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Multivariate analysis of some Ethiopian field pea (*Pisum sativum* L.) genotypes

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The information on the nature and degree of diversity in the genotypes is crucial for efficient utilization of existing genetic resources. Thirteen (13) field pea genotypes along with two standard and one local checks were evaluated in triplicate randomized complete block design for three consecutive years to estimate the genetic variability and identify superior genotypes that generate putative transgressive segregantes. Genotypes differed significantly in respect to phonological, yield and some yield related traits, and were highly influenced by the environment. Large magnitude of variability among the genotypes contributed to pod length and reaction to Ascochyta blight. High heritability was observed for days to flower (39.11%) and moderate for seed yield (15.98%). Genetic gains that could be expected from selecting the top 5% of the genotypes was 17.36% for seed yield. Four of the twelve principal components accounted for more than 89% of the total variations. The sixteen (16) genotypes were grouped into five clusters based on D^2 values for which the maximum distance was found between cluster three and five. Thus, crossing of Tegengech with col 26 and col 23 would result high magnitude of heterosis that would produce superior breeding materials that can be utilized in future breeding program.

Key words: Field pea, genetic variability, multivariate analysis, principal component, cluster.

INTRODUCTION

Field pea (*Pisum sativum* L.) is one of the world's oldest domesticated crops cultivated before 10th and 9th millennia BC (Zohary et al., 2000). *Pisum sativum* comprises both the wild species (P. *fulvum* and P. *eratius*) and cultivated species (P. *abyssinicum*) originnated from the Mediterranean region, primarily in the Middle East (Ellis et al., 2011). However, the exact center of its diversity is not known yet due to significant change in the areas of origin and loss of passport data of the early accessions (Petr et al., 2012). The crop is grown in many countries and currently ranks fourth among the pulses in the world with cultivated area of 6.33 million hectares (ha) (FAOSTAT, 2012).

In Ethiopia, the crop is widely grown in mid to high altitude and ranks fourth in area coverage reaching 212, 890 ha with an annual production of 2,632,663.87 tons (t) (CSA, 2012; FAOSTAT, 2012). It is the major food legumes with a valuable and cheap source of protein having essential amino acids (23 to 25%) that have high nutritional values for resource poor households (Nawab et al., 2008). The crop has important ecological and economical advantages in the highlands of Ethiopia, as it plays a significant role in soil fertility restoration and also serves as a break crop suitable for rotation to minimize the negative impact of cereal based mono-cropping (Angaw and Asnakew, 1994). It is also used as a source

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Abbreviations: ANOVA, Analyses of variance; **GA,** genetic advance; **GAM,** genetic advance mean; **IBC,** Institute of Biodiversity Ethiopia; **RCBD,** randomized complete block design; **m^2,** meter square; **kg,** kilograms; **kg ha^1,** kilograms per hectare; **masl,** meter above sea level.

Table 1. List of 16 genotypes along with their origin/source.

S/N	Material	Source
1	PGRC/E 32563-1	IBC*
2	MG 102029	IBC
3	PGRC/E 32642-1	IBC
4	PGRC/E 32642-2	IBC
5	MG 1004-46	IBC
6	Col 23	Local Collection
7	Col 34	Local Collection
8	Col 26	Local Collection
9	Col 8	Local Collection
10	Col 6	Local Collection
11	Col 12	Local Collection
12	Col 38	Local Collection
13	Col 24	Local Collection
14	Tegegnech (Standard Check)	Holota Agricultural Research Center
15	Markos (Standard Check)	Holota Research Center
16	Local Check	Farmer

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of income for the farmers and foreign currency for the country (Girma, 2003).

Having all these multiple benefits in the economic lives of the farming communities, however, the average yield of the crop is only 1.24 t ha^{-1} in Ethiopia (CSA, 2012, FAOSTAT, 2012) which is far below the potential 40 to 50 t ha^{-1} traditionally achieved in Europe (Netherlands, France and Belgium) and the worldwide average yield of 1.7 t ha^{-1} (Petr et al., 2012). Lack of improved high yielder varieties resistance to diseases, insects and abiotic calamities for specific location with appropriate agronomic recommen-dations can be cited as a major reason for this low productivity.

Employing effective breeding program that can exploit the existing genetic variability in the genotypes is paramount important to fill these yield gaps and feed the ever increasing population. To this effect, the knowledge of nature and degree of divergence in genotypes, the extent of transmissibility of the given trait and their interaction with environments are extremely valuable (Johnson et al., 1995; Nisar et al., 2008).

Recently, several studies have been conducted to assess the genetic diversity of field pea based on morpho-agronomic traits using multivariate procedures including principal component and cluster analysis (Singh and Singh, 2006; Katyar and Dixit, 2009; Million, 2012). However, to date, there is no information on genetic variability and environmental interaction of these elite genotypes under eastern Ethiopian conditions.

As the genotypes differently perform under different agro-climatic conditions (Khan et al., 2013), this study was initiated with elite genotypes of Ethiopian collections so as to provide the information on the extent and nature of genetic diversity and the interrelationship among characters and their environment based on the multivariate analysis postulated by Mahalanobis (1936). Therefore, the present investigation was designed to estimate the genetic varia-bility among elite field pea genotypes and identify supe-rior genotypes that would generate putative transgressive segregantes on hybridization under agro-climatic conditions of Eastern Ethiopia.

MATERIALS AND METHODS

Description of the study area

This study was conducted at Haramaya and Hirna districts of Eastern Ethiopia. Haramaya is located at 9°26′N and 42°03′E with an altitude of 1980 m above sea level (masl) 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). While Hirna district is situated in 9°13'N longitude and 41°6'E latitude of the semi-arid and sub-humid agro-ecological zones of the country. It has an altitude of 1750 to 1990 masl with average rain fall of 1064 mm and annual temperature of 18.2 to 27.5°C (Ayalneh, 2006; Dawit etal., 2012).

Experimental materials and design

Thirteen (13) samples of elite field pea genotypes along with two commercial varieties (*Tegegnech* and *Markos*) and a local check were evaluated for three consecutive years, 2006 to 2008 cropping seasons at Haramaya and Hirna locations. List of 16 genotypes along with their sources are given in Table 1. The treatments were arranged in randomized complete block design with three replications. Seeding was done in a plot size of 0.8 × 4 m and regular spacing of 5 cm between plants and 20 cm between rows. Other cultural practices were done as per the recommendations adopted for the respective sites.

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, Ascochyta blight and powdery mildew (1-9 scale), Plant height, pod length, number of pods per plant, number of seeds per pod and per plant, thousand seeds weight in gram and seed yield in gram from 1.6 m^2 harvestable plot (Table 2). Qualitative and disease data were transformed using appropriate data transformation techniques. The traits were quantified using pooled analyses of variance over two locations and three years using the following model:

$$\mathbf{P}_{imkt} = \mu + y_m + l_t + r_{i(m)(t)} + g_k + (gy)_{km} + (yl)_{mt} + (gl)_{kt} + (ylg)_{mtk} + e_{imkt}$$

Where, $\mathbf{P}_{ijmkt}$ = phenotypic value of k^{th} genotype under i^{th} replication during m^{th} year and at t^{th} location with replication i, location t and year m; y_m= m^{th} year; l_t= t^{th} location; $r_{i(m)(t)}$ = the effect of replication i within year m and location t; g_k = the effect of k^{th} accession; μ= grand mean and $(gy)_{km}$, $(yl)_{mt}$, $(gl)_{kt}$ and $(ylg)_{kmt}$ = the interaction effects and e_{imkt} = random error.

The data were subjected to the analyses of variance (ANOVA) performed using the SAS program software (SAS, 2001). Significant

of the result was illustrated under each analysis of the following sub-categories.

Coefficient of variations

The coefficients of variations at phenotypic and genotypic levels were estimated using the formula adopted by Johnson et al. (1995). Significance of variability for each trait was tested against 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. (1995) using the SAS software package (SAS, 2001).

Clustering and estimation of distance

Genetic diversity between clusters based on correlation matrix was calculated using the SAS software package (SAS, 2001). Thus, the analysis 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). Squared distance (D^2) for each pair of genotype combinations was computed as per Singh and Chaudhary (1999). Based on the squared distances (D^2), clustering of genotypes was done using Tocher's method as described by Singh and Chaudhary (1999). SAS software package (SAS, 2001) was used for all statistical analysis.

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.

RESULT

Analysis of variance

Before proceeding with performing analysis of variance, test was made to confirm the homogeneity of variances which all turned out to be so. It can be seen from Table 2 that the mean squares due to year were highly significant ($P \leq 0.01$) for all traits except for the disease Ascochyta blight and number of pods per plant which were significant.

Similarly, mean squares due to location were highly significant for all traits indicating that there are differences between the six environments, which are significant enough to see the genetic performance of field pea germplasm. It is evident from the results that mean squares due to genotypes were highly significant for all temporal data, thousand seed weight and seed yield, whereas, non significant for disease reaction as well as seed contributing traits, indicating the existence of sufficient genetic variability among the tested genotypes.

Mean squares due to the interaction between location and genotype were highly significant for all temporal data and seed yield whereas non significant for the rest of the traits. Mean squares due to the interaction between year, location and genotype were highly significant for the temporal traits, plant height and seed yield. The field pea accessions in this study showed significant phenotypic variability in terms of phenology and yield attributes.

Estimation of genotypic and phenotypic variations

High genotypic coefficient of variation (32.52%) and (32.07%) were observed for Ascochyta blight and number of seeds per pod, respectively. Whereas, the lowest value of genotypic coefficient of variation was estimated for powdery mildew (0.24%). Likewise phenotypic coefficient of variation was high for the number of seeds per pod (241.13%) followed by Ascochyta blight (173.59%).

The estimated values of phenotypic variances were in the range of 12.40 for number days to flowering to 134038.68 for seed yield (Table 3). The lowest and highest genotypic variances were found 0.18 and 21415.10 for the powdery mildew reaction and seed yield, respectively.

Estimation of broad sense heritability and genetic advance

High heritability was observed for temporal trait, days to flower, moderate for seed yield. However, the rest of the traits exhibited for low values of heritability indicating limited possibility of improvement for those characters through selection (Table 4). The highest genetic advance accompanied with moderate estimate of heritability observed for the seed yield (120.67, 15.98%) and thus about 17% of yield improvement can be made per selection cycles in field pea. While, high heritability coupled with low genetic advance found in date of flowering (39%, 2.84).

Principal component analysis

Principal component analysis was done to assess the pattern of variations by considering all the 12 variables simultaneously. Four of the 12 principal components accounted for more than 89% of the total variation in the field pea accessions (Table 4). 40.26% of the total variation was explained by the first principal component.

Out of the 12 traits considered, half of them considered exerted posi-tive and half negative effects on this component. Among those traits having positive and greater influence include: plant height, Ascochyta blight, number of seeds per pod and thousand seed weight. Whereas, seed yield and grain filling periods were among the traits exerted negative influence.

The second component accounted for an additional

Table 2. Analysis of variance for 12 traits of *Pisum sativum* L. genotypes tested over three cropping seasons (2006-2008) and two locations (Haramaya and Hirna).

Variable	MSY(2)[β]	MSL(1)	MSR(2)	MSG(15)	MSYL(2)	MSYG(30)	MSLG(15)	MSYLG(30)	MSE	CV (%)
DF	42.73**	17.67**	5.92^{ns}	97.25**	27.13**	13.35**	50.64**	11.17**	1.70	2.21
GFP	1193.82**	199.09**	0.91^{ns}	68.23**	1508.57**	12.16**	36.13**	7.86**	2.85	3.22
DM	833.76**	335.40**	4.19^{ns}	27.40**	1134.00**	11.35**	6.14**	7.07**	1.60	1.13
PWM	45.63**	499.60**	10.71**	2.42^{ns}	2.12^{ns}	2.05**	0.91^{ns}	2.34^{ns}	1.56	23.04
ASBL	350.34*	8.92^{ns}	15.29^{ns}	82.48^{ns}	3.01^{ns}	85.23^{ns}	0.83^{ns}	10.42^{ns}	74.93	182.62
PH	141744.96**	270450.74**	370.03**	206.62**	110064.61**	193.42**	100.10^{ns}	146.25**	64.92	12.54
PL	161.75**	170.66**	2.55^{ns}	8.43^{ns}	21.31^{ns}	23.19^{ns}	22.01^{ns}	20.30^{ns}	13.18	59.02
PPPL	174.69*	3922.57**	61.15^{ns}	47.76^{ns}	157.47*	39.69^{ns}	26.00 ^{ns}	34.72^{ns}	47.57	40.77
SPP	3582.80**	4608.38**	218.83^{ns}	340.69^{ns}	2027.25**	393.50^{ns}	330.10^{ns}	391.84^{ns}	333.42	240.79
SPPL	53218.49**	270229.75**	5983.49^{ns}	2443.70^{ns}	4479.02^{ns}	3080.59^{ns}	2224.64^{ns}	2724.66^{ns}	2924.95	63.71
TSW	120908.00**	65426.31**	649.11^{ns}	25362.06**	61429.04**	8989.49^{ns}	9615.59^{ns}	7481.43^{ns}	7679.27	50.67
SYLD	793195.13**	6875135.72**	30513.09^{ns}	431647.52**	228588.38**	81029.71**	94416.42**	83482.09**	36374.88	27.30

*, **Significant at 0.05 and 0.01 probability level respectively and ^{ns}non significant. MSY = Mean square due to year, MSL = mean square due to location, MSR = mean square due to replication, MSG = mean square due to genotypes, MSYL = mean square due to the interaction between year and location, MSYG = mean square due to the interaction between year and genotypes, MSLG = mean square due to the interaction between location and genotypes, MSYLG = mean square due to the interaction between year and location and genotypes, MSE = mean square due to error, CV% = Coefficient of variation in percentage. [β]Figures in parenthesis indicate degrees of freedom. DF = days to 50% flowering, DM = Days to 90% maturity, GFP = grain filling period, PWM = Powdery mildew (1-9 scale), ASBL = Ascochyta blight (1-9 scale), PH = plant height in cm, PL = pod length, PPPL = number of pods per plant, SPP = number of seeds per pod, SPPL = number of seeds per plant, TSW = thousand seeds weight in gram, SYLD = seed yield in gram.

Table 3. 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 11 traits of *Pisum sativum* L.

Variable	Min	Mean	Max	σ^2p	σ^2g	GCV%	PCV%	h^2%	GA	GAM
DF	54.55	59.05	63.48	12.401	4.850	3.73	5.96	39.11	2.84	4.81
GFP	48.83	52.32	55.94	35.544	2.647	3.11	11.39	7.45	0.92	1.75
DM	109.72	111.37	113.72	25.335	0.851	0.83	4.52	3.36	0.35	0.31
PWM	2.11	4.93	6.87	13.282	0.180	0.24	0.31	1.35	0.10	2.03
ASBL	2.26	5.09	11.98	78.187	2.744	32.52	173.59	3.51	0.64	12.57
PH	57.84	63.64	68.47	4422.701	47.305	10.81	104.50	1.07	1.47	2.31
PPPL	13.95	16.92	20.80	75.849	0.291	3.19	51.47	0.38	0.07	0.41
SPP	4.42	8.18	17.32	389.211	6.884	32.07	241.13	1.77	0.72	8.80
SPPL	67.83	86.06	118.96	5321.791	10.165	3.70	84.77	0.19	0.29	0.33
TSW	123.66	175.54	273.01	10068.422	738.212	15.48	57.16	7.33	15.18	8.65
SYLD	456.04	695.30	1046.91	134038.681	21415.10	21.05	52.66	15.98	120.67	17.36

DF = days to 50% flowering, DM = days to 90% maturity, GFP = grain filling period, PWM = powdery mildew (1-9 scale), ASBL = ascochyta blight (1-9 scale), PH = plant height in cm, PPPL = number of pods per plant, SPP = number of seeds per pod, SPPL = number of seeds per plant, TSW = thousand seeds weight in gram, SYLD = seed yield in gram.

Table 4. The Eigen values and vectors of the correlation matrix for 12 traits of *Pisum sativum* L genotypes.

Parameter	PRIN1	PRIN2	PRIN3	PRIN4
Eigen value	4.88	2.78	1.94	1.19
% variance	40.26	23.21	16.25	9.93
Cumulative	40.26	63.47	79.72	89.65
Character				
DF	0.206	-0.159	-0.044	0.770
GFP	-0.246	0.215	0.460	-0.332
DM	-0.106	0.115	0.576	0.406
PWM	-0.061	0.550	0.028	0.018
ASBL	0.436	0.055	0.129	-0.108
PH	-0.193	-0.222	-0.509	-0.090
PL	0.439	0.004	0.050	-0.036
PPPL	-0.165	0.474	-0.265	0.208
SPP	0.420	0.183	-0.037	-0.047
SPPL	0.054	0.517	-0.295	0.123
TSW	0.414	-0.040	0.069	-0.118
SYLD	-0.290	-0.183	0.112	0.189

PRIN1, PRIN2, PRIN3 and PRIN4 = principal component 1, 2, 3 and 4 respectively, DF = days to 50% flowering, DM = days to 90% maturity, GFP = grain filling period, PWM = powdery mildew (1-9 scale), ASBL = Ascochyta blight (1-9 scale), PH = plant height in cm, PL = pod length, PPPL = number of pods per plant, SPP = Number of seeds per pod, SPPL = number of seeds per plant, TSW = thousand seeds weight in gram, SYLD = seed yield in gram.

23.21% of the total variation. About 67% of the traits under consideration were found to have positive impacts on the second component which primarily illustrated by the patterns of variations in powdery mildew and yield component traits such as number of seeds per pod and number of seed per plant. While, plant height and seed yield were among those traits which influenced negatively. The third principal component accounted for16.25% of the total variation and was eluded with the variations in temporal traits, number of maturity days and grain filling period, exhibiting positive effects on one hand; and plant height with negative impacts on the other. The fourth component accounted 9.93% of the total variation which accounted by days flower contributed the largest positive effect. In this component, about 67% of the trait excreted negative impact of which grain filling period has contributed high negative impact.

Clustering of genotypes

The clustering is based on the squared Euclidean distance and the average linkage technique of clustering was used as illustrated by Rai et al. (2003) using SAS software (SAS,2001) and produced a more understandable portrayal of the 16 field pea genotypes by grouping them into five clusters as indicated in Figure 1 and 2, 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 (Mathura et al., 2006; Million, 2012; Saeed et al., 2009; Singh and Singh, 2006). Table 5 indicates the range and mean of genetic divergence in phonological, morphological and seed traits of the five clusters and the detail account of the characteristics of each cluster is presented hereunder.

Cluster I: consisted of four accessions, PGRC/E32642-2, Col 26, MG102029 and MG1004-46, which exhibited earlier days for flowering, requires longer periods for grain filling, longer in plant height and large number of pods per plants. The remaining traits laid in the intermediate between the other clusters. The result revealed that accessions included in this cluster require shorter for flowering but longer time for grain filling period and had longer height which can bear larger numbers of pods.

Cluster II: consisted of six accessions, Col 8, Col 12, Col 38, local, Col 24 and Col 6, which were early in days to flowering, short in height, shorter pod length, small in seed size as a result low yielder. The accessions in this cluster required longer time to grain filling and susceptible to the disease powdery mildew where as they became intermediate for the rest of the traits under studied.

Cluster III: consisted of two accessions, Col 23 and Col 34, characterized by inferior performance for most of the

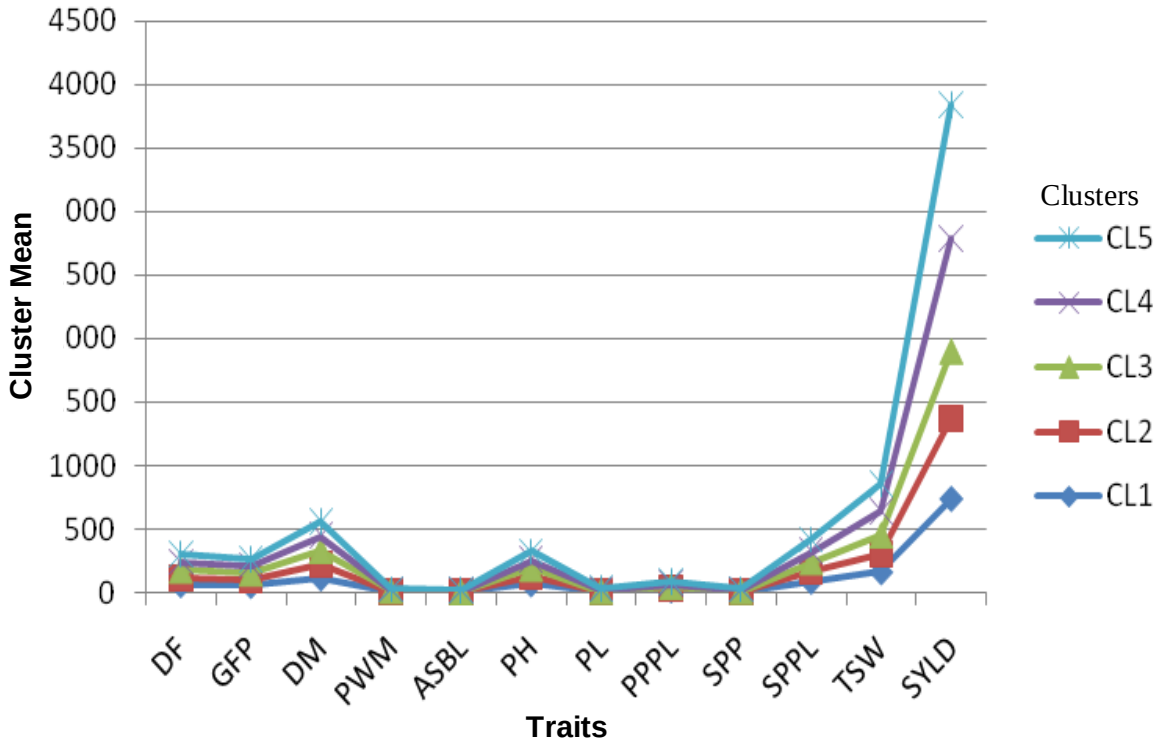

Figure 1. Plotting of cluster mean over traits of interest.

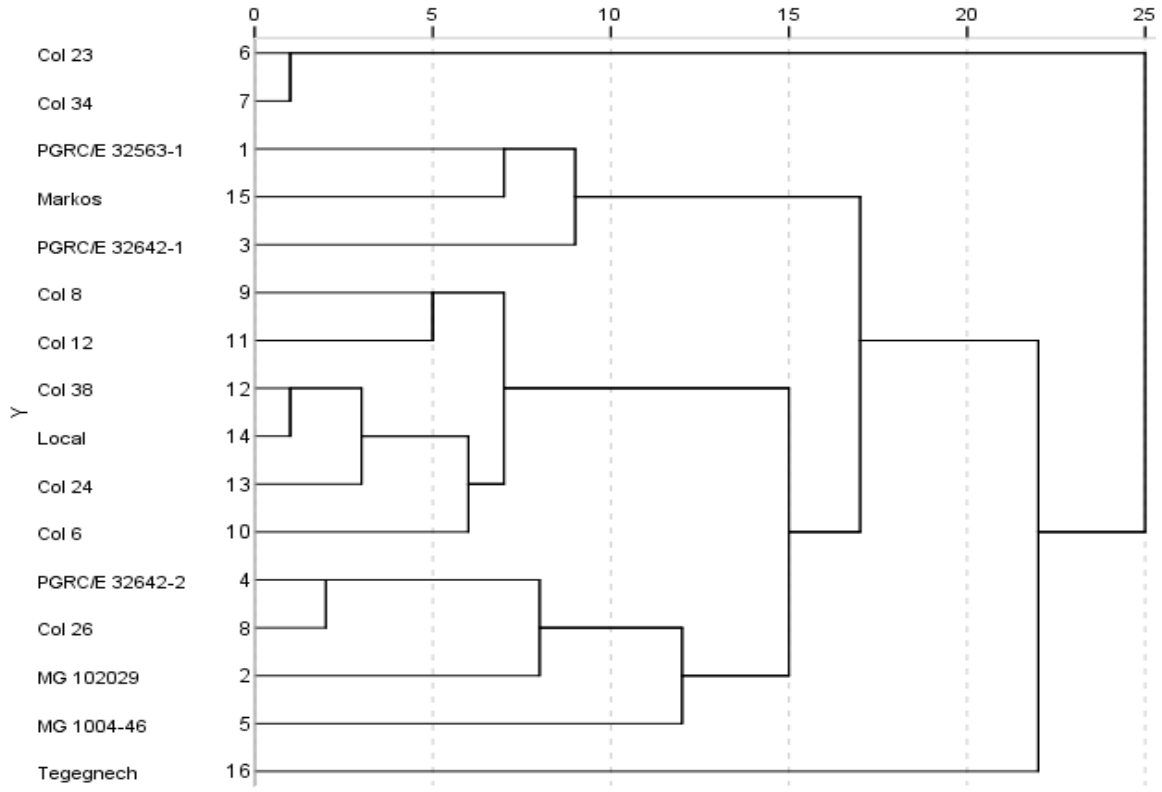

Figure 2. Dendrogram of sixteen elite field pea genotypes derived from squared ecludian linkage cluster analysis.

Table 5. Mean and range of genetic divergence in morphological and seed traits of the five clusters of *Pisum sativum* L.

Character	I			II			III			IV			V		
	Min	Mn	Max	Min	Mn	Max	Min	Mn	Max	Min	Mn	Max	Min	Mn	Max
DF	56.11	58.89	62.28	57.06	58.35	61.61	60.28	61.89	63.50	54.56	58.07	60.83	-	61.00	-
GFP	50.61	52.44	54.33	51.22	53.17	55.94	48.78	49.81	50.83	50.56	52.54	55.39	-	50.89	-
DM	109.83	111.33	112.89	109.72	111.51	113.72	111.11	111.70	112.28	109.94	110.61	111.39	-	111.89	-
PWM	4.58	5.08	5.50	5.00	5.59	6.17	5.50	5.63	5.75	4.92	4.95	5.00	-	4.58	-
ASBL	2.75	2.94	3.22	2.13	2.92	3.33	2.75	3.13	3.50	2.33	2.46	2.67	-	2.33	-
PH	63.74	65.70	68.24	59.64	63.13	67.91	61.48	64.42	67.36	61.48	65.92	68.50	-	63.7	-
PL	5.22	5.36	5.56	4.56	5.04	5.44	4.78	5.00	5.22	5.44	5.89	6.56	-	6.44	-
PPPL	17.18	17.70	18.18	13.95	16.83	19.54	16.82	17.03	17.23	15.76	17.16	18.13	-	17.21	-
SPP	4.37	4.68	4.92	4.42	4.55	4.67	4.26	4.48	4.69	4.51	4.74	4.93	-	5.02	-
SPPL	80.47	86.65	95.13	67.83	80.08	92.00	73.72	78.03	82.33	71.20	83.27	92.72	-	88.09	-
TSW	150.07	160.44	180.56	124.87	142.45	153.79	145.95	152.11	158.27	164.14	184.72	210.68	-	213.22	-
SYLD	727.43	738.59	753.62	601.28	632.54	683.81	523.16	524.65	526.14	875.97	895.26	926.51	-	1046.91	-

Min, Mn and Max stands for minimum, mean and maximum value, SD = standard deviation, DF = days to 50% flowering, DM = days to 90% maturity, GFP = grain filling period, PWM = powdery mildew (1-9 scale), ASBL = ascochyta blight (1-9 scale), PH = plant height in cm, PL = pod length, PPPL = number of pods per plant, SPP = number of seeds per pod, SPPL = number of seeds per plant, TSW = thousand seeds weight in gram, SYLD = seed yield in gram.

traits in general. The genotypes took longer period to flower but required shorter time for grain filling. They are shorter in pod length, bear small number of seeds per pod as well as number of pods and seeds per plant, lower thousand seed weight and seed yield. The accessions also exhibited high susceptible to the diseases, powdery mildew and ascochyta blight.

Cluster IV: had three accessions, PGRC/E 32563-1, Markos and PGRC/E 32642-1, which generally exhibited intermediate for all traits of interest except for plant height which exhibited longer in height than the rest of field pea genotypes.

Cluster V: consisted of single genotype, Tegegnech, exhibited superior in most of the traits. The genotypes required longer periods for flowering and resistance to the disease reaction such as powdery mildew and Ascochyta blight. This accession showed largest in pod length which can hold large number of seeds per the pod and per plant. This accession exhibited with bold seed size and gave the highest seed yield.

Divergence analysis

From the estimated distance analysis, under this investigation, differences between all of the ten possible pairs of clusters were highly significant ($P \leq 0.01$) (Table 5). The maximum distance was found between cluster three and five (D^2 = 53032377). Cluster three constitutes two genotypes while cluster five constitutes a single accession. The second most divergent clusters were cluster three and four (D^2 = 22919871). Cluster four constitutes three accessions.

The third most divergent clusters were cluster two and three (D^2 = 16662613). Cluster two constituting from six accessions. The forth most divergent clusters were bet-ween cluster one and three (D^2 = 13853386) and so on, indicated the wide diversity of the genotypes. The minimum distance between cluster I and II (D^2 = 140914) indicate the genotypes falling in this cluster have genetically close relationship.

Genotypes grouped into the same cluster also presumably diverge little from one another as the aggregate characters are measured (Table 6 and Figure 2).

Association of the traits

Table 7 reveals that seed yield had negative and significant genotypic correlations with the reaction of the disease Ascochyta blight. Whereas, phenoltypic association showed the seed yield had positive and highly significant with grain filling periods, number of seeds per pod and per plant, pod length

Table 6. Pair wise generalized squared distance (D^2) among 5 clusters constructed from *Pisum sativum* L genotypes.

Cluster	C_1	C_2	C_3	C_4	C_5
C_1		140914**	13853386**	1137262**	12676135**
C_2			16662613**	525989**	10260044**
C_3				22919871**	53032377**
C_4					6230799**
C_5					

Table 7. Estimates of correlation coefficients at phenotypic (above diagonal) and genotypic (below diagonal) levels of 12 traits in *Pisum sativum* Lgenotypes.

Traits	DF	GFP	DM	PWM	ASBL	PH	PL	PPPI	SPP	SPPL	TSW	SYLD
DF		-0.688**	0.177ns	-0.268*	0.293**	-0.121ns	0.382**	-0.177ns	0.286**	-0.057ns	0.302**	-0.116ns
GFP	-0.883**		0.591**	0.389**	-0.322**	-0.264*	-0.441**	0.173ns	-0.387**	-0.046ns	-0.390**	0.277**
DM	0.559*	-0.104ns		0.229*	-0.110ns	-0.493**	-0.172ns	0.037ns	-0.207ns	-0.125ns	-0.193ns	0.246*
PWM	-0.423ns	0.182ns	-0.574*		-0.043ns	-0.294**	-0.122ns	0.692**	0.147ns	0.707**	-0.239*	-0.204ns
ASBL	0.693**	-0.584*	0.436ns	-0.129ns		-0.542**	0.953**	-0.362**	0.922**	0.108ns	0.883**	-0.620**
PH	-0.717**	0.699**	-0.283ns	0.247ns	-0.875**		-0.413**	0.083ns	-0.425**	-0.079ns	-0.394**	0.252*
PL	0.848**	-0.676**	0.602*	-0.384ns	0.900**	-0.872**		-0.369**	0.927**	0.101ns	0.880**	0.541**
PPPI	-0.273ns	-0.044ns	-0.658**	0.601*	-0.396ns	0.281ns	-0.464ns		-0.087ns	0.847**	-0.443**	0.022ns
SPP	0.732**	-0.690**	0.332ns	0.015ns	0.877**	-0.869**	0.845**	-0.091ns		0.403**	0.792**	0.651**
SPPL	-0.030ns	-0.252ns	-0.508*	0.595*	-0.114ns	0.002ns	-0.150ns	0.902ns	0.253ns		0.011ns	0.293**
TSW	0.584*	-0.422ns	0.491ns	-0.431ns	0.758**	-0.812**	0.837**	-0.499*	0.616*	-0.254ns		-0.477**
SYLD	-0.103ns	0.082ns	-0.071ns	-0.387ns	-0.514*	0.313ns	-0.209ns	0.145ns	-0.459ns	0.043ns	0.037ns	

*, ** Significant at 0.05 and 0.01 probability level respectively. DF= days to 50% flowering, DM= Days to 90% maturity, GFP= grain filling period, PWM= Powdery mildew (1-9 scale), ASBL= Ascochyta blight (1-9 scale), PH= Plant height in cm, PL= pod length, PPPL= number of pods per plant, SPP= Number of seeds per pod, SPPL=Number of seeds per plant, TSW= thousand seeds weight in gram, SYLD= Seed yield in gram.

and plant height. Positive and significant phenotypic association was existed between seed yield and plant height and number of days to physiological maturity. Whereas, the seed yield became negatively and highly significant phenotypic association with ascochyta blight and thou-sand seed weight.

DISCUSSION

The existence of significant genetic variability among the tested genotypes for all temporal data, thousand seed weight and seed yield that differently performed across the testing sites indicating the need to establish location specific variety releasing mechanism for field pea (Mathura et al., 2006; Singh and Singh, 2006). The environmental variance was greater than the genetic variance for temporal data and all other traits indicating polygenic traits which are inconsistence with the earlier finding (Tezera, 2000; Gemechu et al., 2005).

The highest genetic advance accompanied with moderate estimate of heritability observed for the seed yield (120.67 g, 15.98%), indicated heritability of the trait is mainly due to additive gene effect and selection may be effective to improve the trait. High heritability coupled with low genetic advance for date of flowering (39%, 2.84 days), indicated that the involvement of non-additive gene action and the high value of heritability is being exhibited due to the favorable influence of the environment than the genotype. Similar results

also reported by Mathura et al. (2006) and Raikumar et al. (2001). Therefore, even if heritability estimates provide basis for phenotypic performance, the estimate of heritability and genetic advance should be considered simultaneously, as high heritability is not always associated with high genetic advance (Johnson et al., 1995).

In earlier studies (Tesfaye, 1999; Tezera, 2000; Million 2012), high heritability estimates for phonological traits, biological yield, number of seeds per plant, per pods and harvest index. 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.

The percent mean of 17.36% seed yield genetic gains that could be expected from selecting the top 5% of the genotypes, indicating an increase of the same magnitude can be made per selection cycle to improve field pea yield under similar conditions.

From the cluster analysis in this study, the differences between the clusters were mainly attributed to the variation in pod length and reaction with Ascochyta blight. These traits were also the major contributors to the principal one and two. Genotypes found in the highly divergent clusters showed a wide spectrum of variability that can be used in breeding program. Therefore, crossing of Tegengech from cluster five with Col 26 and Col 23 from cluster three would result potential transgressive segregants that would produce superior breeding materials utilized in future breeding program (Figure 2). While, genotypes grouped into the same cluster or closing clusters (Cluster I and II) presumably diverge little from one another and selection of parents from such clusters may be avoided because it may results in narrow genetic base (Singh and Singh, 2006).

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 (Million, 2012). 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 (Nigussie and Becker, 2002, Gemechu et al., 2005; Fikreselassie et al., 2012).

The strong positive correlation of pod length with seed yield indicates that pod length should be used as selection criteria for maximizing seed yield (Musa et al., 2003). 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. The existence of a positive association between pods per plant and seed yield indicated that plants bearing more number of pods per plant produce more seed yield and thus, selection for number of pods at earlier stage will bring improvement in seed yield.

Similar result also reported by Saeed et al. (2009) and Sharma et al. (2007). The negative and highly significant phenotypic associa-tion exhibited between seed yield and thousand seed weight may due to shriveled large size seed per pod resulted from the frequent terminal moisture stress in the study sites. This result is inconsistent with the earlier studies from Ethiopia (Tesfaye, 1999; Tezera, 2000) and hence Haramaya and Hirna can be a potential testing site for drought tolerance breeding to tackle frequent terminal drought.

The positive significant correlations observed between seed yield with plant height are in agreement with the results reported by Fikreselassie et al. (2012) and McCormic (2004) but contradict with the earlier studies from Ethiopia (Tesfaye, 1999; Tezera, 2000) and elsewhere (Singh, 1990; Rathore, 1993a, 1993b).

Conclusion

In this study, genotypes differed significantly in respect to phonological, yield and some yield related traits and were highly influenced by environment. High magnitude of variability among the genotypes contributed to pod length and reaction to Ascochyta blight. Therefore, the presence of diversity within these advanced genotypes appears to be great interest in providing valuable materials for further breeding programs. Even though, high genotypic coefficient of variations was observed in the genotypes, most of the traits under study except days to flowering and seed yield exhibited low broad sense heritability as the variability was highly influenced by environment. The percent mean of 17.36% seed yield genetic gains that could be expected from selecting the top 5% of the genotypes.

Four of the twelve principal components accounted for more than 89% of the total variation in the field pea accessions. Each trait exerts both positive and negative impact on different principal components with variable magnitude. The average linkage technique clustered the sixteen elite field pea genotypes into five clusters having different number of genotypes. The differences between the clusters were mainly attributed to the variation in pod length and reaction with Ascochyta blight. The maximum genetic distance was observed between cluster three and five. Thus, crossing of Tegengech with col 26 and col 23 would result high magnitude of heterosis that would produce superior breeding materials that can be utilized in future breeding program. Positive correlation of some

yield component traits with seed yield indicates that these traits should be used as selection criteria at earlier breeding stage to maximize the seed yield and hence the study sites can be used as a potential testing site for field pea drought tolerance breeding to tackle terminal drought frequently occurring in the region.

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