



Assessing of Genetic Variability and Character Associations of Collected Ethiopian Field pea Landraces (*Pisum sativum* var. *abyssinicum* L.) at Southeastern Ethiopia

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Abstract

The experiments were carried out during 2021 cropping season (June, 2021–November, 2021) at three locations (Bekoji, Asasa and Kofele). The objective of the experiment was to assess the quantity of genetic variability and character association of agronomic traits. A total of 45 dekokko field pea genotypes were collected and evaluated at three locations (Bekoji, Asasa, and Kofele) using a randomized complete block design (RCBD). The analysis of variance revealed that the presence of highly significant differences among evaluated genotypes for most traits and genotype×location interaction showed a non-significance difference. The genetic parameter results of PCV, GCV, heritability in the broad sense and genetic advance were recorded from lower to highest values. Higher heritability estimates and genetic advances were observed from plant height, powdery mildew, thousand seed weight and grain yield ha⁻¹. Grain yield showed a highly significant ($p<0.01$) and positive association with days to 50% flowering, days to maturity, plant height, number of seeds plant⁻¹, pod length, thousand seed weight and powdery mildew at the genotypic level. The path analysis result revealed that days to flowering, plant height, and pod length had positive direct effects on grain yield, while the remaining traits have negative direct effects on the grain yield performance of genotypes. The result showed the presence of sufficient variability among collected landraces for further field pea breeding improvement programs.

Keywords: Heritability, genetic advance, path analysis

1. Introduction

Dekoko field pea (*Pisum sativum* var. *abyssinicum* L.) is the most commonly grown pulse crops in Ethiopia and it ranks fourth in terms of total production and area coverage next to faba bean, haricot bean and chickpea (Anonymous, 2022). Ethiopia is the center of diversity for field pea and is grown in an altitude of 1,800–3,000 masl with annual rainfall of 700–1,000 mm. According to the central statistics agency (Anonymous, 2022), it has grown in 220,209 ha of land and it accounts for 13.79% from total pulse production with a total of production 368,519,065 t and its productivity is 1.67 t ha⁻¹. In Ethiopia, it plays a significant role in the livelihood of the agricultural communities and serves as a source of food and feed with a valuable and cheap source of protein. It also plays a great role in soil fertility restoration as a suitable rotational crop and as a source of animal feed (Gemechu et al., 2016). Regardless of its economic and nutritional importance for the farmers, the production and productivity

of the crop do not grow significantly with the potential of the country. The productivity of the crop is mainly constrained by many biotic and abiotic factors, including disease (powdery mildew, aschochyta blight), pests, water lodging, frost, lack of genotypes that perform consistently across different environments and seasons, unimproved traditional practices, weeds, drought, salinity and acidity. There is a wide range of field pea genotypes in Ethiopia, making the country the second center of genetic diversity (Gemechu et al. (2012)). The presence of wide genetic variability in the field pea crop is a prerequisite for an effective breeding program. Achenef et al. (2024), Haile and Tesfaye (2024) and Yilma et al. (2021) reported the presence of highly significant ($p<0.05$) variation among field pea genotypes, and they showed a significant environmental interaction with genotypes. Genetic variability is important and a primary consideration for the development of improved varieties by selection and hybridization of diverse gene sources. Heritability describes the observed difference among genotypes that arises because of genetic makeup or



due to environmental factors. Genetic advance gives an idea of the possible improvement of a new population through selection, when compared to the original population. The concept of correlation with yield and yield-related traits is essential in studying the magnitude and direction of association of each character with another (Kalapchieva et al., 2021). Correlation coefficient and path analysis provide a means for determining the importance of traits affecting the dependent variables. Yilma et al. (2021) reported a significant and positive association of grain yield with plant height, days to 50% flowering and number of pods per plant. Characterization and evaluations of field pea germplasm are good tool for estimating the genetic variability, heritability and related genetic parameters. To select elite breeding materials from the population, it must have high genetic variability among the genotypes (Tiwari and Lavanya (2012)). For efficient and optimum selection of elite genotypes knowledge of genetic variability, genetic advance, heritability and associations among traits is essential (Singh, 1990). Different scholars

reported the presence of significant genetic variation among the field pea genotypes (Yimam et al. (2024), Argaye et al., (2023), Tolessa (2017), Tamene et al. (2013), and Jagadeesh et al. (2023), Yimam et al. (2020)). In view of this, the research was conducted with the objectives of to estimate genetic variability and assess associations of yield and yield related traits of collected dekoko field pea genotypes.

2. Materials and Methods

2.1. Experimental sites

The experiments were carried out during June–November, 2021 at three locations (Bekoji, Asasa and Kofele). These three testing locations were high-potential growing environments for field pea production. A total of forty-five collected dekoko genotypes, including two standard checks (Adi and Local), were used for the experiment. The three experimental sites' descriptions were presented in Table 1 below.

Table 1: Description of the experimental sites

Location	Year	Geographical position		Altitude	Temperature		Rainfall (mm)
		Latitude	Longitude		Minimum	Maximum	
Bekoji	2021/22	07032'37"N	39015'21"E	2780	7.9	16.6	1020
Asasa	2021/22	0707'09"N	3911'56"E	2340	5.8	23.6	620
Kofele	2021/22	07004'28"N	38047'11"E	2300	5.8	23.6	1211

E: Environments, Min: Mminimum, Max: Maximum

2.2. Experimental design

The experiment was carried out using randomized complete block designs (RCBD) with four replications. Each treatment was randomly assigned to each plot within the replication. The plot size of the experiment was 4 m long and 0.8 m wide, i.e. 3.2 m² area with a spacing of 0.2 m and 5 cm between rows and plants, respectively. Each plot had four rows, and the spacing between each treatment and replications was 1 m and 1.5 m, respectively. Recommended rate of fertilizer (100 kg ha⁻¹) of DAP (Di ammonium Phosphate) was applied at each location, and all other agronomic practices were done throughout the growing season.

2.3. List of experimental materials

A total of 45 collected landrace dekoko materials including one released (Adi) and local varieties were evaluated. The list of materials and codes were described in Table 2 below.

2.4. Data collected on plot basis

Days to 50% Flowering (DF): number of days which takes 50% of the plants showed the first flower, Days to Maturity (DM): number of days taken to the stages when 90% of physiological maturity, Thousand seed weight (TSW): weight of 100 randomly taken seeds weighed and adjusted at 10% moisture content and converted in to 1000 seed weight, Grain yield (GY): weight of grain seed obtained from the plots and

converted into kg ha⁻¹ by adjusting at 10% moisture content, Powdery mildew (PM) and Ascochyta blight (AB): Based on 1 to 9 scale were, 1 for nil: No visible disease symptom (Immune), 3 for slight: Some small discrete and a few large lesions (resistant), 5 for medium: Some coalesced lesions many spotting (moderately resistant), 7 for severe: Large coalesced lesions with about 50% defoliation and few dead stems/plants (susceptible), 9 for very severe: Extensive lesion, severe defoliation, stem girdling, many dead plants (highly susceptible).

2.5. Data collected on sample plant basis

Plant height (PLH): the average height of five randomly taken plants, Number of pods per plant (NPP): the average number of pods per plant counted from five randomly taken plants, Number of seeds per Pod (SPP): the average number of seeds in five pods each from five randomly selected plants, Pod length (PL): the average length of five randomly taken pods and expressed as an average of five pod length.

2.6. Data analysis

2.6.1. Statistical analysis

The analysis of variance (ANOVA) for combined data over location were estimated using a mixed linear model to assess the differences among genotypes. R software version 4.4.0 with the packages "agricolae" and "metan" were used. The



Table 2: List of experimental materials used for the trial

Sl. No.	G-code	Variety name	Source	Sl. No.	G-code	Variety name	Source
1.	G1	FP-COLL-1/07	collection	24	G24	FP-COLL-24/07	collection
2.	G2	FP-COLL-2/07	collection	25	G25	FP-COLL-25/07	collection
3.	G3	FP-COLL-3/07	collection	26	G26	FP-COLL-26/07	collection
4.	G4	FP-COLL-4/07	collection	27	G27	FP-COLL-27/07	collection
5.	G5	FP-COLL-5/07	collection	28	G28	FP-COLL-28/07	collection
6.	G6	FP-COLL-6/07	collection	29	G29	FP-COLL-29/07	collection
7.	G7	FP-COLL-7/07	collection	30	G30	FP-COLL-30/07	collection
8.	G8	FP-COLL-8/07	collection	31	G31	FP-COLL-31/07	collection
9.	G9	FP-COLL-9/07	collection	32	G32	FP-COLL-32/07	collection
10.	G10	FP-COLL-10/07	collection	33	G33	FP-COLL-33/07	collection
11.	G11	FP-COLL-11/07	collection	34	G34	FP-COLL-34/07	collection
12.	G12	FP-COLL-12/07	collection	35	G35	FP-COLL-35/07	collection
13.	G13	FP-COLL-13/07	collection	36	G36	FP-COLL-36/07	collection
14.	G14	FP-COLL-14/07	collection	37	G37	FP-COLL-37/07	collection
15.	G15	FP-COLL-15/07	collection	38	G38	FP-COLL-38/07	collection
16.	G16	FP-COLL-16/07	collection	39	G39	FP-COLL-39/07	collection
17.	G17	FP-COLL-17/07	collection	40	G40	FP-COLL-40/07	collection
18.	G18	FP-COLL-18/07	collection	41	G41	FP-COLL-41/07	collection
19.	G19	FP-COLL-19/07	collection	42	G42	FP-COLL-42/07	collection
20.	G20	FP-COLL-20/07	collection	43	G43	FP-COLL-43/07	collection
21.	G21	FP-COLL-21/07	collection	44	G44	Adi	Released
22.	G22	FP-COLL-22/07	collection	45	G45	Local	Local
23.	G23	FP-COLL-23/07	collection				

following RCBD models were used for combined analysis.

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + \beta(E)_{jk} + \varepsilon_{ijk}$$

Where; Y_{ij} was the grain yield of the i^{th} genotype in the j^{th} environment, μ =the grand mean, G_i =the effect of the i^{th} genotype, E_j =the effect of the j^{th} environment, GE_{ij} =the interaction of the i^{th} genotype with the j^{th} environment, (E) =the effect of the k^{th} replication in the j^{th} environment, and ε_{ijk} =the error.

2.6.2. Estimation of genetic parameters

The phenotypic and genotypic variance, heritability, phenotypic and genotypic coefficient of variations, genetic advance and genetic advance as percentage of mean for combined location were calculated separately using the following equations suggested by biometricians (Allard 1960, Falconer and Mackay 1996).

$$\sigma^2_g = (MS_g - MS_g * I) / r_l, \sigma^2_g * I = (MS_g * I - MSe) / r, \sigma^2_p = \sigma^2_g + \sigma^2_p / r_l + (\sigma^2_g * I) / I,$$

$$PCV = (\sqrt{\sigma^2_p / \bar{X}}) * 100, GCV = (\sqrt{\sigma^2_g / \bar{X}}) * 100, H^2_b = (\sigma^2_g / \sigma^2_p) * 100, GA = K * \sqrt{\sigma^2_p} * H^2_b, GAM = (GA / \bar{X}) * 100$$

Where, σ^2_g =Genotypic variance, σ^2_e =Environmental variance, σ^2_p =Phenotypic variance, MS_g =mean square due to genotypes, MSe =Error mean square, r =Number of replication, $MS_g * I$ =Mean square due to genotypes×location, I =number of environment, PCV =Phenotypic coefficient of variation, GCV =genotypic coefficient of variation, H^2_b =Heritability in broad sense, GA =Genetic advance, K =Selection differential at 5% selection intensity which accounts to a constant value 2.063, GAM =Genetic advance as percent of mean, $\bar{X}$ =Population Mean.

2.6.3. Estimation of correlation coefficient

Phenotypic and genotypic correlation coefficients of grain yield ha^{-1} with other traits were estimated using the components of variance and covariance of combined location based on the standard procedure by using the cov2cor function of R software using the stats package.

$$\text{Phenotypic correlation coefficient (r}_{pxy}) = Pcov_{xy} / \sqrt{(\sigma^2_{px})(\sigma^2_{py})}$$

$$\text{Genotypic correlation coefficient (r}_{gxy}) = Pcov_{xy} / \sqrt{(\sigma^2_{px})(\sigma^2_{py})}$$

The level of significance of phenotypic and genotypic



correlation coefficients was tested using the formula suggested by Robertson (1959).

3. Results and Discussion

3.1. Combined analysis of variance

The combined analysis result showed that the presence of sufficient amount of genotypic variance among evaluated genotypes. As shown in Table 3, highly significant ($p < 0.01$) differences were observed between genotypes for all traits except number of pods per plant, number of seed pod⁻¹ and aschocyta blight. The highly significant difference between genotypes indicated that the existence of wide genetic variability among genotypes. Mean square from location showed that highly significant location effect on genotypes

performance for all evaluated traits and this indicated that the differential performance of genotypes across the tested environments. Similar to this finding, high genetic diversity in Ethiopian field pea landraces was reported by Gemechu et al. (2005). Tiwari and Lavanya (2012), Tezera (2000), Million (2012), Tamene et al. (2013), Yilma et al. (2021) and Tolessa (2017) reported significant genotypic variations among field pea breeding lines for most of the traits.

The location×genotype interaction showed a non-significant difference for all traits (Table 3), indicated that similar performances of dekoko field pea genotypes across the three testing locations or no importance of evaluating these genotypes across different environments, because of non-differential performance of genotypes across environments.

Table 3: Mean square from the analysis of variance of 10 traits for combined analysis result

Source of variation	Genotype	Location	Location: Replication	Genotype: Location	Residuals
Traits	df=44	df=2	df=6	df=88	df=263
FLD	130.2***	3930.3***	35.4	7	19.7
MTD	106.2***	91347.2***	21.6	16.3	18.7
PLH	1131.5***	25471.4***	1304.4***	149.5	263.5
PPL	13.2	4189.3***	125.5***	9.5	11.6
SPP	0.9	33.4***	4.5***	0.6	0.6
PL	0.9***	4.1***	1.3***	0.4	0.4
TSW	1355.4***	6529.2***	92.1	84.1	211.1
GYH	5663797***	75388873***	2745023	1115680	1554549
AB	0.5	18.2***	2.1**	0.6	0.6
PM	0.8***	21.3***	1.9***	0.2	0.2

FLD: Days to flowering, MTD: Days to maturity, PLH: Plant height, PPP: Number of pods plant⁻¹, SPP: Number of seeds pod⁻¹, PL: Pod length, TSW: Thousand seed weight, AB: Aschochyta blight, PM: Powdery mildew, GYH: Grain yield ha⁻¹

3.2. Mean performances of traits

Mean performance of the genotypes for 10 traits was presented in Table 4. The result of the mean performances of parameters suggested that there were considerable differences observed in all of the traits under investigation. The genotypes required 54 to 73 days for flowering and 116 to 133 days to physiological maturity. All collected dekoko field pea genotypes which recorded less mean grain yield performance than the standard check Adi and local varieties. This poor performance might be caused because of the less adaptability performances of the dekoko field pea genotypes to the environment and their physiological differences. From those genotypes G-42 was recorded the maximum mean grain yield (3,649 kg ha⁻¹) followed by G-35 (3,285 kg ha⁻¹), G-6 (2,958 kg ha⁻¹) and G-39 (2,187 kg ha⁻¹). The mean grain yield performance of genotypes showed that there were significant differences across three locations. The combined mean performance result showed that lowest mean grain

yields were recorded from G-19 (969 kg ha⁻¹), G-34 (1095 kg ha⁻¹), G-13 (1254 kg ha⁻¹) as presented in Table 4 below.

3.3. Estimation of genetic parameters

3.3.1. Phenotypic and genotypic coefficient of variation

The genetic parameters of ten traits were estimated and results were presented in Table 5 below. The result showed that the phenotypic variance was higher than the genotypic variance for all traits, indicated that the differential environmental influences on the expression of the traits. The differences were not as larger for all traits. The PCV value were ranged from 2.9% for days to maturity to 42.9% for grain yield and the GCV value also ranged from 0% for aschochyta blight to 37.2% for grain yield (Table 5). According to Deshmukh et al. (1986), phenotypic and genotypic coefficients of variation values more than 20% are considered as high, between 10 and 20% as moderate and less than 10% considered as low. According to this bench mark, higher phenotypic and



Table 4: Combined mean performances of 10 traits

Genotype	GYH	TSW	FLD	MTD	PLH	PPL	SPP	PL	AB	PM
G1	1676 ^{ef}	104 ^{de}	55 ^c	117 ^d	69 ^{efgh}	10 ^{bcdefg}	5 ^{abcdef}	4.4 ^{cdef}	3.9 ^{abcde}	1.2 ^{def}
G2	1513 ^{ef}	102 ^e	55 ^c	117 ^d	72 ^{efgh}	12 ^{abcdef}	4 ^{cdefg}	4.7 ^{cde}	3.9 ^{abcde}	1.2 ^{def}
G3	1675 ^{ef}	102 ^e	54 ^c	117 ^d	69 ^{efgh}	8 ^g	4 ^{defg}	4.4 ^{cdef}	3.8 ^{abcde}	1.2 ^{def}
G4	1477 ^{ef}	101 ^e	56 ^c	117 ^d	73 ^{defgh}	11 ^{abcdefg}	5 ^{abcdef}	4.3 ^{cdef}	3.7 ^{abcde}	1.1 ^{ef}
G5	1545 ^{ef}	106 ^{de}	55 ^c	118 ^d	67 ^{efgh}	11 ^{abcdefg}	5 ^{abcde}	4.3 ^{cdef}	3.7 ^{abcde}	1.3 ^{cdef}
G6	2958 ^{bcd}	117 ^{cd}	64 ^b	123 ^{bc}	99 ^{bc}	12 ^{abcdef}	5 ^{ab}	4.7 ^{cde}	3.4 ^{cde}	1.7 ^c
G7	1448 ^{ef}	103 ^{de}	55 ^c	120 ^{cd}	67 ^{efgh}	10 ^{abcdefg}	4 ^{cdefg}	4.1 ^{ef}	3.6 ^{bcde}	1.2 ^{def}
G8	1514 ^{ef}	100 ^e	56 ^c	117 ^d	71 ^{efgh}	10 ^{cdefg}	5 ^{abcdef}	4.4 ^{cdef}	3.8 ^{abcde}	1.2 ^{def}
G9	1726 ^{ef}	101 ^e	56 ^c	117 ^d	71 ^{efgh}	11 ^{abcdefg}	4 ^{efg}	4.2 ^{def}	4.1 ^{abc}	1.2 ^{def}
G10	1615 ^{ef}	102 ^e	55 ^c	117 ^d	76 ^{defg}	12 ^{abcdef}	4 ^{cdefg}	4.3 ^{cdef}	4 ^{abcd}	1.1 ^{ef}
G11	1738 ^{ef}	107 ^{de}	56 ^c	118 ^d	77 ^{defg}	10 ^{cdefg}	5 ^{bcdefg}	4.7 ^{cde}	3.8 ^{abcde}	1.1 ^{ef}
G12	1761 ^{ef}	106 ^{de}	55 ^c	117 ^d	80 ^{de}	11 ^{abcdefg}	5 ^{abcdef}	4 ^f	4 ^{abcd}	1 ^f
G13	1254 ^{ef}	100 ^e	55 ^c	117 ^d	71 ^{efgh}	10 ^{cdefg}	4 ^{cdefg}	4.2 ^{def}	3.9 ^{abcde}	1 ^f
G14	1746 ^{ef}	107 ^{de}	55 ^c	118 ^d	78 ^{def}	10 ^{cdefg}	5 ^{abcd}	4.2 ^{def}	3.8 ^{abcde}	1.2 ^{def}
G15	1817 ^{def}	103 ^{de}	54 ^c	117 ^d	72 ^{efgh}	12 ^{abcdef}	4 ^{cdefg}	4.6 ^{cdef}	3.6 ^{bcde}	1.3 ^{cdef}
G16	1588 ^{ef}	10 ^{3e}	56 ^c	118 ^d	73 ^{defgh}	11 ^{abcdef}	5 ^{abcdef}	4.4 ^{cdef}	3.8 ^{abcde}	1.1 ^{ef}
G17	1583 ^{ef}	104 ^{de}	56 ^c	118 ^d	72 ^{efgh}	12 ^{abcdef}	4 ^{defg}	4.2 ^{def}	3.7 ^{abcde}	1.1 ^{ef}
G18	1405 ^{ef}	104 ^{de}	56 ^c	118 ^d	70 ^{efgh}	11 ^{abcdefg}	4 ^{bcdefg}	4.3 ^{cdef}	3.8 ^{abcde}	1.3 ^{cdef}
G19	969 ^f	101 ^e	55 ^c	118 ^d	62 ^{gh}	10 ^{bcdefg}	4 ^{cdefg}	4.6 ^{cdef}	4.3 ^a	1.1 ^{ef}
G20	1294 ^{ef}	97 ^e	56 ^c	117 ^d	67 ^{efgh}	10 ^{abcdefg}	4 ^g	4.1 ^{ef}	3.9 ^{abcde}	1.1 ^{ef}
G21	1528 ^{ef}	101 ^e	55 ^c	116 ^d	69 ^{efgh}	11 ^{abcdef}	5 ^{abcdef}	4.3 ^{cdef}	3.9 ^{abcde}	1.1 ^{ef}
G22	1916 ^{def}	99 ^e	56 ^c	117 ^d	71 ^{efgh}	13 ^{abc}	4 ^{cdefg}	4.7 ^{cde}	3.9 ^{abcde}	1.4 ^{cde}
G23	1892 ^{def}	100 ^e	56 ^c	117 ^d	72 ^{efgh}	10 ^{cdefg}	5 ^{abc}	4.4 ^{cdef}	4.1 ^{abc}	1.4 ^{cde}
G24	1605 ^{ef}	100 ^e	56 ^c	116 ^d	72 ^{efgh}	13 ^a	4 ^{efg}	4.6 ^{cdef}	3.6 ^{bcde}	1.2 ^{def}
G25	1605 ^{ef}	101 ^e	56 ^c	117 ^d	73 ^{defgh}	12 ^{abcdef}	4 ^{cdefg}	4.3 ^{cdef}	4.1 ^{abc}	1.1 ^{ef}
G26	1959 ^{def}	107 ^{de}	56 ^c	118 ^d	70 ^{efgh}	11 ^{abcdef}	5 ^{abcdef}	4.6 ^{cdef}	3.4 ^{cde}	1.4 ^{cde}
G27	1818 ^{def}	99 ^e	55 ^c	118 ^d	66 ^{efgh}	12 ^{abcd}	5 ^{abcde}	4.6 ^{cdef}	4.2 ^{ab}	1.3 ^{cdef}
G28	1563 ^{ef}	100 ^e	55 ^c	118 ^d	59 ^h	10 ^{defg}	4 ^{bcdefg}	4.4 ^{cdef}	3.8 ^{abcde}	1.3 ^{cdef}
G29	1662 ^{ef}	102 ^e	56 ^c	117 ^d	64 ^{fgh}	12 ^{abcde}	4 ^{bcdefg}	4.3 ^{cdef}	3.3 ^{de}	1.2 ^{def}
G30	1525 ^{ef}	100 ^e	56 ^c	117 ^d	68 ^{efgh}	12 ^{abcd}	4 ^{bcdefg}	4.2 ^{def}	3.8 ^{abcde}	1.3 ^{cdef}
G31	1357 ^{ef}	100 ^e	55 ^c	117 ^d	67 ^{efgh}	10 ^{bcdefg}	4 ^{efg}	4.3 ^{cdef}	3.8 ^{abcde}	1.1 ^{ef}
G32	1964 ^{def}	105 ^{de}	56 ^c	118 ^d	71 ^{efgh}	10 ^{abcdefg}	5 ^{abcdef}	4.3 ^{cdef}	4.1 ^{abc}	1.3 ^{cdef}
G33	1473 ^{ef}	100 ^e	56 ^c	118 ^d	68 ^{efgh}	9 ^{efg}	4 ^{cdefg}	4.1 ^{ef}	4.1 ^{abc}	1.4 ^{cde}
G34	1095 ^{ef}	101 ^e	56 ^c	117 ^d	66 ^{efgh}	9 ^{fg}	4 ^{fg}	4.1 ^{ef}	3.9 ^{abcde}	1.1 ^{ef}
G35	3285 ^{bc}	135 ^b	63 ^b	125 ^b	88 ^{cd}	12 ^{abcd}	5 ^{abcdefg}	4.9 ^{bc}	3.4 ^{cde}	1.6 ^{cd}
G36	1717 ^{ef}	98 ^e	56 ^c	118 ^d	69 ^{efgh}	11 ^{abcdefg}	4 ^{cdefg}	4.2 ^{def}	3.9 ^{abcde}	1.1 ^{ef}
G37	1957 ^{def}	99 ^e	55 ^c	118 ^d	68 ^{efgh}	12 ^{abcde}	5 ^{abcde}	4.8 ^{bcd}	3.6 ^{bcde}	1.2 ^{def}
G38	1592 ^{ef}	108 ^{de}	55 ^c	118 ^d	66 ^{efgh}	10 ^{bcdefg}	4 ^{bcdefg}	4.2 ^{def}	4 ^{abcd}	1.3 ^{cdef}
G39	2187 ^{cde}	96 ^e	54 ^c	118 ^d	70 ^{efgh}	13 ^{abcd}	5 ^{bcdefg}	4.2 ^{def}	3.9 ^{abcde}	1.3 ^{cdef}
G40	1942 ^{def}	99 ^e	55 ^c	118 ^d	65 ^{efgh}	13 ^{ab}	5 ^{abcde}	4.4 ^{cdef}	3.9 ^{abcde}	1.3 ^{cdef}



Genotype	GYH	TSW	FLD	MTD	PLH	PPL	SPP	PL	AB	PM
G41	1909 ^{def}	98 ^e	55 ^c	118 ^d	64 ^{efgh}	13 ^{abcd}	5 ^{bcdefg}	4.4 ^{cdef}	3.9 ^{abcde}	1.2 ^{def}
G42	3649 ^b	101 ^e	56 ^c	117 ^d	70 ^{efgh}	11 ^{abcdefg}	4 ^{cdefg}	4.6 ^{cdef}	3.7 ^{abcde}	1.3 ^{cdef}
G43	1644 ^{ef}	103 ^{de}	56 ^c	118 ^d	72 ^{efgh}	11 ^{abcdefg}	5 ^{bcdefg}	4.3 ^{cdef}	3.8 ^{abcde}	1.2 ^{def}
G44	5484 ^a	174 ^a	72 ^a	132 ^a	110 ^{ab}	12 ^{abcd}	5 ^a	5.8 ^a	3.2 ^e	2.1 ^b
G45	4021 ^b	130 ^{bc}	73 ^a	133 ^a	120 ^a	12 ^{abcdef}	5 ^a	5.3 ^{ab}	3.7 ^{abcde}	2.9 ^a
Mean	1881	105	56.6	118.5	72.8	11.1	4.5	4.4	3.8	1.3
LSD	1166	14.5	4.4	4.4	15.2	0.1	0.7	0.6	0.7	0.4

FLD: Number of days to flowering; MTD: Number of days to maturity; PLH: Plant height in cm; PPP: Number of pods plant⁻¹; SPP: Number of seeds pod⁻¹; PL: pod length in cm; TSW: Thousand seed weight (g); AB: Aschochyta blight; PM: Powdery mildew; GYH: Grain yield ha⁻¹ in (kg ha⁻¹)

Table 5: Estimates of genetic parameters for 10 traits

Traits	GV	PV	H%	GA%	GAM%	GCV%	PCV%	CV%
FLD	12.96	14.96	0.87	6.91	12.22	6.36	6.83	7.49
MTD	9.53	11.77	0.81	5.73	4.83	2.60	2.90	3.79
PLH	101.56	127.73	0.80	18.54	25.46	13.84	15.52	21.07
PPL	0.24	1.47	0.16	0.41	3.68	4.42	10.95	30.05
SPP	0.03	0.10	0.30	0.19	4.30	3.79	6.88	17.22
TSW	140.35	162.42	0.86	22.72	21.63	11.28	12.14	13.42
PL	0.05	0.10	0.51	0.33	7.43	5.04	7.04	14.77
GYH	489564	651413	0.75	1251.4	66.5	37.2	42.9	64.2
AB	0.00	0.06	0.00	0.00	0.00	0.00	6.55	19.64
PM	0.08	0.09	0.81	0.51	39.18	21.16	23.58	31.21

FLD: Number of days to flowering; MTD: Number of days to maturity; PLH: Plant height in cm; PPP: Number of pods plant⁻¹; SPP: Number of seeds pod⁻¹; PL: Pod length in cm; TSW: Thousand seed weight (g); AB: Aschochyta blight; PM: Powdery mildew; GYH: Grain yield ha⁻¹ in (kg ha⁻¹); GV: Genotypic variance; PV: Phenotypic variance; H: Broad sense heritability; GA: Genetic advance; GAM: Genetic advance as percent of mean; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; CV: Coefficient of variation

genotypic coefficient of variation were recorded from traits of grain yield and powdery mildew, in this finding it showed existence of high genetic variability that could be exploited to improve grain yield. In agreement to this finding, significantly higher PCV than GCV values were reported for number of pods plant⁻¹, grain yield, and powdery mildew disease incidence (Tolessa (2017), Tiwari and Lavanya (2012) and Million (2012)). Moderate genotypic and phenotypic coefficient of variation observed from thousand seed weight and plant height. Number of pods plant⁻¹ showed moderate PCV values. Jagadeesh et al. (2023) reported higher genotypic coefficient of variation from plant height, while days to flowering, days to maturity, number of seeds plant⁻¹, pod length and aschocyta blight recorded lower estimates of phenotypic and phenotypic coefficient of variation. The low value of GCV and PCV indicated that selection was not effective for these traits, because of the narrow range of genetic variations on the expression of these traits.

3.3.2. Estimation of heritability and genetic advance

Heritability estimates were ranged from 0% for aschochyta blight to 87% for days to flowering. Heritability estimates in broad sense was categorized as high (>60%), moderate (30–60%) and low (<30%) as recommended by Dabholker (1992). Accordingly, to this estimation, high estimates of heritability were found for days to 50% flowering, days to maturity, plant height, powdery mildew, thousand seed weight and grain yield ha⁻¹. The higher heritability value of such traits indicated that direct selection could be working at phenotypic level to improve the traits as the environmental influence on the expression of the phenotype was low. In agreement of this finding, similar finding was reported by Yilma et al. (2021) for days to 50% flowering and thousands seed weight. Jagadeesh et al. (2023) reported higher heritability estimates for days to 50% flowering, days to maturity, primary branches plant⁻¹, secondary branches plant⁻¹, plant height, pod length, 100 seed weight. However, moderate heritability value was observed



from pod length while traits of number of pods plant⁻¹, number of seed plant⁻¹, and aschochyta blight showed lower estimates of heritability values. Low heritability estimates for those traits implied that the expression of these traits was highly influenced by environments. Hence, simple selection was impossible for improvement of such traits.

3.3.3. Genetic advance as percent of mean

Genetic advance as percent of mean were ranged from 0% for aschochyta blight to 66.5% for grain yield (Table 5). Johansen et al. (1955) classified genetic advances as a percentage of the mean (GAM) as high (>20%), moderate (10–20%) and low (<10%). According to this benchmark, high genetic advance as percent of mean were observed from plant height, thousand seed weight, grain yield and powdery mildew. This indicated that the possibility to select the genotypes with better performance on genetic improvement for these traits. Similar to this result higher genetic advance were reported by Yilma et al. (2021), and Yimam et al. (2024), for grain yield and thousands seed weight. Days to 50% flowering showed moderate genetic advance as percent of mean, while days to maturity, number of pods plant⁻¹, number of seed plant⁻¹, pod length and aschochyta blight showed lowest genetic advance as percent of mean. The low genetic advance as percent of mean result indicated that selection of genotype based on those traits would not make any improvement due to narrow range of variation. The same finding was reported by Yilma et al. (2021) and Yimam et al. (2024) for plant height, seed yield and days to 50% flowering, number of seeds plant⁻¹, days to flowering and days to maturity.

Selecting superior individuals based on heritability estimated alone might not be evidence for genetic improvement. High heritability coupled with high genetic advance as percent of mean was very essential to improve traits of interest (Johnson et al., 1955). According to this suggestion, plant height, thousand seed weight, grain yield and powdery mildew

showed high heritability estimates coupled with high genetic advance as percent of mean. This indicated that those traits were controlled by genetic factor and less influenced by environments so higher chances of improvement of traits through direct phenotypic selection. Days to maturity showed highest estimates of heritability but it observed lowest genetic advance. This indicated that selection of genotypes by their better heritability character was not efficient for the improvement of traits but must consider other genetic parameters.

3.4. Association of traits at genotypic and phenotypic level

Estimates of genotypic and phenotypic correlation coefficients among nine traits were presented in (Table 6) below. The present study showed that, genotypic correlation coefficients are higher than the phenotypic correlation coefficients for most of traits, which showed greater contribution of the genetic factors than the environmental factors in the expression of these traits. The correlation analysis result showed that, highly significant ($p < 0.01$) and positive association of grain yield with days to 50% flowering, days to maturity, plant height, number of seed per plant, pod length, thousand seed weight and powdery mildew at genotypic level. This indicated that the improvement of positively correlated traits with grain yield could result the simultaneous effect on grain. So, to improve grain yield more emphasis should be given to those traits. In agreement with this finding positive and highly significant association of grain yield with days to 90% maturity and number of seeds plant⁻¹ were reported by Yimam et al. (2024) and Fikreselassie et al. (2012). But Yilma et al. (2021) reported a significant and negative genotypic association of grain yield with plant height and stand count.

Days to maturity had positively and significant associations with days to flowering, plant height, number of pods plant⁻¹, number of seed plant⁻¹, pod length, thousand seed weight grain yield and powdery mildew. This implied that when

Table 6: Genotypic correlation (above diagonal) and phenotypic correlation (below diagonal)

Traits	FLD	MTD	PLH	PPL	SPP	PL	TSW	GYH	PM
FLD	1.0	0.82***	0.999***	0.492	0.809***	0.763***	0.893***	0.952***	0.98***
MTD	0.846	1.0	0.987***	0.636***	0.63***	0.521	0.925***	0.979***	0.422**
PLH	0.815	0.736	1.0	0.325*	0.786***	0.452**	0.872***	0.944***	0.902***
PPL	0.085	0.055	0.218	1.0	0.276	0.968***	0.421**	0.561	0.325*
SPP	0.357	0.305	0.322	0.232	1.0	0.66***	0.459**	0.591***	0.818***
PL	0.531	0.510	0.447	0.111	0.370	1.0	0.359*	0.858***	0.463**
TSW	0.801	0.773	0.683	0.049	0.352	0.534	1.0	0.948***	0.763***
GYH	0.643	0.623	0.591	0.205	0.390	0.439	0.659	1.0	0.912***
PM	0.706	0.705	0.653	0.207	0.393	0.476	0.553	0.568	1.0

FLD: Number of days to flowering; MTD: Number of days to maturity; PLH: Plant height in cm; PPP: Number of pods plant⁻¹; SPP: Number of seeds pod⁻¹; PL: Pod length in cm; TSW: Thousand seed weight (g); AB: Aschochyta blight; PM: Powdery mildew; GYH: Grain yield ha⁻¹ in (kg ha⁻¹)



the number of days to maturity increases, then positive and significantly associated traits tend to become taller in plant height and pod length, high number of pods and seeds plant⁻¹, and high in thousand seed weight and grain yield.

3.5. Genotypic path coefficient analysis

The direct and indirect genotypic path coefficient analysis of eight independent traits on grain yield was presented in Table 7 below. The analysis result showed that days to flowering, plant height, and pod length had positive direct effects on grain yield, while days to maturity, number of pods plant⁻¹, number of seed plant⁻¹, thousand seed weight and powdery mildew had negative direct effects on the grain yield performance of genotypes. Yimam et al. (2024) reported a positive direct effect of plant height, number of seeds plant⁻¹ and days to 50% flowering on seed yield, whereas negative direct effect of days to 90% maturity, number of pods plant⁻¹ and ascochyta blight on seed yield. The positive direct effect of these traits on grain yield implied that direct selection of such traits would

improve the grain yield if the correlation with grain yield was positive and significant. In this result days to flowering, plant height, and pod length has positive association with grain yield and have positive direct effect on grain yield. Thus, efficient selection would be done to these traits in order to obtaining maximum grain yield.

Number of days to maturity, number of pods plant⁻¹, number of seed plant⁻¹, thousand seed weight and powdery mildew exhibited a negative direct effect on grain yield, thus negative selection on these traits had positive effects on yield improvement. Plant height had positive indirect effect on grain yield through days to flowering and pod length, while negative indirect effect through days to maturity, number of pods plant⁻¹, number of seed plant⁻¹, thousand seed weight and powdery mildew. Thousand seed weight also have negative indirect effect on grain yield through all traits. The phenotypic path analysis result showed that all evaluated traits have positive direct effects on grain yield performance (Table 8).

Table 7: Genotypic direct (diagonal) and in direct effect of eight traits on grain yield

Traits	FLD	MTD	PLH	PPL	SPP	PL	TSW	PM
FLD	2.095	-0.181	0.392	-0.106	-0.559	0.211	-0.145	-0.755
MTD	1.717	-0.221	0.387	-0.137	-0.435	0.144	-0.151	-0.326
PLH	2.094	-0.218	0.392	-0.07	-0.543	0.125	-0.142	-0.695
PPL	1.031	-0.141	0.128	-0.215	-0.191	0.268	-0.069	-0.25
SPP	1.695	-0.139	0.308	-0.059	-0.691	0.182	-0.075	-0.63
PL	1.598	-0.115	0.177	-0.208	-0.455	0.276	-0.058	-0.357
TSW	1.87	-0.205	0.342	-0.09	-0.317	0.099	-0.163	-0.588
PM	2.053	-0.093	0.354	-0.07	-0.565	0.128	-0.124	-0.771

FLD: Number of days to flowering; MTD: Number of days to maturity; PLH: Plant height in cm; PPP: Number of pods plant⁻¹; SPP: Number of seeds pod⁻¹; PL: Pod length in cm; TSW: Thousand seed weight (g); AB: Aschochyta blight; PM: Powdery mildew; GYH: Grain yield ha⁻¹ in (kg ha⁻¹)

Table 8: Phenotypic direct (diagonal) and in direct effect of eight traits on grain yield

Traits	FLD	MTD	PLH	PPL	SPP	PL	TSW	PM
FLD	0.071	0.079	0.051	0.009	0.037	0.01	0.285	0.1
MTD	0.06	0.094	0.046	0.006	0.031	0.009	0.275	0.1
PLH	0.058	0.069	0.063	0.023	0.033	0.008	0.243	0.093
PPL	0.006	0.005	0.014	0.107	0.024	0.002	0.017	0.029
SPP	0.026	0.029	0.02	0.025	0.102	0.007	0.126	0.056
PL	0.038	0.048	0.028	0.012	0.038	0.018	0.19	0.068
TSW	0.057	0.073	0.043	0.005	0.036	0.01	0.356	0.079
PM	0.05	0.066	0.041	0.022	0.04	0.009	0.197	0.142

FLD: Number of days to flowering; MTD: Number of days to maturity; PLH: Plant height in cm; PPP: Number of pods plant⁻¹; SPP: Number of seeds pod⁻¹; PL: Pod length in cm; TSW: Thousand seed weight (g); AB: Aschochyta blight; PM: Powdery mildew; GYH: Grain yield ha⁻¹ in (kg ha⁻¹)



4. Conclusion

The ANOVA results for Dekoko field pea genotypes reveal significant genetic variability across most traits. This implied that the existence of sufficient amount of genetic variability among genotypes for field pea improvement. High heritability and genetic advance for plant height, seed weight, and yield suggested that phenotypic selection was effective for improvement. Since most traits positively correlated with grain yield, breeding programs should prioritize parent materials based on their specific direct effects on yield performance.

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