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Variability, Heritability and Association of Some Morpho-agronomic Traits in Field Pea (*Pisum sativum* L.) Genotypes

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Abstract: In order to best exploit the available genetic wealth in the crop, the information would have paramount important. Therefore, this study was conceived to examine the variability, heritabilities and determines the relative importance of primary and secondary traits as selection criteria to improve productivity. The field experiment was conducted at Haramaya University research field, Ethiopia during 2011 main cropping season. Twenty-five elite field pea genotypes along with two commercial varieties were arranged in randomized complete block design with three replications. The data were subjected to the analyses of variance using the SAS program software. The mean squares of the genotypes were highly significant for all of the characters. The genotypic coefficient of variation ranged from 11.19% for days to mature to 25.72% for number of seeds per plant. The estimated broad sense heritability ranged from 19.24% for stand count to 50.81% for days to flowering. Genetic gains that could be expected from selecting the top 5% of the genotypes varied from 11.45% for stand count to 33.08% for number of seeds per plant. The first five principal components accounted for more than 77% of the total variation. The first principal component accounted for about 43.75% of the variability due to Phenological traits. The materials were grouped into eight clusters based on Mahalanobis' D^2 statistic. Seed yield per plant had significant associations with most of the traits. The path analysis at genotypic level revealed that harvest index and biomass yield contributed major positive direct effects on seed yield.

Key words: Variability, heritability, association, morpho-agronomic, *Pisum sativum*

INTRODUCTION

The pulse as a group in Ethiopia constitutes a considerable number and diversity of crop species (Vavilov, 1926), one of which is the field pea (*Pisum sativum* L.) which is an annual grain legume of the Papilionaceae family. As suggested by Cousin *et al.* (1985) and Santalla *et al.* (2001), since the crop has high protein content (23-33%), peoples raised their interest on it for animal feed as well as human nutrition.

According to FAO (1998) center of origin/diversity of field pea are East Africa and West Asia with secondary center in South Asia and South and East Mediterranean sub-regions. The species *P. sativum* is dominant in Ethiopia even though wild and primitive forms are also known to exist in the high elevation of the country (Amare and Adamu, 1994; Mussa *et al.*, 2003).

According to CSA (2011), field pea covers about 226,532.57 ha of the total arable lands with a total production of 235,872 t. This constitutes about 15.21% of the total area covered by pulses and 12.43% of the total annual production of pulses in the country.

Besides to the aforementioned fact field pea plays a significant role in the socio-economic lives of the farming communities of Ethiopia. It serves as a source of food and feed with a valuable and cheap source of protein (Cousin *et al.*, 1985). It also plays a significant role in soil fertility restoration as suitable rotation crop that fixes atmospheric nitrogen (Angaw and Asnakew, 1994). It also a good source of cash to farmers and foreign currency to the country (Girma, 2003).

Despite its importance, however, the productivity of the crop is only 1.04 t ha^{-1} (CSA, 2011) which fluctuates and is far below the potential as compared to the research plot yields of 2.5-3.5 t ha^{-1} (Mussa *et al.*, 2003). The production has been constrained by several yield limiting factors. Among them, the important one are the inherent low yielding potential of the indigenous cultivars (Asfaw *et al.*, 1994), space diseases like Ascochyta blight (*Mycosphaerella pinodes*) and powdery mildew (*Erysiphe polygoni*) (Dereje and Tesfaye, 1994), poor soil fertility, unimproved cultural practice such as as poor seed bed preparation and lack of fertilizer use (Amare and Adamu, 1994).

Therefore, in order to best exploit the available genetic wealth, unraveling the information on the extent and nature of genetic diversity of the population and the interrelationships among characters that would help in formulating efficient scheme of selection based on multiples of traits is of utmost importance. In line with

this, the objective of the study was to examine the existence of genetic variability, to establish such fundamental genetic facts as heritabilities and to determine the relative importance of primary and secondary traits as selection criteria to improve productivity.

MATERIALS AND METHODS

Description of experimental location: The field experiment was conducted at Haramaya University research field during 2011 main cropping seasons. Haramaya has an altitude of 1980 meter above sea level. It was in semi-arid sub-tropical belt of eastern Ethiopia. The area receives an average annual rainfall of 870 mm. The soil is characterized as a fluvisol with a pH of 7.4 (Solomon, 2006).

Experimental material and design: Twenty seven samples of elite field pea genotypes along with two commercial varieties (Burkitu and Latu) were considered in this study. The commercial varieties were released by Ethiopian Institute of Agricultural Research after fulfilling the requirements set by the National Variety Release Committee for national production. The materials were advanced from preliminary observation nursery collected from Kulumsa Agricultural Research Center, Ethiopia. Treatments were arranged in randomized complete design with three replications. Seeding was done in a plot of two rows with four meter length and regular spacing of 5 cm between plants and 20 cm between rows. The layout and randomization were as per the standard procedure set by Cochran and Cox (1957). Weeding and other cultural practices were done as per the recommendations adopted for the location.

Data collected and analysis: The following data were collected either from whole plot or from ten sample plants randomly from each plot. Days to 50% flowering, Grain filling period, Days to 90% maturity, Stand count, Aschochyta blight , Powdery mildew, Plant height in cm, Number of pods per plant, Number of seeds per pod, Number of seeds per plant, Biomass yield, Thousand seeds weight in gram, Harvest index in percentage, Seed yield per plot. The data were subjected to the analyses of variance (ANOVA) performed using the SAS program software (SAS, 1996). Significance of the result was illustrated under each analysis of the following sub category.

Analysis of variance: The coefficients of variations at phenotypic and genotypic levels were estimated using the formula adopted by Johnson *et al.* (1955). Significance of variability for each trait was tested against the tabulated F-values at 5% probability level.

Heritability and genetic advance: Broad-sense heritability (h^2) for the traits was estimated using the formula adopted by Allard (1960). Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of the superior 5% of the genotypes, was estimated in accordance with the methods illustrated by Johnson *et al.* (1955).

Clustering and estimation of distance: Genetic diversity between clusters based on correlation matrix was computed based on multivariate analysis using Mahalanobis D^2 statistic (Mahalanobis, 1936). The important traits in each principal component that significantly contributed to the variation observed were identified as suggested by Johonson and Wichern (1988). Based on the squared distances (D^2), clustering of genotypes was done using Tocher's method as described by Singh and Chaudhary (1999). Squared distance (D^2) for each pair of clusters combinations was computed as per Singh and Chaudhary (1999). Significance of the squared distances for each cluster was tested against the tabulated χ^2 values at p degree of freedom at 5% probability level. where, p is number of characters used for clustering genotypes.

Association of the traits: Phenotypic and genotypic correlation coefficients were estimated using the standard procedure suggested by Miller *et al.* (1958) from the corresponding variance and covariance components. The coefficients of correlation r were tested for their significance as per described by Robertson (1959). Path coefficient analysis was estimated as suggested by Wright (1921) and conducted out by Dewey and Lu (1959) using both phenotypic and genotypic correlation coefficients to determine the direct and indirect effects of yield components on seed yield.

RESULTS AND DISCUSSION

Results from the analysis of variance are given in Table 1. In order to assess the extent to which the observed variation is due to genetic effect, different parameters were estimated and presented in Table 2. The detail accounts of each of these are discussed hereunder.

It was revealed from the results that mean squares due to block/replication were non-significant for all traits, except stand count, number of seeds per pod and per plant which were highly significant. Mean squares due to

genotypes were highly significant for all the traits studied and this revealed the presence of variability for these traits in field pea genotypes investigated.

The field pea genotypes evaluated in this study showed significant phenotypic variability in terms of plant morphology, phenology and yield attributes. These results are similar with the findings of other scholars like Tesfaye (1999) and Tezera (2000). In this study in general efficiency of randomized complete design was generally trait specific.

Range of parameters: Table 2 suggested that there was substantial difference observed in all of the traits under consideration. The commercial variety, Burkitu, along with two tested genotypes, EH-04049-1 and EH-05033-3, required longer days for maturity and both are statistically different from the population mean (97.30). Generally, all accession required 34 to 44.67 days for grain filling and 55.33 to 60.33 days for vegetative growth. The result from this investigation is in agreement with the previous reports of Mussa *et al.* (2003).

In general, the genotypes showed shorter days to maturity and grain filling periods thus may be suitable to lower rainfall regions whereas the late types can be adapted to the highland areas with dependable rainfall. Thus, the variability that has been exhibited by these genotypes can offer great flexibility for the development of suitable varieties for the various agro-ecological zones of Ethiopia. Here, genotypes showed shorter grain filling period can be suitable for the areas where the terminal drought frequently occurs.

From the results, the broad spectrum of variability observed among these genotypes of field pea for different traits generally indicates possibilities for genetic improvement of the crop through selection and cross breeding as well.

Table 1: Analysis of variance for 14 traits of elite field pea genotypes tested in 2011 cropping season at Haramaya University research field

Variables	MSR(2)$^{\beta}$	MSG(26)	MSE	CV (%)
DF	3.60^{ns}	168.06**	6.40	11.52
GFP	91.31*	91.42**	5.06	12.80
DM	241.98^{ns}	473.41**	10.85	11.41
STD	5594.87**	390.12**	11.97	1642.00
AB	0.12^{ns}	2.23*	0.97	25.69
MLDW	0.02^{ns}	2.31**	0.88	24.27
PH	2055.11^{ns}	2438.44**	30.66	16.61
PPP	3.24^{ns}	8.62**	1.91	22.60
SPP	3.85**	1.48**	0.65	22.80
SPPL	603.52**	163.01**	6.51	26.42
BIOM	0.80^{ns}	1.78**	0.78	19.54
TSW	21.88^{ns}	2966.38**	37.15	19.93
HI	39.55^{ns}	78.31**	5.25	28.26
SYLD	72.63^{ns}	126403.10**	228.26	30.21

*,**Significant at 0.05 and 0.01 probability level, respectively, ^{ns}Non significant, MSR: Mean Square due to replication, MSG: Mean Square due to genotypes, MSE: Mean Square due to error, CV%: Coefficient of variation in percentage. $^{\beta}$Values in parenthesis indicate degrees of freedom, DF: Days to 50% flowering, GFP: grain filling period, DM: Days to 90% maturity, STD: Stand count, AB: Aschochyta blight , MLDW: Powdery mildew, PH: Plant height in cm, PPP: No. of pods per plant, SPP: No. of seeds per pod, SPPL: No. of seeds per plant, BIOM: Biomass yield, TSW: Thousand seeds weight in gram, HI: Harvest index in percentage and SYLD: Seed yield in g per plant

Estimation of genotypic and phenotypic variations: High genotypic coefficient of variation (25.72%) was observed for number of seeds per plant followed by Harvest Index (22.15%) and seed yield (20.83%). Likewise phenotypic coefficient of variation was high for the number of seeds per plant (41.25%) followed by seed yield (36.70%). In general, the environmental variance was greater than the genetic variance for all the traits.

The estimated values of phenotypic variances were in the range of 0.90 for number of seeds per plant to 76870.40 for seed yield (Table 2). The lowest and highest genotypic variances were found 0.35 and 24766.30 for the

Table 2: Estimates of minimum, mean and maximum value, variance and coefficient of variation at phenotypic (σ^2p), genotypic (σ^2g) level, heritability in broad sense (h^2%), genetic advance in absolute (GA) and percent of mean (GAM) for fourteen traits of field pea

Traits	Min	Mean	Max	σ^2p	σ^2g	GCV (%)	PCV (%)	h^2 (%)	GA	GAM
DF	55.33	57.05	60.33	83.35	42.35	11.41	16.00	50.81	9.57	16.78
GFP	34.00	40.25	44.67	49.97	21.94	11.64	17.56	43.91	6.40	15.91
DM	92.00	97.30	100.33	240.90	118.55	11.19	15.95	49.21	15.76	16.20
STD	33.28	71.69	87.10	427.52	82.26	12.65	28.84	19.24	8.21	11.45
AB	1.00	3.77	5.00	1.37	0.43	17.40	31.00	31.50	0.76	20.14
MLDW	1.00	3.64	5.00	1.29	0.51	19.58	31.20	39.40	0.92	25.35
PH	148.00	188.28	223.33	1481.00	499.37	11.87	20.44	33.72	26.77	14.22
PPP	2.73	8.44	11.67	5.30	1.66	15.27	27.27	31.37	1.49	17.65
SPP	0.59	2.86	4.88	0.90	0.35	20.76	33.23	39.03	0.77	26.76
SPPL	4.80	24.65	48.00	103.39	40.20	25.72	41.25	38.88	8.16	33.08
BIOM	1.37	4.01	6.00	1.01	0.39	15.56	25.05	38.56	0.80	19.93
TSW	65.00	186.60	229.67	1909.89	527.89	12.31	23.42	27.64	24.92	13.35
HI	4.50	18.57	28.92	44.92	16.92	22.15	36.09	37.67	5.21	28.05
SYLD	184.33	755.49	1080.80	76870.40	24766.30	20.83	36.70	32.22	184.28	24.39

DF: Days to 50% flowering, GFP: Grain filling period, DM: Days to 90% maturity, STD: Stand count, AB: Aschochyta blight , MLDW: Powdery mildew, PH: Plant height in cm, PPP: No. of pods per plant, SPP: No. of seeds per pod, SPPL: No. of seeds per plant, BIOM: Biomass yield, TSW: Thousand seeds weight in gram, HI: Harvest index in percentage and SYLD: Seed yield in g per plant

same traits, respectively. This finding is inconsistence with the earlier findings by Tesfaye (1999), Tezera (2000) and Keneni *et al.* (2005).

Moderate heritability was observed for temporal traits (days to flower, grain filling period and days to maturity). However, low values of heritability were estimated for stand count, indicating limited possibility of improvement for those characters through selection. In earlier studies of Tesfaye (1999) and Tezera (2000), high heritability estimates for phonological traits, biological yield, number of seeds per plant, per pods and harvest index were estimated. These findings are thus only partially in agreement with the results obtained in the present investigation. The probable cause of the disparity could be due to the fact that the heritability of a given trait refers to a particular population under a particular condition or environment.

Generally, heritability determines the effectiveness of selection. The effectiveness of selection for a trait depends on the relative importance of the genetic and environmental factors in the expression of phenotypic differences among genotypes in a population.

Genetic gains that expected from selecting the top 5% of the genotypes, as a percent of the mean, varied from 11.45% for stand count to 33.08% for number of seeds per plant, indicating an increase of 11.45-33.08% the same magnitude can be made by selection based on these traits under similar conditions to this study.

The low values of expected genetic advance for the traits like aschochyta blight, powdery mildew and number of seeds per pod in spite of higher heritability is due to low variability for the trait indicated by the low genotypic and phenotypic variance values (Table 2). This indicates the importance of genetic variability in improvement through selection. Therefore, even if heritability estimates provide basis for selection on phenotypic performance, the estimates of heritability and genetic advance should always be considered simultaneously, as high heritability is not always associated with high genetic advance (Johnson *et al.*, 1955).

Principal component analysis: In order to assess the pattern of variations, principal component analysis was done by considering all the 14 variables simultaneously. Five of the 14 principal components accounted for more than 77% of the total variation in the field pea genotypes (Table 3).

The first principal component accounted for 43.75% of the total variation. All the 14 traits considered exerted positive effects on this component. Temporal data (Days to flower and maturity and grain filling periods and plant height were among those traits having positive and

Table 3: The eigenvalues and vectors of the correlation matrix for 14 traits of 27 elite field pea germplasms

Parameter	PRIN1	PRIN2	PRIN3	PRIN4	PRIN5
Eigenvalue	6.999	1.811	1.498	1.064	1.000
% variance	43.750	11.320	9.360	6.650	6.250
Cumulative	43.750	55.060	64.420	71.070	77.320
		Eigenvectors			
DF	0.345	-0.184	-0.070	0.166	-0.034
GFP	0.324	-0.158	-0.155	0.103	-0.209
DM	0.350	-0.180	-0.112	0.145	-0.115
STD	0.229	-0.178	0.388	0.225	-0.357
AB	0.201	-0.245	0.043	-0.150	0.547
MLDW	0.214	-0.031	0.069	0.437	0.294
PH	0.309	-0.114	0.235	0.070	0.098
PPP	0.222	0.078	-0.475	-0.174	-0.436
SPP	0.235	0.410	-0.154	0.200	0.390
SPPL	0.205	0.489	-0.398	0.035	0.071
BIOM	0.246	-0.227	-0.106	-0.333	0.164
TSW	0.275	-0.088	-0.072	-0.126	-0.060
HI	0.244	0.292	0.345	-0.313	-0.104
SYLD	0.249	0.204	0.289	-0.542	0.042

PRIN1, PRIN2, PRIN3, PRIN4, PRIN5: Principal component 1, 2, 3, 4 and 5, respectively, DF: Days to 50% flowering, GFP: Grain filling period, DM: Days to 90% maturity, STD: Stand count, AB: Aschochyta blight, MLDW: Powdery mildew, PH: Plant height in cm, PPP: No. of pods per plant, SPP: No. of seeds per pod, SPPL: No. of seeds per plant, BIOM: Biomass yield, TSW: Thousand seeds weight in gram, HI: Harvest index in percentage and SYLD: Seed yield in g per plant

greater influence. The second component accounting for an additional 11.32% of the total variation, primarily illustrates the patterns of variations in seed bearing traits (number of seeds per pod and per plant) which were found to have positive impacts on the second component. About 64% of the traits under consideration exerted negatively on this component and of which, Aschochyta blight and biomass yield exerted greater negative coefficients. The third principal component accounted for 9.36% of the total variation and was alluded with the variations in number of stand count and harvest index, both of which exhibited positive effects on one hand and number of seeds and pods per plant with negative impacts on the other. Here, in contradiction with the third component, in the forth component, more than 55% of the traits exerted negative impact. Of which powdery mildew exerted the maximum positive effect whereas, seed yield and its contributing traits like biomass and harvest index exerted high and negative effect on it. From the correlation matrix biomass and harvest index were highly and positively correlated with seed yield. In fifth principal component, 50% of the traits exerted positive and the rest act negatively. Among them aschochyta blight, number of seeds per pod and powdery mildew exerted maximum positive impact while number of pods per plant, stand count and the phonological traits exerted maximum and negative impact on the component. In general, the traits considered in this experiment contributed in the total variability in different degree and component.

Clustering of genotypes and divergence analysis: Genetic diversity plays an important role in plant breeding, because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains. The average linkage technique of clustering produced a more understandable portrayal of the 27 field pea genotypes by grouping them into eight clusters, whereby different members within a cluster being assumed to be more closely related in terms of the trait under consideration with each other than those members in different clusters. Table 4 indicates the range and mean of genetic divergence in morphological and seed traits of the eight clusters and the detail account which is presented hereunder:

- **Cluster I:** It consisted five genotypes which characterized by maximum in phonological traits and stand count, Intermediate which the disease reactions (Aschochyta blight and powdery mildew) and yield contributing traits. However, genotypes under this category bear low seed yielding potential. The result revealed that genotypes included in this cluster require longer time for flowering, maturing and grain filling period and had high stand establishment
- **Cluster II:** It consisted of twelve genotypes which required longer period for flowering and maturity, high in stand count, thousand seed weight and harvest index and susceptible for Aschochyta blight. The genotypes categorized under this cluster are suitable for the area exhibited by terminal drought
- **Cluster III:** It consisted two genotypes characterized by longer in phonological traits and exhibited high in yield contributing traits (number of seeds per pods and plant) whereas intermediate for the rest of the traits. According to the output of principal component, the major contributing factors that cause differentiation of this cluster from the rests of the clusters were stand count, number pods and seeds per plant and Harvest index (Table 3)

Table 4: Mean and range of genetic divergence in morphological and seed yield traits of the eight clusters of *Pisum sativum* L.

	Cluster														
	I					II					III				
Character	Min.	Mean	Max.	SD	CV (%)	Min.	Mean	Max.	SD	CV (%)	Min.	Mean	Max.	SD	CV (%)
DF	55.33	56.86	58.33	0.88	1.54	55.67	57.14	59.00	1.64	2.87	56.00	56.50	57.00	0.82	1.44
GFP	37.33	40.07	42.00	1.71	4.27	37.00	39.92	42.67	2.18	5.46	39.33	41.83	44.33	2.86	7.14
DM	95.67	96.93	98.33	1.03	1.06	95.67	97.06	99.67	1.53	1.57	96.33	98.33	100.33	2.04	2.11
STD	59.63	71.73	82.41	5.28	7.36	57.62	74.10	87.10	7.26	9.80	74.37	78.50	82.63	15.04	19.44
AB	3.00	3.53	4.33	0.97	21.34	3.00	4.06	5.00	0.96	23.77	3.00	3.67	4.33	0.82	22.27
MLDW	3.00	3.53	4.33	0.63	17.90	3.00	3.72	5.00	0.83	22.26	3.67	4.00	4.33	0.82	24.49
PH	148.00	183.60	213.00	26.09	14.21	180.67	193.06	216.00	17.60	9.11	183.33	187.33	191.33	22.05	11.14
PPP	7.47	9.70	11.67	1.06	10.93	7.13	8.40	9.87	1.59	18.91	8.00	8.77	9.53	1.55	18.32
SPP	2.43	2.84	3.26	0.52	18.39	1.92	2.87	3.56	0.54	18.84	3.09	3.99	4.88	0.31	10.71
SPPL	24.13	27.08	30.40	4.35	16.07	15.93	24.05	32.40	5.53	22.98	23.53	35.77	48.00	7.67	32.52
BIOM	3.40	3.79	4.30	0.59	15.59	3.00	4.11	4.80	0.49	12.04	3.70	4.02	4.33	0.86	20.74
TSW	168.53	189.65	219.03	17.89	9.43	167.77	200.78	229.67	26.57	13.23	176.77	180.87	184.97	21.02	10.99
HI	15.01	16.85	18.48	7.79	46.26	17.26	20.86	28.92	3.30	15.84	16.34	18.57	20.80	0.35	1.79
SYLD	585.80	630.12	656.13	259.87	41.24	796.83	843.61	880.87	147.2	17.45	754.50	770.70	786.90	143.5	17.60

	IV					V					VI	VII	VIII
Character	Min.	Mean	Max.	SD	CV (%)	Min.	Mean	Max.	SD	CV (%)	Mean	Mean	Mean
DF	55.67	57.56	60.33	1.33	2.31	55.33	55.67	56.00	0.73	0.41	57.00	58.33	18.67
GFP	38.67	42.22	44.67	3.84	9.10	42.33	42.67	43.00	3.83	1.63	39.67	38.00	14.00
DM	99.00	99.78	100.33	2.60	2.61	98.33	98.33	98.33	1.24	1.22	96.67	96.33	32.67
STD	63.65	69.38	80.40	7.90	11.39	71.75	75.18	78.61	9.55	7.18	76.66	62.31	33.28
AB	3.00	3.67	4.33	1.15	31.49	3.00	3.67	4.33	22.27	0.82	3.67	5.00	1.00
MLDW	3.00	3.89	5.00	0.66	17.12	3.67	3.67	3.67	0.00	0.00	3.00	5.00	1.00
PH	155.67	174.56	199.00	30.00	17.18	188.00	191.67	195.33	0.85	1.63	176.00	223.33	68.33
PPP	6.53	7.64	8.87	0.55	7.14	9.40	9.60	9.80	10.21	0.98	9.13	7.00	2.73
SPP	2.19	2.65	3.04	0.43	16.31	2.97	2.98	2.99	3.97	0.12	2.47	3.51	0.59
SPPL	16.53	20.38	24.33	4.32	21.22	28.60	29.14	29.67	6.44	1.88	21.27	24.60	4.80
BIOM	3.60	3.91	4.20	0.29	7.42	4.17	4.42	4.67	4.16	0.18	6.00	3.97	1.37
TSW	160.17	173.65	190.17	12.72	7.32	143.80	167.59	191.37	45.36	76.02	204.90	192.77	65.00
HI	10.36	11.73	14.42	2.03	17.32	23.22	24.54	25.85	15.11	3.71	15.86	25.12	4.50
SYLD	409.27	443.46	489.30	9.32	2.10	1070.9	1075.84	1080.8	11.06	119.00	919.77	996.77	184.33

DF: Days to 50% flowering, GFP: Grain filling period, DM: Days to 90% maturity, STD: Stand count, AB: Aschochyta blight, MLDW: Powdery mildew, PH: Plant height in cm, PPP: No. of pods per plant, SPP: No. of seeds per pod, SPPL: No. of seeds per plant, BIOM: Biomass yield, TSW: Thousand seeds weight in gram, HI: Harvest index in percentage and SYLD: Seed yield in g per plant

- **Cluster IV:** It had three genotypes which exhibited late in the phonological traits and low in harvest index and seed yield. Whereas, intermediate for the rest of the traits. Here, even if the genotypes requires long period for mature they bear low seed yielding potential. Among the studied traits, powdery mildew and seed yield are the most contributing traits that create variability of this cluster from the rest. The commercial variety, Burkitu, is clustered along with the genotypes as a result the genotypes under this cluster can be adapted in the area where the Burkitu recommended for production
- **Cluster V:** It consisted of 2 genotypes were relatively superior in most of the traits under considered. Among the other traits, reaction with aschochyta blight and yield contributing traits like number of pods per plant are the most contributing traits that create variability of this cluster from the rest of characters. Cluster vi-viii: Each of the clusters, six, seven and eight constitutes single genotypes. Among these the genotype in cluster eight exhibited inferior in all of the traits. This is confirmed with the most divergent from the rests of genotypes in another cluster (Table 5). In general, the differences between the clusters were mainly attributed to the variation in number of seeds per pod and number of pods per plant reaction of powdery mildew

From the estimated of distance, under this investigation, differences between all of the twenty-eight possible pairs of clusters were highly significant ($p<0.01$) (Table 5). The maximum distance was found between cluster five and eight (D^2 = 15174.00). Cluster five constitutes two elite genotypes while cluster eight constitutes a single accession. The second most divergent clusters were cluster six and eight and six (D^2 = 14971). Both clusters were constituted a single genotype. The third most divergent clusters were cluster seven and eight (D^2 = 14487.00). The forth most divergent clusters were between cluster two and eight (D^2 = 13027.00) and so on.

Genotypes grouped into the same cluster presumably diverge little from one another as the aggregate characters are measured. In the present investigation, therefore, crossing of accessions from cluster five and eight will give rise to maximum genetic segregation.

Among the eight clusters formed, cluster one showed the maximum intra-cluster D^2 value of 21.67 followed by cluster three and two, 15.69 and 15.52, respectively. Since clusters six, seven and eight contains a single accession; the intra-cluster D^2 value is zero (Table 5). This result revealed, the genotypes grouped in the fourth cluster are more similar as compared with the rest of the genotypes in the rest of the clusters.

It is worthy to note that in calculating cluster mean, the superiority of a particular accession with respect to a given character could get diluted by other accessions that are grouped in the same cluster but are inferior or intermediate for the character in question. Hence, apart from selecting genotypes from the clusters which have higher inter-cluster distance for hybridization one can also think of selecting parents based on the extent of divergence with respect to a character of interest (Fikreselassie *et al*., 2012).

Association of the traits: Table 6 reveals the seed yield per plant had positive and highly significant genotypic correlations with the temporal traits (days to flower, maturity and grain filling periods), plant height, biomass yield per plant, thousand seed weight and harvest index. Positive and significant genotypic associations were also observed with stand count and yield contributing traits like seed per pod and per plant and pods per plant. The strong positive correlation of thousand seed weight with seed yield indicates that thousand seed weight is less affected by the environment factors and phenotype could reflect the genotype (Mussa *et al*., 2003). Negative and highly significant genotypic correlation of seed yield was observed with aschochyta blight.

The positive significant correlation observed between seed yield and plant height indicates that tall plants supporting many leaves could increase total biomass production through increase carbon fixation that can ultimately be partitioned to reproductive organ. Pods per plant exhibited a positive association with seed yield per plant. This is an indication that plants bearing more

Table 5: Pair wise generalized squared distance (D^2) among 5 clusters constructed from 27 elite field pea genotypes

Cluster	C_1	C_2	C_3	C_4	C_5	C_6	C_7	C_8
C_1	21.67	193.83**	103.12**	180.81**	731.69**	484.87**	650.01**	11712.00**
C_2		15.52	42.75**	675.60**	189.24**	136.53**	58.82**	13027.00**
C_3			15.69	498.84**	327.60**	259.06**	278.17**	12531.00**
C_4				5.51	1549.00**	1087.00**	1405.00**	10308.00**
C_5					9.63	165.94**	59.40**	15174.00**
C_6						0.00	250.28**	14971.00**
C_7							0.00	14487.00**
C_8								0.00

**Significant at 1%

Table 6: Estimates of correlation coefficients at phenotypic (above diagonal) and genotypic (below diagonal) levels of 14 traits in field pea

Traits	DF	GFP	DM	STD	AB	MLDW	PH	PPP	SPP	SPPL	Biomass	TSW	HI	SYLD
DF		0.84**	0.97**	0.59**	0.51**	0.53**	0.79**	0.53**	0.48**	0.36**	0.63**	0.67**	0.40**	0.39**
GFP	0.86**		0.95**	0.57**	0.44**	0.46**	0.62**	0.61**	0.42**	0.41**	0.50**	0.59**	0.44**	0.38**
DM	0.97**	0.95**		0.61**	0.50**	0.52**	0.75**	0.59**	0.48**	0.40**	0.60**	0.66**	0.43**	0.41**
STD	0.69**	0.53**	0.65**		0.28^{ns}	0.33**	0.59**	0.14*	0.15*	-0.01*	0.30**	0.34**	0.43**	0.36**
AB	0.61**	0.54**	0.61**	0.34^{ns}		0.25^{ns}	0.46**	0.15*	0.26*	0.11*	0.38**	0.39**	-0.29**	-0.30**
MLDW	0.65**	0.483*	0.60**	0.42*	0.43*		0.50**	0.18^{ns}	0.38**	0.24*	0.29**	0.31**	0.29**	-0.26*
PH	0.85**	0.63**	0.78**	0.60**	0.61**	0.68**		0.26*	0.43**	0.210^{ns}	0.54**	0.56**	0.53**	0.54**
PPP	0.59**	0.74**	0.68**	0.39*	0.36^{ns}	0.16^{ns}	0.32^{ns}		0.27*	0.64**	0.38**	0.45**	0.30**	0.29**
SPP	0.63**	0.65**	0.66**	0.47**	0.34^{ns}	0.45*	0.61**	0.42*		0.84**	0.27*	0.35**	0.41**	0.38**
SPPL	0.479*	0.64**	0.57**	0.36^{ns}	0.21^{ns}	0.26^{ns}	0.35^{ns}	0.71**	0.86**		0.21^{ns}	0.30**	0.38**	0.35**
BIOM	0.68**	0.58**	0.66**	0.46*	0.53**	0.38^{ns}	0.62**	0.38*	0.28^{ns}	0.15^{ns}		0.54**	0.17^{ns}	0.55**
TSW	0.78**	0.62**	0.74**	0.50**	0.52**	0.37^{ns}	0.73**	0.354^{ns}	0.55**	0.33^{ns}	0.57**		0.37**	0.43**
HI	0.51**	0.52**	0.53**	0.45*	0.459*	0.36^{ns}	0.56**	0.52**	0.55**	0.57**	0.21^{ns}	0.48*		0.87**
SYLD	0.52**	0.49**	0.52**	0.44*	-0.50**	-0.34^{ns}	0.62**	0.45*	0.45*	0.42*	0.57**	0.50**	0.87**	

*,**Significant at 0.05 and 0.01 probability level, respectively, ^{ns}Non significant, DF: Days to 50% flowering, GFP: Grain filling period, DM: Days to 90% maturity, STD: Stand count, AB: Aschochyta blight, MLDW: Powdery mildew, PH: Plant height in cm, PPP: No. of pods per plant, SPP: No. of seeds per pod, SPPL: No. of seeds per plant, BIOM: Biomass yield, TSW: Thousand seeds weight in gram, HI: Harvest index in percentage and SYLD: Seed yield in g per plant

Table 7: Estimates of direct (bold and under lined diagonal values) and indirect effects (off-diagonal) at genotypic level of 12 traits on seed yield in elite field pea genotypes

Variables	DF	GFP	DM	STD	AB	PH	PPP	SPP	SPPL	BIOM	TSW	HI
DF	-0.078	-0.067	-0.076	-0.054	-0.048	-0.066	-0.046	-0.049	-0.037	-0.053	-0.061	-0.040
GFP	0.021	0.024	0.023	0.013	0.013	0.015	0.018	0.016	0.015	0.014	0.015	0.012
DM	0.098	0.095	0.100	0.065	0.060	0.078	0.068	0.066	0.057	0.066	0.074	0.053
STD	-0.137	-0.105	-0.128	-0.197	-0.066	-0.119	-0.077	-0.092	-0.070	-0.091	-0.099	-0.088
AB	-0.033	-0.029	-0.032	-0.018	-0.053	-0.032	-0.019	-0.018	-0.011	-0.028	-0.028	-0.024
MLDW	-0.034	-0.025	-0.031	-0.022	-0.023	-0.035	-0.008	-0.023	-0.013	-0.020	-0.019	-0.019
PH	-0.061	-0.045	-0.056	-0.043	-0.044	-0.072	-0.023	-0.044	-0.025	-0.045	-0.052	-0.041
PPP	-0.136	-0.170	-0.156	-0.091	-0.083	-0.073	-0.231	-0.096	-0.163	-0.089	-0.082	-0.119
SPP	-0.151	-0.154	-0.158	-0.111	-0.082	-0.145	-0.099	-0.238	-0.206	-0.066	-0.130	-0.132
SPPL	0.137	0.182	0.162	0.102	0.058	0.100	0.201	0.246	0.285	0.043	0.094	0.163
BIOM	0.455	0.387	0.441	0.309	0.352	0.415	0.256	0.184	0.100	0.668	0.379	0.140
TSW	-0.030	-0.023	-0.028	-0.019	-0.020	-0.028	-0.013	-0.021	-0.013	-0.022	-0.038	-0.018
HI	0.490	0.498	0.510	0.431	0.442	0.543	0.496	0.533	0.551	0.202	0.460	0.963

Residual effect (RP): 0.36; DF: Days to 50% flowering, GFP: Grain filling period, DM: Days to 90% maturity, STD: Stand count, AB: Aschochyta blight, MLDW: Powdery mildew, PH: Plant height in cm, PPP: No. of pods per plant, SPP: No. of seeds per pod, SPPL: No. of seeds per plant, BIOM: Biomass yield, TSW: Thousand seeds weight in gram, HI: Harvest index in percentage

number of pods per plant produce more seed yield. Thus, selection for pods number during the earlier stage alone will bring about a definite improvement in seed yield. This result is in consistent with the earlier studies on field pea from Ethiopia (Tesfaye, 1999; Tezera, 2000; Singh, 1990; Rathore *et al*., 1993a, b).

The genotypic and phenotypic correlations were further analyzed by path-coefficient technique which involves partitioning of the correlation coefficients into direct and indirect effects via alternative characters or pathways. Seed yield being the complex outcomes of various characters, were considered to be as resultant variables and the rest of the variables as causal variables (Fikreselassie *et al*., 2012).

The path analysis at genotypic level revealed that, harvest index (0.963) and biomass yield (0.668) contributed major positive direct effects (Table 7). These traits showed positive and highly significant genotypic correlations with seed yield (Table 6). As a result, these characters will be considered as main components for selection in a breeding program for higher seed yield in field pea. The other characters that had positive direct effects include number of seeds per plant days to maturity and grain filling period. These positive direct effects indicate that given other characters are kept constant, increasing one of these characters will increase seed yield which implies that these characters are the major contributors for the improvement of seed yield at genotypic level.

Negative direct effect exerted on seed yield by number of seeds per pod, number of pods per plant. This negative direct effect was counter balanced by the positive indirect influences through harvest index, biomass yield and number of seeds per plant (Table 7). These traits as shown earlier had positive and highly significant genotypic correlations with seed yield (Table 6). These results are found to be consistent with that of Devendra *et al*. (1995), Golaszewski and Pusio (1996) and Tesfaye (1999). Earlier studies on another crop have also indicated direct negative effect of seed weight (Singh *et al*., 1993), pod number (Singh *et al*., 1993; Raghuvanshi and Singh, 1984) and plant height (Raghuvanshi and Singh, 1984) on seed yield.

Table 8: Estimates of direct (bold diagonal values) and indirect effects (off-diagonal) at phenotypic level of 12 traits on seed yield in elite field pea genotypes

Variables	DF	GFP	STD	AB	MLDW	PH	PPP	SPP	SPPL	BIOM	TSW	HI
DF	**-0.265**	-0.257	-0.157	-0.135	-0.141	-0.210	-0.141	-0.128	-0.096	-0.167	-0.177	-0.105
GFP	-0.025	**-0.030**	-0.017	-0.013	-0.014	-0.018	-0.018	-0.013	-0.012	-0.015	-0.018	-0.013
STD	-0.019	-0.018	**-0.032**	-0.009	-0.011	-0.019	-0.004	-0.005	0.000	-0.010	-0.011	-0.014
AB	-0.029	-0.025	-0.016	**-0.057**	-0.014	-0.026	-0.008	-0.015	-0.006	-0.022	-0.022	-0.016
MLDW	-0.024	-0.021	-0.015	-0.011	**-0.045**	-0.022	-0.008	-0.017	-0.011	-0.013	-0.014	-0.013
PH	0.077	0.060	0.058	0.045	0.048	**0.097**	0.025	0.041	0.020	0.052	0.055	0.052
PPP	-0.071	-0.082	-0.019	-0.020	-0.024	-0.035	**-0.134**	-0.036	-0.086	-0.051	-0.061	-0.040
SPP	-0.037	-0.032	-0.012	-0.020	-0.029	-0.033	-0.021	**-0.077**	-0.065	-0.021	-0.027	-0.032
SPPL	0.037	0.041	-0.001	0.011	0.025	0.021	0.065	0.085	**0.101**	0.021	0.031	0.039
BIOM	0.419	0.334	0.199	0.254	0.192	0.356	0.253	0.180	0.138	**0.665**	0.360	0.115
TSW	-0.043	-0.038	-0.022	-0.025	-0.019	-0.036	-0.029	-0.022	-0.019	-0.035	**-0.064**	-0.024
HI	0.382	0.422	0.415	0.276	0.276	0.514	0.291	0.398	0.367	0.167	0.358	**0.963**

Residual effect (RP): 0.35; DF: Days to 50% flowering, GFP: Grain filling period, DM: Days to 90% maturity, STD: Stand count, AB: Aschochyta blight, MLDW: Powdery mildew, PH: Plant height in cm, PPP: No. of pods per plant, SPP: No. of seeds per pod, SPPL: No. of seeds per plant, BIOM: Biomass yield, TSW: Thousand seeds weight in gram, HI: Harvest index in percentage

The high positive correlation observed between days to flower and stand count and seed yield was partially explainable by its high positive indirect effect through harvest index and biomass yield. An overall analysis of path coefficient suggested that selection should be made for plants with high biomass yield followed by harvest index to increase seed yield on field pea.

The trend with respect to phenotypic path coefficient (Table 8) of seed yield with other traits was more or less the same. The residual effect was somehow low for both phenotypic (0.35) and genotypic (0.36) level indicating that the twelve traits included in this study account for almost the whole variation in seed yield.

CONCLUSION

Significant variability existed for the traits in field pea genotypes generally indicated possibilities for genetic improvement of the crop through selection and cross breeding. The study reveals high genotypic coefficient of variation and moderate broad heritability for the traits under considered. The experiment confirmed there was an increase of 11.45-33.08% can be made in the tested traits by selection. Five of the fourteen principal components accounted for more than 77% of the total variation in the field pea genotypes. Plant height and temporal data were among those traits having positive and greater influence in PCA1. The average linkage technique clustered the field pea genotypes into eight. From the estimated distance analysis, crossing of accessions from cluster five and eight will give rise to maximum genetic segregation. From the association and path analysis, most of the traits exhibited significant correlation with the seed yield and from the path analysis, harvest index and biomass yield will be considered as main components for selection in a breeding program for higher seed yield. Therefore, generally, substantial variability in the considered traits among the field pea genotypes was observed and this might be used as important inputs for the future field pea breeding program.

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