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Preliminary Evaluation of Dekoko Field Pea (*Pisum sativum* var. *abyssinicum*) Accessions at Kulumsa and Dehera, South Eastern Ethiopia

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ABSTRACT

The experiment was conducted during July to September, 2021 at Kulumsa and Dhera, Ethiopia to study the genetic variability among yield and yield related traits of abyssinian field pea. Thirteen accessions of field pea (*Pisum sativum* var. *abyssinicum*) along with one standard and one local check from the species Pisum sativum were evaluated at two locations in a randomized complete block design with three replications. Combined analysis of variance revealed highly significant (p<0.01) for locations. Grain yield performances of the accessions were ranged from low of 1539 kg ha^{-1} to high yield of 4520 kg ha^{-1} followed by 3728 kg ha^{-1} for standard check Megeri, respectively. The estimated values for phenotypic coefficient of variation (PCV) are higher than their counter genotypic coefficient of variation (GCV) values. A heritability as high as 98% were recorded for days to flowering and days to maturity. Cluster analysis grouped into three distinct classes with number of genotypes in each cluster ranged from two to nine. Principal component (PCs) analysis revealed the first two PC were contributed for 70.7% of the entire phenotypic variation observed among the 15 field pea genotypes. Generally, the use of multivariate analysis including principal component and cluster analysis, and coefficient of variance analysis were effectively used to estimate the level of existing genetic variability in field pea genotypes under study. The result indicated that there is a potential for genetic improvement through selection in this field pea species.

KEYWORDS: Abyssinicum, collections, variability, correlation, genotypic, phenotypic, cluster, principal

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1. INTRODUCTION

Field pea (*Pisum sativum L.*) is the fourth most important legume crop in Ethiopia after faba bean, haricot bean and chick pea in terms of both area and total amount of production. Field pea covers over 203,990.64 ha with a total production of 257,031.41 tons which accounts for 12.37% of the total grain legume production (Anonymous, 2018).

Even though the origin of field pea is controversial, Ethiopia is undoubtedly the center of diversity for this crop since wild and primitive forms are known to exist in the high elevations of the country. Ethiopia is one of the major Vavilovian centers of diversity for several grain legume crops including lupine, field pea and wild ancestors of cow pea (Ali et al., 2003).

Cultivated Pisum is dominated by *P. sativum* species but Pisum sativum species abyssinicum (or simply *P. abyssinicum*) is a unique sub-species independently developed and cultivated in Ethiopia. The existing germplasm in the country shows tolerance to disease (Sentayehu, 2009); (Jing et al., 2010). *Pisum sativum* is widespread across the Middle East and has affinity with the wild Pea elatius while Pea abyssinicum is restricted to highland regions of Ethiopia (South Tigray and North Wello) and Southern Yemen and shows a greater affinity to P. fulvum (Yemane and Skjelvag, 2002; Jing et al., 2010). However, P. fulvum is found around the eastern edge (Syria, Lebanon, Israel, Palestine and Jordan) and not common in Ethiopia (Maxted and Ambrose, 2001).

Pisum sativum abyssinicum is locally known as Dekoko (minute seeded) in Tigrigna and Yagere Ater (pea of my country) or Tinishu Ater (the smallest pea) in Amharic. This variety sells for about twice the price of fava beans, Farmers and consumers call it as the "Dero-Wot of the poor" (chicken stew of the poor) due to its special taste and high nutritional value. Most often, the dry seeds of Dekoko are decorticated and split ('split peas') before boiling. Regarding to its earliness, Abyssinian pea (dekoko) is named as "fetnoderash" (early maturing) referring to its short life cycle.

A large genetic diversity has been found in Pea sativum collections from both Africa (e.g. Ethiopia) and Asia. High to medium field pea genetic diversity in Ethiopia was observed in collections from Shoa, Gojam, Gondar, Wello, and Tigray while low to trace genetic diversity was observed in collections from Arsi, Gamo-gofa, Wellega, Illubabur and Kafa (Ali et al., 2003).

Land races are the genetic wealth that a crop acquires over many years of its existence and have considerable breeding values as they contain valuable adaptive genes to different circumstances (Messiaen et al., 2006; Ali et al., 2003). In Ethiopia, many cultivars of field pea, with better yield potential, seed size, seed color and disease resistance than the farmers' varieties, have been released for different agro-ecological conditions (Anonymous, 2008). Some of these varieties were obtained from local collections while others were obtained through hybridization of landraces with introduced germplasm. Two variety of dekeko released by Alamata Agricultural research center (AARC) under Tigray Agricultural research institute (TARI) (Anonymous, 2008)

Even though Dekoko (*P. sativum* var. *abyssinicum*) is important both for the local farmers and consumers, it is at risk of disappearing due to lack of improved Varieties and improper management.

However apart from a study conducted on genetic diversity for attributes of biological nitrogen fixation (Gemechu et al., 2013), there were no information regarding the existing variability in yield and its component traits of this botanical species. Therefore, the current study is initiated aimed to evaluate abyssinian field pea accessions for genetic variability, character association and adaptability performance for yield and yield related traits.

2. MATERIALS AND METHODS

2.1. Planting materials and test locations

The experiment was conducted during July–September 2021 at Kulumsa and Dhera, Ethiopia to study the genetic variability among yield and yield related traits of abyssinian field pea. Thirteen random samples of field pea (*Pissum sativum* var. *abyssinicum*) accessions collected from the northern part of the country including one standard and one local check from the species *Pisum sativum* were used for this study. Descriptions of the planting materials are indicated in Table 1 below. The accessions were evaluated at two locations, Kulumsa (08°01'00"N, 39°09'32"E) and Dhera (08°19'10"N, 38°19'13"E) in Arsi during the year 2021 main cropping season. Kulumsa, with an altitude of 2200 meters above sea level and receiving an average annual rainfall of 820 mm, represents the major mid-altitude field pea production areas of the country while Dhera, with an altitude of 1650 meters above sea level and an average annual rainfall of 596 mm, represents the major low-altitude production areas. Kulumsa is represented by a dark-clay loam soil, while Dhera is by light sandy soil with very low water holding capacity.

2.2. Experimental design

The trials are laid down in a randomized complete block design with three replications. Each plot consists four rows of 4 m long with a spacing of 20 cm between rows and 5 cm between plants. The trial was managed following research recommendations specific to each location. Data on days to

Table 1: Description of field pea (*P. sativum* var. *abyssinicum*) accessions studied

Sl. No.	Accession name	Sl. No.	Accession name
1.	Coll-016-21	9.	Megeri (St. Check)
2.	Coll-019-21	10.	Local check
3.	Coll-021-21	11.	Coll-002-21
4.	Coll-025-21	12.	Coll-024-21
5.	Coll-027-21	13.	Coll-026-21
6.	Coll-030-21	14.	Coll-032-21
7.	Coll-040-21	15.	Coll-041-21
8.	Coll-043-21		

50% flowering, days to 95% physiological maturity, grain yield (g), seed size (g), ascochyta blight (1–9), and powdery mildew (1–9) were conducted on a plot bases, while number of pods plant^{-1}, number of seeds pod^{-1} and plant height (cm) were collected from randomly selected 5 plants. The seed yield was converted into hectare basis at 10% standard seed moisture content and used for statistical analysis.

2.3. Statistical analysis

The coefficients of variations at phenotypic and genotypic levels were estimated using the formula adopted by Johnson et al. (1955a). Genetic diversity between the field pea accessions under study was computed through clustering and principal component analysis of the multivariate procedure using PROC CLUSTER and PROC PRINCOMP procedure of statistical analysis software (Anonymous, 2002 and R software).

2.4. Data analysis

2.4.1. Analysis of variance

2.4.1.1. Analysis of variance for each location

The data collected from each location were subjected to analysis of variance (ANOVA) and computed with R statistical software. The data were collected in simple lattice (partially balanced or incomplete block) design (Gomez and Gomez, 1984) and analysis of variance for individual location was computed considering the general linear model as follows.

$Yijl=\mu+rj+gi+P\ l(j)+\varepsilon ijl$

Where: *Yij*=the observed value of the trait Y for the i^{th} genotype in j^{th} replication

μ=the general mean of trait Y, *rj*=the effect of j^{th} replication

gi=the effect of i^{th} genotypes and (*j*)=block within replicate effect

εijl= the experimental error associated with the trait y for the i^{th} genotype in l^{th} block with in replication and j^{th} replication.

2.4.1.2. Combined analysis of variance over location

Homogeneity test of error variances using F-test as stated by Gomez and Gomez (1984) was accomplished for each trait prior conducting the combined analysis of variance over locations. For combined analysis homogeneity of error variance were computed using the error variance ration i.e. F-max method is better to check variances homogeneity the results were no serious violation of the assumption. The ANOVA for combined location was conducted using the following model:

$Pijk=\mu+gi+bk(j)(s)+rj(s)+ls+(gl)is+eijks$

Where: Pijks=phenotypic value of i^{th} genotype under j^{th} replication at s^{th} location and k^{th} incomplete block within replication j and location s; μ=grand mean; g_i=the effect of i^{th} genotype; $b_{k(j)(s)}$=the effect of incomplete block k within replication j and location s; $rj_{(s)}$=the effect of replication j within location s; ls=the effect of location s; $(gl)_{is}$=the interaction effects between genotype and location; and e_{ijks}=the residual or effect.

Analysis of variance model for individual location

Source of variation	DF	SS	Mean square	F value
Replication	r-1	SSr	MSr	MSr/Mse
Treatments	t-1	SSt	MSt	MSt/Mse
Block within replication (b)	r (b-1)	SSb	SSb	MSb/Mse
Intra block error	(b-1) (rb-b-1)	SSe	Mse	
Total	TSS			

r: No. of replication; t: No. of treatments; df: Degree of freedom; b: Block; SS: Sum of squares; MS: Mean squares; SSr and MSr are sums of squares and mean of replication; respectively; SSt and MSt are sums of squares and mean of treatments respectively; SSb and MSb are sums of squares and mean of blocks within replication respectively; SSe and MSe are sums of squares and mean of intra-block error; respectively and SST is sum of squares of the total.

The two locations homogeneity test of error variances indicated the homogeneous of error variances for all traits and accordingly the comparison of genotypes was conducted based on pooled mean performance over locations. The comparison of mean performance of genotypes was carried using Duncan's Multiple Range Test (DMRT) at 5% level of significance (Gomez and Gomez, 1984). The combined analysis of variance (ANOVA) was conducted using R Statistical software version 3.6 (Anonymous, 2019).

2.4.2. Estimation of phenotypic and genotypic variances

The phenotypic and genotypic variances of each trait estimated from the analysis of variance. The expected mean squares under the assumption of random effects model was

computed from linear combinations of the mean squares. The phenotypic and genotypic coefficients of variations were computed as per the methods suggested by. Temesgen et al., 2022. The genetic variance of the components was estimated by considering the effects in the model as random variable using the lme4 package of R software v 3.6 (R core team, 2019). The genotypic variance (σ^2g) and the environmental variance (σ^2e) were obtained directly from variance component table generated by the software.

2.4.3. Genotypic variance for over locations

Analysis of variance model of simple lattice design for combined analysis over locations

Source of variation	Degree of freedom	Mean square (MS)	Expected mean square (EMS)
Location (L)	L-1	MSL	$\sigma^2e+r\sigma^2gl+rg\sigma^2l$
Replication with in location	(r-1)L	MSr	$\sigma^2e+g\sigma^2r$
Blocks within replication(b)	rL(b-1)	MSb	$\sigma^2e+r\sigma^2gl+r\sigma^2g$
Genotype (g)	g-1	MSg	$\sigma^2e+r\sigma^2gl+rL\sigma^2g$
G×L interaction(i)	(g-1) (L-1)	MSg×L	$\sigma^2e+r\sigma^2gl$
Error (e)	Lg(r-1)-(rb-1)	Mse	σ^2e
Total	Lrb^2-1	MSt	

b=Blocks; L=No. of locations; g=No. of genotypes; r=No. of replications; σ^2g=Genotypic variance; σ^2L=Location variance; σ^2r=Replication variance; σ^2gl=Genotype by location interaction variance and σ^2e=Environmental variance.

The estimates of genotypic variance computation over locations considered the expected mean squares from combined analysis of variance (Table 4).

$\sigma^2g = (Msg-Msgl)/rl$

$\sigma^2gl = (Msgl-Mse)/r$

$\sigma^2e = \sigma^2e/rl$

Where, σ^2g=genotypic variance, σ^2gl=genotype by environment variance, σ^2e=environment or error variance, r= replication and l=location. Msg=genotype/treatment mean square, Msgl=mean square due to genotype by environment interaction, Mse=pooled error mean square/Phenotypic variance $(\sigma^2_{ph})=\sigma^2_g+\sigma^2_{gl}/l+\sigma^2_e$

2.4.4. Estimation of genotypic and phenotypic coefficient of variations

The genotypic and phenotypic coefficients of variability were undertaken according to the formulae of Singh and Chaundary (1977).

Genotypic Coefficient of Variation (GCV) (%)=(σ^2_g/grand mean)×100

Phenotypic Coefficient of Variation (PCV) (%)=(σ^2_{ph}/grand mean)×100

Where, σ^2_g and σ^2_{ph} are genotypic and phenotypic standard deviations, respectively.

2.4.5. Estimation of heritability and genetic advance

Heritability in broad sense for all traits was computed as suggested by Hanson et al. 1956).

Heritability in broad sense (H^2b) (%) = (σ^2_g/σ^2_{ph})×100

Then, the genetic advance for selection intensity (k) at 5% (2.06) was estimated by the formula (Johnson et al., 1955a; Allard, 1960; Rasmusson and Glass, 1967):

$EGA=k^* \sigma_{ph} {}^*H^2b$

Where, EGA represents the expected genetic advance under selection; σ^2_{ph} is the phenotypic standard deviation; H^2b is heritability in broad sense and k is selection intensity.

The genetic advance as percent of population mean was also estimated following the procedure of Johnson et al. (1955a). Genetic advance population^{-1} mean GMA) (%)=(EGA/ grand mean)×100

2.4.6. Estimation of phenotypic and genotypic correlations

Phenotypic and genotypic correlation coefficients were estimated using the formulae of Temesgen et al., 2024.

$$rg\ (xy)=\frac{Gcov(x,y)}{\sqrt{\sigma^2_{gx}\times\sigma^2_{gy}}}$$

Where rg=genotype correlation coefficient, Gcov (x.y)=genotype co-variance between Variable x and y, σ^2_{gx}=genotype variance for variable x, σ^2_{gy}=genotype variance for variable y. The phenotypic correlation was calculated as follow:

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

Where rp=phenotype correlation coefficient, Pcov (x.y)=phenotype co-variance between variable x and y, σ^2_{px}=phenotype variance for variable x, σ^2_{py}=phenotype variance for variable y.

2.4.7. Path coefficient analysis

In path coefficient analysis, yield plot^{-1} was taken as a dependent variable while the rest of the characters were considered as independent variables. The direct and indirect effects of the independent traits on field pea yield plot^{-1} were estimated by the simultaneous solution of the following general formula suggested by ().

$rij=pij+\sum r_{ik}P_{jk}$

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

2.4.8. Genetic divergence

The Mahalanobis D^2 genetic distance (Rao, 1952) was estimated by considering the mean data and the variance covariance matrix of the traits using the bio-tools package of R (da Silva, 2017). Based on the estimated distance, the Hierarchical cluster analysis was employed to cluster the field pea genotypes using the UPGMA clustering method using the R base function hclust. After the appropriate number of clusters determined based on the above analysis the intra and inter genetic distance within and among the cluster groups were estimated using clv package of R (Nieweglowski, 2020), respectively.

The manhalobis genetic distance among the 15 field pea genotypes was estimated as follow

$$D^2=\sum X^{-1} V^{-1} X$$

Where D^2 is the Mahalanobis genetic distance between genotype i and j, X the mean performance of the genotypes of the traits, V is the variance covariance matrix of the traits under consideration.

The distance matrix from phenotype traits were used to construct dendrogram based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis are presented in the form of dendrogram. Using the mean data the principal component analysis was conducted to see the distribution of the genotypes in two dimensional plots using the princomp" package of R (Anonymous, 2019).

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

The combined analysis of variance over the two test locations revealed highly significant (p<0.01) differences in mean squares of locations for all traits evaluated except for seed size and grain yield (Table 2). Likewise, there were significant differences (p<0.01) among the field pea accessions for traits including days to flowering, days to maturity, plant height, 1000 seed weight, and grain yield (kg ha^{-1}), however, there were no differences among accessions for ascochyta blight and powdery mildew disease incidences. The overall mean values of accessions for all traits investigated were found varied (Table 3). Grain yield performances of the accessions were ranged from low yield of 1539 kg ha^{-1} for Coll-019-21 and Coll-040-21, to high yield of 4520 kg ha^{-1} followed by 3728 kg ha^{-1} for Coll-043-21 and standard check Megeri, respectively with overall mean of 2331 kg ha^{-1}.

Most of the evaluated accessions were earlier by almost one month in flowering and by nearly two months to rich their physiological maturity when compared to the standard and local checks in the trail. The checks were found to have longer plant height, higher number of pods $plant^{-1}$,

Table 2: Mean squares from 9 traits from fifteen field pea accessions evaluated in 2 locations

	Mean Square				
Source	Location	Bloc (Location)	Entry	Loc*Entry	Error
DTF	2538.7^{**}	62.2^{***}	433.7^{***}	6.1^{ns}	3.4
DTM	332.5^{***}	2.97^{ns}	2588.7^{***}	18.23^{***}	3.39
PHT	11514.7^{**}	355.9^{ns}	6672.5^{**}	1257.5^{***}	249.7
PPP	1869.6^{***}	4.01^{ns}	71.03^{ns}	49.0^{***}	17.17
SPP	48.1^{**}	0.78^{ns}	0.56^{ns}	0.59^{ns}	0.33
TSW	624.1^{ns}	127.2^{ns}	1848.4^{**}	455.1^{*}	212.5
Grainyield	1612505.8^{ns}	1876588.5^{ns}	3982501.9^{**}	1008249.2^{ns}	793024
AB	24.5^{**}	0.41^{ns}	0.49^{ns}	0.83^{ns}	0.46
PM	134.4^{***}	0.92^{*}	0.79^{ns}	0.35^{ns}	0.26

FLD: Days to 50% flowering; MTD: Days to 90% maturity; PLHT: Average plant height (cm); PPP: Average no. of pods $plant^{-1}$; SPP: average no. of seeds pod^{-1}; TSW: Mean 1000 seed weight (g); GYDH: Grain yield (kg ha^{-1}); AB: Ascochyta blight disease score (1-9); PM: Powdery mildew disease score (1–9) score

Table 3: Mean agronomic performance of 15 field pea accessions evaluated across two locations during 2021 main cropping season

Entry	Genotypes	DTF	DTM	PHT	PPP	SPP	TSW	GY	AB	PM
1	Coll-016-15	45.00	78.67	67.78	9.43	5.37	101	2079	3.50	2.50
2	Coll-019-15	44.33	78.33	55.44	7.90	5.10	97	1539	3.67	2.50
3	Coll-021-15	44.50	76.33	66.44	10.37	5.40	101	2725	3.33	2.50
4	Coll-025-15	44.33	78.17	65.94	10.40	5.00	96	2236	3.50	2.67
5	Coll-027-15	45.17	79.67	54.61	9.40	5.80	104	1869	3.33	2.33
6	Coll-030-15	45.50	77.50	58.50	9.47	5.63	102	2015	3.67	2.33
7	Coll-040-15	46.17	80.83	65.78	9.03	5.93	103	1539	3.33	2.33
8	Coll-043-15	45.67	78.83	88.72	8.77	5.57	152	4520	3.17	2.67
9	Megeri	64.67	134.17	164.00	18.17	5.50	147	3728	3.83	3.67
10	Local check	72.67	141.00	147.67	19.33	5.33	116	2206	3.50	2.83
11	Coll-002-15	43.67	78.33	64.17	10.60	5.07	98	2161	3.17	2.50
12	Coll-024-15	46.00	80.33	65.89	7.83	5.50	104	1989	4.17	2.17
13	Coll-026-15	46.67	78.67	57.72	8.97	5.80	99	1865	3.33	2.17
14	Coll-032-15	43.00	78.83	66.94	10.83	4.97	97	2675	3.83	2.50
15	Coll-041-15	45.67	79.17	58.06	8.47	5.67	102	1824	3.83	2.33
	Mean	48.20	86.59	76.51	10.60	5.44	108	2331	3.54	2.53
	CV (%)	3.85	2.13	20.66	39.09	10.49	13.52	38.20	19.11	19.95
	LSD (p<0.05)	2.15	2.13	18.28	4.79	0.66	16.86	1030	0.78	0.58

DTF: Days to 50% flowering; DTM: Days to 90% maturity; PHT: Average plant height (cm); PPP: Average no. of pods plant^{-1}; SPP: Average no. of seeds pod^{-1}; TSW: Mean 1000 seed weight (g); GY: Grain yield (kg ha^{-1}); AB: Ascochyta blight disease score (1-9); PM: Powdery mildew disease score (1-9) score

and larger seed size compared to the remaining accessions. All genotypes evaluated were showed non-significant differences for their reaction against ascochyta blight disease, however, the analysis revealed that the accessions had good level of resistance to powdery mildew compared to both checks in the trail.

On the other hand, the interaction effect of accessions with locations were highly significant (p<0.01) for days to maturity, plant height, number of pods plant^{-1} and at (p<0.05) for 1000 seed weight (Table 2). These significant effects due to accessions, locations, and accessions by environment interaction indicate that the accessions and locations were diverse to show substantial variations in useful agronomic traits for field pea breeding.

3.2. Estimate of coefficient of variation, heritability, and genetic advance

The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (H), and expected genetic advance (GA) are presented in Table 4. The estimated values for GCV ranged from 2.06% for number of seeds pod^{-1} to 35.6% for plant height, while the PCV estimates is ranged from 6.33% for number of seeds pod^{-1} to 41.8 for plant height. In most of the traits under study, the estimated values for PCV are higher than their counter GCV values except for days to flowering and maturity. As PCV is usually the reflection of the effects of genotypes and environment, the higher PCV than GCV values suggests a significant contribution of environment and genotype by environment interactions to the expression of the traits under investigation (Abo et al., 2025).

On the other hand, the highest broad sense heritability value of 98.0% and 98.7% were estimated for days to flowering and days to maturity, while the lowest value of 10.5% was recorded for number of seeds pod^{-1}. This indicates that traits with high heritability can easily select based on phenotype. The estimated genetic advance values in the present study ranged from 1.4% for number of seeds pod^{-1} to 62.3% for plant height. Six traits (days to flowering, days maturity, plant height, number of pods plant^{-1}, seed size, and grain yield) have shown relatively high estimates of GA, indicating their responsiveness for improvement through selection.

Table 4: Estimates of genotypic (GCV) and phenotypic (PCV) coefficient of variation, broad sense heritability (H), and genetic advance (GA) as percent of the mean for seven traits in 15 field pea accessions evaluated in Kulumsa and Dhera in 2021

Traits	Mean	Range	PCV	GCV	H_2	GA (%)
Days to flowering	48.2	43-72.67	15.35	15.19	98	30.98
Days to maturity	86.59	76.33-141	20.86	20.73	98.73	42.43
Plant height (cm)	76.51	54.61-164	41.8	35.55	72.32	62.28
No. of pods plant^{-1}	10.6	7.83-19.33	36.35	20.55	31.95	23.92
No. of seeds pod^{-1}	5.44	4.97-5.93	6.33	2.06	10.53	1.37
1000 seed weight (g)	108	96-152	15.42	12.76	68.46	21.74
Grain yield (kg ha^{-1})	2331	1539–4520	31.47	26.63	71.58	46.41

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; H: broad sense heritability; GA: genetic advance as percent of the mean

3.3. Association among yield and yield components

3.3.1. Genotypic and phenotypic correlation of grain yield with other traits

The results of genotypic correlation analysis are presented in Table 5 at two locations (Kulumsa and Dehera). Grain yield had positive and highly significant correlations with plant height, pod plant^{-1} and thousand seed weight at genotypic levels for combined analysis (Table 5). Asfakun et al. (2013) reported a positive and highly significant genotypic correlation of grain yield with day to maturity and pod length.

Grain yield had positive and highly significant correlations with plant height and thousand seed weight at phenotypic levels at two locations (Table 6). The presence of highly significant and positive correlation of these traits with grain yield at genotypic and phenotypic levels indicated prime importance of these traits in selection program to identify field pea genotypes with high grain yield. Direct selection only for higher yield could be misleading because many factors interact to determine crop yield. Similar results were reported by Alemu, (2017) for thousand seed weight and plant height. Days to flowering days to maturity and pod plant^{-1} at both locations (Kulumsa and Dehera) have non-significant correlations with grain yield at genotypic and phenotypic level (Table 5 and Table 6). The presence of non-significant correlations of the traits with grain yield indicated that the two traits are independent of each other. Also Barkat et al. (2019) reported positive and highly significant correlation seed yield between plant heights.

Table 5: Genotypic (above diagonal) correlation coefficients among seven traits for the combined analysis

T	DTF	DTM	PHT	PPL	TSW	GY	PM
1	1	0.999***	0.543**	0.743*	0.567	0.287	0.949
2	0.999	1	0.635	0.614**	0.58	0.334*	0.98*
3	0.543	0.635	1	0.316	0.685**	0.585**	0.983**
4	0.743	0.614	0.316	1	0.537	0.685**	0.365**
5	0.567	0.58	0.685	0.537	1	0.413**	0.891
6	0.287	0.334	0.585	0.685	0.413	1	0.765
7	0.949	0.98	0.983	0.365	0.891	0.765	1

T: Traits; [1]DTF: Days to flowering; [2]DTM: Days to maturity; [3]PHT: Plant height; [4]PPL: Pod plant^{-1}; HI: Harvest index; [5]TSW: Thousand seed weight; [6]GY: Grain yield; [7]PM: Powdery mildew

3.3.2. Path coefficient analysis

3.3.2.1. Genotypic and phenotypic path analyses of yield and other traits

Only characters that had significant relationship with grain yield were included in the path analysis (Dewey and Lu., 1959). The results of genotypic path coefficient analysis of grain yield with other traits are presented in Table 7 at combined analysis. While, phenotypic path coefficient analysis of grain yield with other traits are presented in Table 8. Days to flowering, Plant height, thousand seed weight and powdery mildew have positive and highly significant direct effect while, days to physiological maturity and pod

Table 6: Phenotypic (below diagonal) correlation coefficients among seven traits for the combined analysis

T	DTF	DTM	PHT	PPL	TSW	GY	PM
1	1	0.961***	0.758**	0.524*	0.399	0.162	0.412
2	0.961	1	0.845	0.66**	0.448	0.206	0.552*
3	0.758	0.845	1	0.77	0.715**	0.454**	0.738**
4	0.524	0.66	0.77	1	0.403	0.166	0.645**
5	0.399	0.448	0.715	0.403	1	0.71**	0.503
6	0.162	0.206	0.454	0.166	0.71	1	0.487
7	0.412	0.552	0.738	0.645	0.503	0.487	1

T: Traits; [1]DTF: Days to flowering; [2]DTM: Days to maturity; [3]PHT: Plant height; [4]PPL: Pod plant^{-1}; HI: Harvest index; [5]TSW: Thousand seed weight; [6]GY: Grain yield; [7]PM: Powdery mildew

Table 7: Genotypic direct (bold face and at the diagonal) and indirect effects (off the diagonal) of six characters on grain yield plot^{-1} for the combined analysis

T	DTF	DTM	PHT	PPL	TSW	PM
1	0.1359	0.30699	0.74259	0.23944	0.13975	-1.2774
2	0.13578	0.30727	0.86805	0.19775	0.14302	-1.3183
3	0.07377	0.19498	1.36797	0.10166	0.16874	-1.3225
4	0.101	0.18861	0.43165	0.32216	0.13238	-0.4913
5	0.07706	0.17832	0.93667	0.17306	0.24643	-1.199
6	0.12898	0.30097	1.3442	0.11759	0.21955	-1.3459
7	0.412	0.552	0.738	0.645	0.503	0.487

T: Traits; [1]DTF: Days to flowering; [2]DTM: Days to maturity; [3]PHT: Plant height; [4]PPL: Pod plant^{-1}; HI: Harvest index; [5]TSW: Thousand seed weight; [6]GY: Grain yield; [7]PM: Powdery mildew; R-Squared: 0.2333; Residual effect: 0.87561; K-value (for collinearity) 0

plant^{-1} had showed negative and significant direct effect at phenotypic level at Kulumsa and Dehera (Table 8). Asfakun et al. (2013) reported a positive direct effect of days to 50% flowering, number of pods plant^{-1} and hundred seed weight on grain yield.

The trait which has positive correlation with grain yield and has large and positive direct effect the trait is considered as an important component of yield. According, days to flowering, days to maturity, plant height, and thousand seed weight have significant and positive association with grain yield at genotypic level. These indicate that those traits had true association with grain yield and their importance in determining these complex traits. Therefore, important consideration should be given while practicing selection aimed at the improvement of grain yield. The path analysis is the partitioning of the total correlation into direct and indirect effects of independent variable(s) on dependent variable (Gebeyew et al., 2022). According to (Gizachew et al., 2024), path coefficient analysis provides a better knowledge of direct and indirect causes of associations.

Legesse (2015) reported higher positive direct effects of days to maturity, biological yield, harvest index and hundred seed weight on seed yield, indicating that selection of superior field pea genotypes for seed yield on the basis of these characters would be effective. Thakur et al. (2018) reported that path coefficients for seed yield plant^{-1} recorded the highest positive direct effect contributing to seed yield plant^{-1} is, harvest index followed by biological yield, pods plant^{-1}, primary branches plant^{-1} plant height, days to 50% flowering. Whereas, negative direct effects on seed yield plant^{-1} were observed due to powdery mildew. Benti and Yohanis (2017) reported a positive direct effect of plant height (0.419), day to maturity (0.189), day to flower initiation (0.066) and number of seed pod^{-1} (0.087) has positively direct effect on seed yield.

Residual effect in genotypic path analyses at over location was 0.87561 (Table 7), showing that 12.44% of the variability in seed yield was explained by the component factors at genotypic levels respectively Gebeyew et al., 2024. The remaining 87.56% variation could be explained by other un explanatory variable not control in this research; While at phenotypic level residual effect was 0.62989 at over location, indicating that 37.02% of variability was explained by component factors (Table 8).

Table 8: Phenotypic direct (bold face and at the diagonal) and indirect effects (off the diagonal) of six characters on grain yield plot^{-1} for the combined analysis

T	DTF	DTM	PHT	PPL	TSW	PM
1	0.02602	-0.1592	0.00087	-0.1417	0.27202	0.16424
2	0.025	-0.1657	0.00097	-0.1786	0.30506	0.21968
3	0.01973	-0.1399	0.00115	-0.2085	0.48762	0.29406
4	0.01363	-0.1093	0.00089	-0.2706	0.27468	0.25678
5	0.01039	-0.0741	0.00082	-0.109	0.68163	0.20015
6	0.01073	-0.0914	0.00085	-0.1745	0.34255	0.39827
7	0.412	0.552	0.738	0.645	0.503	0.487

T: Traits; [1]DTF: Days to flowering; [2]DTM: Days to maturity; [3]PHT: Plant height; [4]PPL: Pod plant^{-1}; HI: Harvest index; [5]TSW: Thousand seed weight; [6]GY: Grain yield; [7]PM: Powdery mildew; R-Squared: 0.2333; Residual effect: 0.87561; K-value (for collinearity) 0; R-Squared: 0.60323; Residual effect: 0.62989; K-value (for collinearity) 0

4.3.4. Cluster analysis

All except the local and standard check were collected from the northern part of the country. Cluster analysis based on means of two locations and nine major quantitative traits grouped the 15 genotypes into three distinct classes (Figure 1). The number of genotypes in each cluster ranged from two in cluster III and nine in cluster I. The standard check Megeri is grouped in cluster III, but local check was grouped in cluster I. The means of traits for the seven clusters in the present study are shown in Table 9. Cluster I consisted of nine genotypes that have an average performance for all the traits under investigation. On the other hand, cluster II consisted of four genotypes, the second largest number Kedir et al., 2024.

The genotypes in this group were characterized by earlier flowering, earlier maturing, shorter plant height, lower number of pods plant^{-1}, and low yielder once, but they are relatively resistant to powdery mildew disease compared to the genotypes in the remaining clusters Temesgen et al.,

Table 9: Means for nine different traits of 15 field pea genotypes grouped into three clusters

Clusters	Number of genotypes	DTF	DTM	PHT	PPP	SPP	TSW	GY	AB	PM
Cluster I	9	42.67	87.04	62.89	5.61	6.12	105.41	2406.33	3.04	3.67
Cluster II	4	40.17	81.00	47.22	3.80	6.35	104.25	2057.06	2.83	3.67
Cluster III	2	49.33	110.17	111.56	12.43	6.07	145.83	3546.19	3.33	4.33

Abbreviations of the variables are as indicated in Table 3

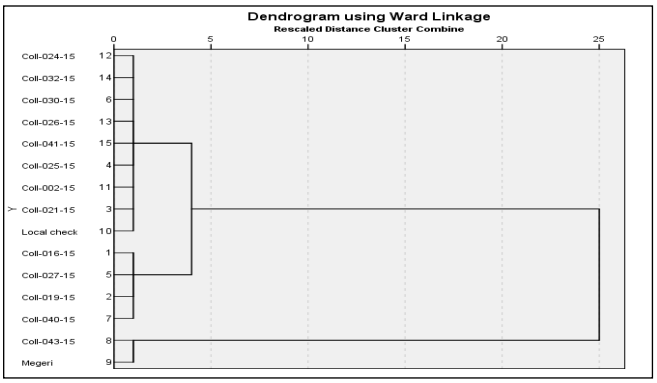

Figure 1: Dendrogram showing hierarchical clustering patterns of 15 field pea genotypes evaluated for nine major quantitative traits

2024. Cluster III have two genotypes. The unique features of genotypes in this cluster are late flowering and maturing dates, taller plant height, higher number of pods plant^{-1}, larger seed size, and higher yielding, but relatively they are susceptible to ascochyta blight and powdery mildew disease compared to those in the remaining groups (Table 9).

3.4.1. Principal component analysis

The first three principal components (PCs) with eigenvalue greater than one contributed for 82.2% of the entire phenotypic variation observed among the 15 field pea genotypes (Table 10). PC1 accounted for 40.4% of the variation among the test genotypes mainly due to the variation in days to flowering, plant height, number of pods plant^{-1}, and ascochyta blight intensity, respectively. PC2 also accounted for 30.4% of the total variation among the test genotypes, whereby 1000 seed weight, grain yield, and number of seeds pod^{-1} were contributing the major part. PC3, on the other hand, has contributed for 11.5% of the total variation of the genotypes mainly resulting from variation in days to physiological maturity Temesgen, 2021.

Table 10: Eigenvectors and values of the first three principal components for 15 field pea genotypes evaluated in Kulumsa and Dhera in 2021

Traits	PC1	PC2	PC3
Days to flowering	0.4724	-0.0164	0.2379
Days to maturity	0.3690	0.2715	0.4914
Plant height (cm)	0.4768	0.1757	0.0555
Number of pods plant^{-1}	0.4374	-0.1575	-0.0114
Number of seeds pod^{-1}	-0.2469	0.3871	0.3218
1000 seed weight (g)	0.2339	0.4258	-0.3898
Grain yield (kg ha^{-1})	0.1411	0.4037	-0.6148
Ascochyta blight (1-9) scale	0.2503	-0.3711	-0.0816
Powdery mildew (1-9) scale	-0.1543	0.4884	0.2422
Eigenvalues	3.63	2.74	1.03
Variance accounted for (%)	40.37	30.39	11.48
Cumulative variance (%)	40.37	70.76	82.23

4. CONCLUSION

Analysis of variance revealed that there were significant differences (p<0.01) among the field pea accessions for traits including days to flowering, days to maturity, plant height, 1000 seed weight, and grain yield kg ha^{-1}.Grain yield performances of the accessions were ranged from low yield of 1539 kg ha^{-1} for Coll-019-15 and to high yield of 4520 kg ha^{-1}.

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