0.624	0.22
PHT	-0.505	0.192	0.105	-0.044	0.002	0.592	0.41
GFP	0.900	0.031	0.007	-0.707	0.007	-0.110	0.06
TSW	0.262	-0.021	0.007	-0.136	0.035	0.034	0.18
TBM	-0.575	0.164	0.062	0.078	0.001	0.999	0.73

R- Squared: = 0.7099; Residual effects: = 0.5386
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.

4. Summary and Conclusions

This study was conducted to assess the genotypic and phenotypic correlations between the field pea genotypes for yield and yield associated traits. Grain yield had positive and highly significant correlations with plant height and total biomass at genotypic levels at two locations. Grain yield had not any negative associations with grain yield traits at genotypic levels, but grain yield had a non-significant association with days to 50% flowering, days to 95% physiological maturity, grain filling period and thousand seed weight at over location.

Similarly grain yield had positive and highly significant correlations with plant height and total biomass at phenotypic levels at over locations, but grain yield had a non-significant association with days to flowering. Days to 95% physiological maturity, grain filling period and thousand seed weight at over locations.

The genotypic path analysis of the combined data shown days to 50% flowering, grain filling period, thousand seed weight, total biomass and plant height has strong positive direct effect on grain yield per plot. The phenotypic path analysis of the combined data shown total biomass yield, thousand seed weight, plant height and days to 95% physiological maturity has strong positive direct effect on grain yield per plot. The traits also have positive significant correlation with grain yield that show the opportunity of using the traits as indirect selection standards in the breeding program.

The study showed the presence of genetic variability between the genotypes that can be exploited in the breeding program. The traits have positive significant association with grain yield and positive direct effect on grain used as direct and indirect selection criteria in the breeding program. The genetic parameter expected in this study should be used to design the breeding program of field pea in the country. In order to have more tangible result and assumption the study should be done by together with more genotypes and tested across locations.

Acknowledgements

References

[1] Asfakun, S., Aminul, A. K. M., M. Golam, R., M., Abdul, K. M. and Jalal, U. A. (2013). Genetic variability in advanced generations of vegetable pea (*Pisum sativum* L.). *International Journal of Plant Breeding* 7 (2), 124-128.

[2] Asfaw Telaye, Beyene Demtsu and Tesfaye Getachew. (1994). Genetics and breeding of field pea. In cool-season Food Legumes of Ethiopia, Asfaw, T. (Ed). ICARDA. Alepo, Syria, PP: 122-137.

[3] Barkat Ali, Raziuddin, Izhar Ullah, Farhatullah, Sajid Khan, Syed Tanveer, Shah, Muhammad Ali, Muhammad Ayoub Khan and Fayaz Khan. (2019). Assessment of genetic variability, genetic advance and correlation coefficient in quantitative traits of field pea (*Pisum sativum* L.) genotypes. BIOSCIENCE RESEARCH, 2019 16 (4): 3769-3780.

[4] Benti O. and Yohannis P. (2017). "Genetic Variability and Association AmongAgronomic Characters in Selected Field Pea (*Pisum sativum* L.) Genotypes at Bale Zone, Sinana Research Center, Oromia Region, Ethiopia." *International Journal of Genetics and Genomics,* 5 (6): 63–75.

[5] CSA, (2020). Agricultural sample survey. Report on area and production of major crops, Volume I. Addis Ababa, Pp. 10.

[6] Davies D. R. (1976). Peas. In: Simmonds N. W. (ed.), Evolution of crop plants Longman, London, pp. 172–174.

[7] Dawit Tadasse, Asfaw Telaye and Geletu Bejiga (1994). Genetic resource in Ethiopia, In: Asfaw Tlaye, Geletu Bejiga, Saxena, M. C. and Solh, M. B. (eds), Cool Season Food Legume of Ethiopia. Proceeding of the first national cool season legume review conference, 16-20 December 1993, Addis Ababa Ethiopia, ICARDA, Syria, pp. 79-96.

[8] Dewey, D. R. and Lu, K. H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, 52: 515-518. *Disease, parasitic nematodes and weeds in cool-season food legumes.* Springer, India. Pp. 147-161.

[9] Duke, J. A (1981). Hand Book of Legumes of World Economic Importance. Plenums press New York. pp. 199-265.

[10] Gemechu K. and Seid A (2016). Genetic options for combating biotic stresses in cool-season food legumes, Indian J. Genet., 76 (4): 437-450 (2016) DOI: 10.5958/0975-6906.2016.00062.

[11] Gemechu Keneni. 2012. Genetic potential and limitations of Ethiopian chickpea (*Cicer arietinum* L.) germplasm for improving attributes of symbiotic nitrogen fixation, phosphorus uptake and use efficiency, and adzuki bean beetle (*Callosobruchus chinensis* L.) resistance. PhD Thesis, Addis Ababa University. Addis Ababa, Ethiopia. pp 292.

[12] Haddis Yirga and Dargie Tsegay. (2013). Characterization of dekoko (*Pisum sativum* var. abyssinicum) accessions by qualitative traits in the highlands of Southern Tigray, Ethiopia. African Journal of Plant Science, 7 (10): pp. 482–487.

[13] McPhee, K. (2003). Dry pea production and breeding, a mini-review. *Food Agricultural Environment* (1): 64-69.

[14] Mussa Jarso, Dereje G, Gemechu Keneni (2009). Procedures of Field Pea Improvement through Hybridization. Technical Manual No. 22, Ethiopian Institute of Agricultural Research. p 12.

[15] Santalla, M., Amurrio, J. M. and de Ron, A. M. (2001). Food and Food potential breeding value of green, dry and vegetal pea germplasm. *Canadian Journal of Plant Science*, 81: 601-610.

[16] Srivastava, Saurabh, Roopa Lavanya, and G. M. Lal. (2017). "Genetic Variability and Character Association for Seed Yield in Chickpea (Cicer Arietinum L.)." *Journal of Pharmacognosy and Phytochemistry,* 6 (4): 748–50.

[17] Temesgen A., Wassu M. and Tesfahun A. (2021). Genetic Variability and Heritability for Various Quantitative Traits in Field Pea (*Pisum sativum* L.) Genotypes in Southern Highlands of Ethiopia. Agricultural and Biological Sciences Journal Vol. 7, No. 3, 2021, pp. 64-71.

[18] Thakur, Monika Chauhan and Abhimanyu Thakur Department of Food Science and Technology, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan – 173230, Himachal Pradesh, India.

[19] Wright, S. 1921. Correlation and causation.. Agric. Res., 20: 257-87.