Variability and Association of Some Morpho-agronomic Traits in Advanced Faba bean (*Viciafaba* L.) Genotypes at Potential Areas of South Eastern Ethiopia

ABSTRACT

Faba bean is an important pulse crop in Ethiopia; however its productivity is low due to lack of biotic and abiotic stresses tolerant varieties. The presence of genetic variability in the germplasm is important for the improvement of yield and other traits. Thus, this study was conducted to understand the extent of genetic variability and association for yield and yield related traits among existing faba bean genotypes. Fiftyfour genotypes were evaluated at two locations (Kulumsaand Asasa)using 9 x 6 alpha lattice design with two replications in 2022/23. The combined/pooled/ analysis of variance revealed that highly significant at ($P \leq 0.01$) and significant ($P \leq 0.05$) differences were observed among genotypes for all the traits. The phenotypic variance were higher than the genotypic variance of the traits, implies that the influence of the environment on the expression of traits.The genotypic coefficient of variation ranged from 1.89% for days to maturity to 16.14% for thousand seed weight and the phenotypic coefficient of variance value ranged from 2.49% for days to maturity to 17% for thousand seed weight. High estimate of heritability were recorded from days to 50% flowering, rust and thousand seed weight. High genetic advance were observed from thousand seeds weight and rust. Highest estimate of heritability with high genetic advance were observed from thousand seeds weight and rust. Seed yield had negative and highly significant correlation with days to maturity and rust at both genotypic and phenotypic levels, respectively. The genotypic path analysis showed that number of pod per plant exerted positive direct effect on seed yield followed by thousand seed weight, plant height and number of seeds per pod. The observed variations indicate the possibility for further improvement of grain yield and associated traits of faba bean genotypes by utilizing selected parental genotypes and targeted crossing schemes in breeding programs.

Key Words: Direct effect, Genotypic association, Genotypic variance, In-direct effect,Phenotypic variance

1. INTRODUCTION

“Faba bean (*Vicia faba* L.) is one of the most important cool season globalfood legume crop in the world belongs to the Fabaceae family. The major faba bean-producing countries include China, Ethiopia, U.K, Australia, Germany, Morocco, France, Egypt, Italy and Sudan” (Yang *et al.,* 2017). “Currently in Ethiopia, faba bean is the first major grain legume crop in terms of both area and total amount of production” (CSA, 2020). “It is grown on 437,106 hectares of land with total production of 9,217,615quintals and productivity of 2.12 tons per hectares” .(CSA, 2020). It is widely cultivated in midland and highland altitude areas of the country at elevations ranging from 1800-3000 msl with receiving 700-1100 mm annual rainfall.

“Faba bean has great versatile purposesin the livelihood of the agricultural societies of the country. It serves as a source of food with valuable and cheap sources of protein for the middle and low income strata of the population who cannot afford animal protein” (Bulti *et al*., 2019). It also provides a significant role in rotation to ameliorate soil fertility for sustainable farming system of the country due to its pertinent atmospheric nitrogen fixing capacity (Kaur *et al*., 2012), break disease cycles and control weeds in areas, where cereal mono-cropping is abundant. “In addition, faba bean is used as a source of animal feed, cash to the farmers and foreign currency earning to the country. Ethiopia is one of the major faba bean producing countries in the world. However, the average national productivity of the crop (2.1t/ha) is low compared to the potential of the crop” (Wondafrash *et al*., 2019). “These is primarily due toinherent low yielding potential of the indigenous cultivars, lack of improved seed, biotic stresses (diseases likechocolate spot, rust, root rot and ascochyta blight), field and storage pests , grass and broad leave weeds and abiotic factors (such as soil acidity,water logging and frost) and, instability of cultivars, poor adaptation and poor crop management” (Mussa *etal*.,2008, Link *et al*.,2010, Mekuria and Ashenafi,2018,Meselu,2019, Wondafrash *etal*.,2019).

On the other hand, currently, in Ethiopia the demand for improved faba bean is increasing as a result of increasing demand of consumers and marketing industry (Bulti *et al*., 2019). “Thus,through plant breeding program,further development and identification of desirable genotypes with high yielding potential, large seed size, wider adaptation, and desirable quality and disease resistant is essential in order to increase the production and productivity of the crop and also in order to meet the growing demand of the stake holders in a sustainable way" (Mekuria and Ashenafi, 2018). "The success of breeding in any crop depends upon the extent of genetic variability, heritable portion and association of traits in the base population within the crop germplasm" (singh,2001; Fikreselassie, 2012; Asnakech *et al*., 2020). Hence, the development of an intensive breeding program needs detailed biological information and knowledge on the existence of genetic variability, heritability, and expected genetic advance in the base population. Kebede *et al*., 2022 reported "significant genotypic differences among the genotypes for all the traits". Mesfin *et al*., 2019 also reported "the presence significant genetic variability among the genotypes". Therefore, the present study was conducted to determine the genotypic and phenotypic variation, heritability, genetic advance of important morpho-agronomic traits and to examine the association among traits and thereby estimate the direct and indirect effects of various traits on seed yield.

2. Materials and Methods

2.1. Experimental Sites and Materials

The experiments were carried out in kulumsa Agricultural Research Center (KARC)at two locations; Kulumsa and Asasa during 2022 main cropping season(June-Augest).A total of fifty four advanced fababean genotypes including two standard checks, which wasreleased recently used inthe experiment. Descriptions of the two study experimental sites were presented in Table **1.**

2.2. Experimental Design

The experiment was sown in mid-June 2022using 9 x 6alpha lattice designs with two replications; each replication containing nine incomplete blocks and each incomplete blockcontaining six genotype. Each genotype was planted in two rows with a length of 4m and 0.8m in width, i.e. 3.2m^2 areas with a spacing of 40cm and 10cm between rows and plants, respectively. Each plot had a spacing of 1m between treatments to separate two genotypes. 121 kg/haof NPS fertilizer was applied and other agronomic practices were done throughout the growing season. The grain yield harvested from a 3.2m^2 plot size was finally converted into hectare and the moisture contents were adjusted to the standard units of faba bean 10%.

Table 1: Description of the test environments

Location	Altitude (m.a.s.l)	Latitude	Longitude	Mean annual Rainfall(mm)	Min T^0	Max T^0	Soil type	Agro-ecology
Kulumsa	2200	0801'10"N	3909'11"E	820	10.5	22.8	clay	MA
Asasa	2340	0707'09"N	3911'56"E	620	5.8	23.6	Clay loam	MA

Where, Min T^0=minimum temperature in degree Celsius, Max T^0=maximum temperature in degree Celsius, MA=Mid-altitude

Data Collection: Data were collected on single plant and plot bases. On a plant basis, data were collected from ten randomly selected plants from each genotype in each replication, namely, pant height (PH) (cm), number of pods per plant (NPPP) (number) and number of seeds per pod (NSPP) (number). While the data on plot basis were collected from the two central rows include days to 50% flowering(DF), gain filling period(GFP), days to 90% maturity(DM), thousand seed weight (TSW) (gram), seed yield (SYPH) (kg ha^{-1}), and rust (1-9) scale, where 1 for nil: No visible disease symptom (Immune), 3 for a slight (resistant), 5 for medium (moderately resistant), 7 for severe (susceptible), 9 for very severe (highly susceptible).

Data Analysis: the analysis of variance was carried out using the procedure of alpha lattice design as described by Gomez and Gomez (1984) for all traits to assess the significance of the difference among the genotypes by using R software version 4.2 (R Core Team, 2019).All the genetic parameter were obtained directly from variance component table generated by the software using lmer function of the lme4 random model package in R software version 4.2 (R core team, 2019) by considering the genotype, location, replication and block in the linear random model as random variables using Residual (restricted) maximum likelihood (REML) variance component estimation method.

Table 2. List of faba bean experimental materials

Code	Genotype	Origin
G-1	EH016025-9	Hybridization
G-2	EH015005-3	Hybridization
G-3	EH016020-3-1	Hybridization
G-4	EH016026-8	Hybridization
G-5	EH017026-3	Hybridization
G-6	EH016001-2	Hybridization
G-7	EH016027-3	Hybridization
G-8	EH016028-4	Hybridization
G-9	EH016030-6	Hybridization
G-10	EH016028-8	Hybridization
G-11	EH017002-2	Hybridization
G-12	EH016031-5	Hybridization
G-13	EH017004-1	Hybridization
G-14	EH014016-1	Hybridization
G-15	EH017036-1	Hybridization
G-16	EH017001-2	Hybridization
G-17	EH016031-4	Hybridization
G-18	EH016021-5	Hybridization
G-19	EH017006-2	Hybridization
G-20	EH016021-4	Hybridization
G-21	EH017036-2	Hybridization
G-22	EH017086-2	Hybridization
G-23	EH016021-2	Hybridization
G-24	Gora	Hybridization
G-25	EH017041-2	Hybridization
G-26	EH016014-2	Hybridization
G-27	EH017026-1	Hybridization
G-28	EH016028-1	Hybridization
G-29	EH016030-9	Hybridization
G-30	EH016028-2	Hybridization
G-31	EH016034-3	Hybridization
G-32	EH014006-3	Hybridization
G-33	EH016027-9	Hybridization
G-34	EH015013-1	Hybridization
G-35	EH017011-6	Hybridization
G-36	EH015001-2	Hybridization
G-37	EH017029-2	Hybridization
G-38	EH016024-4	Hybridization
G-39	EH017022-1	Hybridization
G-40	EH017026-2	Hybridization
G-41	EH017001-1	Hybridization
G-42	EH016021-11	Hybridization
G-43	EH016006-1	Hybridization
G-44	EH017033-2	Hybridization
G-45	EH014020-1	Hybridization
G-46	EH016025-3	Hybridization
G-47	EH016032-1	Hybridization
G-48	EH016010-4	Hybridization
G-49	EH017029-1	Hybridization
G-50	EH017022-3	Hybridization
G-51	EH014006-1	Hybridization
G-52	Numan	Hybridization
G-53	EH016025-6	Hybridization
G-54	EH017109-1	Hybridization

3. RESULTS AND DISCUSSION

The combined analyses of variance for different traits are presented in table 3.The combined/pooled/ analysis of variance revealed that highly significant (*$P \leq 0.01$*) to significant *($P \leq 0.05$)* differences were observed among tested genotypes for all the traits under study (Table 3). The significant differences obtained in the present experiment indicated the presence of considerable variation among faba bean genotypes studied (Table 3).Different researchers reported significant differences for one or more of the studied traits(El-Shal and El-Sayed, 2019;Kumar and Kaushik, 2020; Kebede *etal*., 2022).Test locations exerted highly significant effects on days to flowering, days to maturity, plant height, pods per plant, 1000-seed weight, seed yield and rust indicating there are differences between the two environments for different phenotypic performance of those traits at both locations.

Significant location effects were also observed for grain filling period and number of seeds per pod (Table 3).The interaction effects of locations and genotypes showed highly significant effects for all traits studied except grain filling period, days to 95% maturity, plant height and rust (Table 3). Highly significant of genotype (G) x location (L) interaction was observed in this studyindicating the differential response of genotypes for those traits at each location. In harmony with this result,highly significant genotype by location interaction was observedfor grain yield, plant height, hundred seed weight, number of pods per plant, and days to 50% flowering(Mesfin*etal*., 2019).

Table 3. Mean square from the analysis of variance for 9 traits of 54 faba bean genotypes tested at across location (Kulumsa and Asasa)in 2022

Source of Variation	DF	GFP	DM	PH	NSPP	NPPP	TSW	Rust	SYPH
Entry(df=53)	20.04**	48.99 **	47.28**	249.99*	0.25**	63.14*	84258.36**	3.06**	6185068.57**
Loc(df=1)	3859.12**	97.34*	2730.67**	2571.86**	1.02*	3955.52**	304410.36**	21.41**	116501727.02**
Rep(Loc)(df=2)	16.21	21.41	19.20	1739.47	0.23	87.20	2441.29	2.82	1609173.91
Entry*Loc(df=53)	2.63**	22.40	18.03	195.95	0.29**	56.18*	8242.23**	0.95	3253020.60*
block(Rep:Loc)(df=32)	1.69	25.50	21.95	257.37	0.19	53.42	3722.09	1.56	2468591.59
Residuals(df=74)	2.19	23.55	20.67	139.44	0.12	37.02	3165.59	0.86	1724751.80

PH = Plant height (cm), NPPP = Number of Pods per Plant (NPPP), NSPP = Number of Seeds per Pod (NSPP), DF = Days to 50% flowering, GFP = Grain filling period, DM = Days to 90% maturity, TSW = Thousand seed weight (gram), SYPH = Seed yield, Loc = Location, Rep = Replication, df = Degree of Freedom

3.1. Range and Mean Performance of Genotypes

Range, mean, and estimate of genetic parameters for the combined data were presented in Table 4 and the mean performances of each genotype were also described in Table 5.Days to 50% flowering was varied from 52.53for G-21 to 61.02 day for G-3 with a mean of 78. Days tomaturity ranged from 133.1 for G-12 to 141.45for G-3 with a mean of 138. Nearly,80% of genotypes mature later than the standard check G-52 (Numan). Twenty-six (48.15%) genotypes have matured in fewer days than the grand mean (138) days from 54 genotypes to reach physiological maturity stage and these genotypes could be early to the study areas. However, Twenty-eight (51.85%) genotypes have matured in larger days than the grand mean (138) days from 54 genotypes.

The magnitude of variation for plant height ranged from 143.49 to 149.44 cm with a mean of 147 cm. The highest plant height was recorded by genotype G-33 (149.44 cm) followed by G-13 (149.32 cm), G-44(148.86 cm) and G-9 (148.84 cm) while the lowest plant height was recorded in genotype G-31 (143.49 cm) as indicated in (Table 5).The number of pods per plant ranged from 22.32 to 23.54 with a mean of 22.9. About 67 % of the genotypes had the highest number of pods per plant over the best check G-24 (Gora). The maximum and minimum number of pods per plant was obtained from G-30 and G-3, respectively. The thousand seed weight exhibited a wider range from 629.57for G-9 to 1329.32 gm for G-3 with a mean of 851.8 gm. Twenty-eight (51.85%) genotypes had higher thousand seed weight over the best check G-52(Numan).

Seed yield of genotypes ranged from 6,094.75 to 8,216.69 kg ha^{-1} with a mean of 7,163.6 kg ha^{-1} (Table 5). About thirty-nine and twenty percent of the genotypes gave higher yield than the standard check G-52 (Numan) and G-24 (Gora) respectively. The highest grain yield was recorded in genotype G-1(8,216.69) followed by G-31(7,983.89), G-53(7,926.23), G-22(7,909.36) and G-28(7,803.56 kg ha^{-1}) while the lowest grain yield was obtained from genotype G-3 (6,094.75)as presented in Table 5.Thus these better yielding genotypes (G-1, G-31, G-53)and other traits genotypes used for future breeding program.

3.2. Estimates of Genetic Parameters

The genetic parameters such as genotypic and phenotypic variance and coefficient of variations, heritability in broad sense and genetic advance as percent of mean were estimated for nine traits and results are presented in Table4.

3.2.1. Phenotypic and Genotypic Coefficient of Variation

The PCV value in the present study ranged from 2.49% for days to maturity to 17% for thousandseed weight, and GCV value ranged from 1.89% for days to maturity to 16.14% for thousandseed weight(Table 4).According to Deshmukh *etal*. (1986), the phenotypic coefficient of variation (PCV) and the genotypic coefficient of variation (GCV) values can be categorized as low (<10%), moderate (10-20%), and high (>20%).Based on these categories,moderate PCV and GCV values were recorded for thousandseed weight, seed yield and rust.These moderate values indicated the existence of enough genetic variation on the studied genotypes to perform selection for improvement.In agreement with this result, Kebede *etal*. (2022) reported moderate PCV and GCV for thousandseed weight and seed yield.

High GCV for grain yield, number of pods per plant, 100-seed weight, chocolate spot and rust disease score were reported by Hiywotu *et al.*, (2022).However, days to 50 % flowering, grain filling period, days to maturity, plant height and number of seeds per pod showed lower phenotypic and genotypic coefficient of variation.Similar result of PCV and GCV was reported for days to maturity by Kumar *etal*. (2017). The low value of this variation indicates that selection is not effective for these traits, because of the narrow range of variations even though it showed less influence of environmental effect on the expression of these traits.Moderate PCV and low GCV values were recorded by number of pods per plant.This would indicate the presence of environmental influence on the phenotypic expression of this trait and low range of genetic variation. Hence, this trait also lowers responsive for selection.

In general, the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits although the differences were not large for most of traits. This would be due to the fact the variation at the phenotypic level was due to the effect of genotypes and influence of environment.

3.2.2.Estimation of Broad Sense Heritability

Heritability estimates in broad sense was categorized as high (> 60%), medium (30 - 60%) and low (< 30%)(Dabholkar, 1992). The broad sense heritability values of the traits were ranged from 12.12% for number of seeds per pod to 90.17% for thousand seed weight in the present study (Table 4).Traits such as days to 50% flowering, rust and thousand seed weight showed higher heritability (>60) (Table 4). Similar results were reported for 100-seed weight, number of pods per plant, days to flowering, rust diseaseand grain yield(Mulualem *et al.,* (2013), Hiywotu *et al.,*(2022)).Higher heritability estimates for those traits indicated that the variation observed was mainly under genetic control and was less influenced by environment.

Hence, direct selection for those traits could be possible at phenotypic level for improvement.In line with this finding, the highest estimate of heritability was reported for Days to 50% flowering and hundred seed weights(Kumar *etal.*, 2017; Kebede *etal.*, 2022). Whereas, moderate heritability (30-60%) was recorded for grain filling period, days to maturity and seed yield. while plant height, number of pods per plant and number of seeds per pod showed lower heritability in the present study.Low heritability estimates for those traits implied that the phenotypic expression of these traits was more influenced by environments. Hence, simple selection is impossible for improvement of such traits. Similarly, lower estimate of heritability was reportedfor number of seeds per pod(Kebede *etal.*, 2022).

3.2.3. Genetic Advance as Percent of Mean

Genetic advance as percent of mean ranged from 2.39% for number of seeds per pod to 31.85% for thousand seeds weight (Table 4). These indicating that selecting the top 5% of the base population could result in an advance of 2.39 to 31.85% over the respective population mean.Genetic advances as a percentage of the mean (GAM) are classified high (>20%), moderate (10-20%) and low (<10%) (Johnson *etal.*,1955). Based on this classification, thousand seeds weight and rust showed high genetic advance as percent of mean (GAM).A result of high GAM indicated the maximum control of characters by additive gene action and the high possibility of using these traits for genetic improvement through selection. Seed yield showed moderate estimate of genetic advance as percent of mean.Likewise, high and moderate GAM was reported for hundred seed weight and grain yield, respectively(Mesfin *etal.*, 2019).However, days to 50% flowering, grain filling period, days to maturity, plant height, number of pods per plant and number of seeds per pod exhibited a lower estimate of genetic advance as percent of mean.This implies selection of genotype based on those traits will not make any improvement in new population due to narrow range of variation for those traits. Similarly, low estimate of Gam was reported for days to 50% flowering, grain filling period, days to maturity and plant height(Mesfin *etal.*, 2019).In opposite to this finding, high GAM was reported for number of pods per plant (Kebede *etal.*, 2022). This could be due to the difference of growing environments and genetic makeup of the evaluated genotypes.

“Selecting superior individuals based on heritability estimates alone may not be evidence for genetic improvement. Hence, heritability estimates along with genetic advance would be more useful in predicting the effectiveness of selecting the best individuals” (Johnson *etal.*, 1955).Accordingly,in the present study,thousand seeds weight and rust coupled high heritability with high genetic advance as a percent of mean.The highest heritability coupled with high GAMwas reported for hundred seed weight in line with this study (Mesfin *etal*,2019). “High heritability and high genetic advance were reported for traits of number of pods per plant, biomass weight per plot and thousand-seed weight” (Mulugeta *et al.* (2018)).Moderate estimate of heritability along with moderate genetic advance as percent of mean was observed for seed yield in the present study. A similar result was obtained for grain yield by Kebede *etal.* (2022).

Generally, moderate to high GCV, heritability and GAM associations suggested that phenotypic selection is possible for improvement of the trait. Hence, the analysis of genetic parameters (GCV, HB and GAM) in the present study showed that, thousand seed weight and rust exhibited moderate GCV along with high heritability and GAM association. Moderate GCV coupled with moderate heritability and GAM associations also observed by seed yield in this study. This indicated that those traitsare controlled by genetic factor and higher chance to improve through phenotypic direct selection.

Table 4. Range, mean and estimates of genetic parameters for 9 traits of faba bean genotypes tested at across location (Kulumsa and Asasa)

Traits	Range	mean	v.g	v.ge	v.e	v.ph	GCV	PCV	HB	GA	GAM
DF	52.53-61.02	55.6	4.23	0.34	1.96	4.89	3.70	3.98	86.53	4.01	7.21
GFP	73.07-89.92	82.4	6.65	0.58	23.55	12.82	3.13	4.34	51.84	3.82	4.64
DM	133.1-141.45	138.0	6.81	0.00	20.04	11.82	1.89	2.49	57.61	4.12	2.98
PH	143.49-149.44	147.0	10.92	16.46	163.02	59.91	2.25	5.27	18.23	6.14	4.17
NPPL	22.39-23.54	22.9	1.74	4.79	37.02	13.39	5.77	16.00	12.99	0.81	3.56
NSPP	2.5-3.5	3.0	0.01	0.09	0.12	0.08	3.33	9.57	12.12	0.07	2.39
TSW	629.57-1329.32	851.8	18908.76	2543.19	3155.83	20969.32	16.14	17.00	90.17	271.31	31.85
Rust	3.97-6.33	5.1	0.43	0.00	0.96	0.67	12.75	15.93	64.05	1.15	22.52
SYH	6094.7-8216.69	7163.6	576396.74	730703.43	1791604.63	1389649.62	10.60	16.46	41.48	1150.22	16.06

v.g= Genotypic Variance, v.ge= Genotype by Location Interaction Variance, v.e=Error Variance, v.ph=Phenotypic Variance, DF = Days to 50% Flowering, GFP= Grain Filling Period, DM = Days to Maturity, PH = Plant Height, NPPL = Number of Pods per Plant, NSPP = Number of Seed per Pod, TSW = Thousand Seed weight, SYH = Seed yield in kgha-1

Table 5. Mean performances of faba bean genotypes combined over locations

code	Genotype	DF	GFP	DM	PH	NPPL	NSPP	TSW	Rust	SYH
G-1	EH016025-9	56.92	82.47	138.57	147.49	23.09	3.0	791.43	5.24	8216.69
G-2	EH015005-3	56.5	83.39	137.27	146.4	22.62	3.4	729.04	5.38	6260.49
G-3	EH016020-3-1	61.02	82.64	141.45	146.01	22.32	3.0	1359.32	5.21	6094.75
G-4	EH016026-8	53.55	73.07	138.86	147.32	22.68	2.9	810.64	5.38	6892.77
G-5	EH017026-3	54.43	87.32	134.25	147.52	23.49	3.1	769.12	5.79	6746.94
G-6	EH016001-2	53.36	86.07	137.7	147.15	22.96	2.7	790.4	5.16	7391.10
G-7	EH016027-3	52.99	78.73	137.85	146.37	23.34	2.8	816.22	4.64	7616.94
G-8	EH016028-4	55.55	80.73	139	147.83	22.72	2.9	851.9	5.05	7744.33
G-9	EH016030-6	58.17	77.99	140.58	148.84	23.25	2.5	629.57	5.71	6601.81
G-10	EH016028-8	54.2	81.67	137.13	148.16	23.04	2.7	860.79	4.73	7508.76
G-11	EH017002-2	55.1	79.24	138.42	147.27	23.13	3.1	824.15	4.81	7140
G-12	EH016031-5	56.79	78.76	133.1	146.89	22.85	3.1	691.06	5.34	6922.16
G-13	EH017004-1	55.49	84.00	140.44	149.32	23.22	3.3	851.12	4.38	7063.78
G-14	EH014016-1	56.36	79.74	140.3	147.65	22.62	2.9	839.4	4.86	6422.68
G-15	EH017036-1	57.73	81.98	139.43	147.17	23.22	3.1	773.03	4.63	7249.14
G-16	EH017001-2	54.27	85.16	138.28	147.09	22.9	2.9	754.16	5.11	7386.21
G-17	EH016031-4	53.59	79.90	135.11	146.99	22.58	3.0	773.96	5.82	6467.93
G-18	EH016021-5	54.44	83.73	138.57	148.54	22.41	2.9	860.79	6.09	6493.21
G-19	EH017006-2	52.94	75.00	135.4	145.17	22.58	3.1	970.81	5.18	7373.34
G-20	EH016021-4	56.77	80.74	139.43	147.1	22.69	3.5	990.8	4.69	6979.09
G-21	EH017036-2	52.53	78.67	134.82	144.82	23.27	3.2	809.3	5.22	7282.91
G-22	EH017086-2	56.07	89.92	137.56	144.79	22.92	3.1	927.67	4.11	7909.36
G-23	EH016021-2	55.58	82.01	140.3	147.5	22.48	2.6	879.89	4.6	6580.96
G-24	Gora	58.34	83.82	137.42	148.68	22.67	2.6	806.29	4.53	7491.36
G-25	EH017041-2	58.02	80.47	139.86	147.75	22.71	3.2	1099.48	4.75	7179.39
G-26	EH016014-2	55.91	81.64	134.68	146.15	23.33	3.0	685.85	5.42	7418.8
G-27	EH017026-1	56.19	85.39	138.86	148.14	22.59	2.7	1043.4	5.26	7013.15
G-28	EH016028-1	55.28	86.64	136.7	144.28	22.58	3.1	937.36	4.48	7803.56

code	Genotype	DF	GFP	DM	PH	NPPL	NSPP	TSW	Rust	SYH
G-29	EH016030-9	53.5	83.64	140.3	146.6	22.99	2.7	640.08	6.33	6215.42
G-30	EH016028-2	53.9	88.54	138.14	147.9	23.54	3.5	759.32	4.89	7558.4
G-31	EH016034-3	55.1	77.20	136.41	143.49	23.14	2.8	810.55	5.55	7983.89
G-32	EH014006-3	52.75	86.94	135.26	145.02	22.8	2.7	668.43	5.77	7045.26
G-33	EH016027-9	55.55	86.45	139.86	149.44	22.65	2.7	934.7	3.97	7515.92
G-34	EH015013-1	55.5	85.77	138.86	147.96	22.98	3.2	894.81	5.51	7135.19
G-35	EH017011-6	54.7	88.94	137.7	147.22	23.18	2.8	770.11	5.45	6802.77
G-36	EH015001-2	54.61	81.77	140.44	147.36	22.75	3.2	944.91	5.02	7762.66
G-37	EH017029-2	57.93	77.49	137.13	146.86	22.98	3.5	747.41	5.27	7180.55
G-38	EH016024-4	53.04	84.24	138.57	146.53	22.58	3.2	834.29	4.81	7149.21
G-39	EH017022-1	55.12	81.22	140.58	146.86	23.23	3.0	895.05	4.95	7450.64
G-40	EH017026-2	54.34	84.49	140.58	148.73	23	3.0	917.95	4.65	7458.65
G-41	EH017001-1	54.63	87.29	137.27	147.85	23.07	2.8	805.68	5.38	7247.88
G-42	EH016021-11	57.31	86.14	135.54	148.06	23.19	2.8	695.74	5.85	7484.16
G-43	EH016006-1	58.17	80.68	140.01	147.22	22.6	2.5	1027.04	5.53	7316.36
G-44	EH017033-2	56.82	78.43	137.13	148.86	22.39	2.8	1140.22	4.63	7370.11
G-45	EH014020-1	57.74	75.86	139.86	148.36	22.97	2.8	773.43	4.57	7472.84
G-46	EH016025-3	54.52	81.93	139.72	144.48	22.58	3.0	822.27	4.72	6583.32
G-47	EH016032-1	56.93	74.93	139.58	144.55	22.65	2.6	1021.75	4.56	7278.76
G-48	EH016010-4	57.69	84.61	138.42	148.48	22.49	3.3	923.96	5.52	6854.44
G-49	EH017029-1	53.82	78.21	135.69	144.17	22.99	3.1	833.28	4.81	6608.92
G-50	EH017022-3	55.78	79.14	137.42	147.24	23.16	3.1	871.66	6.1	7423.11
G-51	EH014006-1	59.45	87.64	137.42	147.06	22.42	2.8	958.76	5.45	6603.23
G-52	Numan	52.65	86.71	136.41	146.73	22.45	2.8	820.88	5.56	7352.68
G-53	EH016025-6	54.94	84.97	134.25	146.22	22.94	2.8	796.31	4.8	7926.23
G-54	EH017109-1	58.18	84.14	137.13	146.39	22.94	3.1	759.75	5.26	6799.84
	Mean	55.6	82.38	138.0	147.0	22.9	3.0	851.8	5.1	7163.6
	CV%	2.7	5.90	3.3	8.0	26.6	11.6	6.6	18.1	18.3
	LSD (0.05)	2.1	6.84	6.4	16.6	8.6	0.5	79.3	1.3	1850.4

3.3. Association of Traits at Genotypic and Phenotypic Level

Estimates of genotypic and phenotypic correlation coefficients among 9 traits are presented in (Table6).The present study showed that for most character pairs, genotypic and phenotypic associations were in the same direction and the magnitudes of genotypic correlation coefficients are higher than the phenotypic correlation coefficients for most of traits analyzed, which shows greater contribution of the genetic factors than the environmental factors in the expression of these traits.

The result of correlation analysis indicated that seed yield showed positive highly significant (< 0.01) and significant (<0.05)association withnumber of pods per plant and number of seeds per pod, respectively at genotypic level. This indicated that the possibility of simultaneously improving seed yield through indirect selection of these traits.Therefore, to improve seed yield more attention should be given to these traits during selection.. In accordance with this result, positive and highly significant association of seed yield with number of pods per plant and number of seeds per pods has been reported by(Kumar *etal.*, 2017; Dewangan *etal.*, 2019).

However, seed yield had negative and highly significant correlation with days to maturity and rust at genotypic, and both at genotypic and phenotypic levelsrespectively.These indicate that genotypes with early flowering and resistant to rust produce high seed yield and vice versa.On the other hand, seed yield showed negative and non-significant genotypic and phenotypic correlation with days to 50% flowering and grain filling period; positively non-significant genotypic and phenotypic association with thousand seed weight; negatively and positively non-significant correlation with plant height at genotypic and phenotypic level, respectively.This implies thatselection for these traits may not improve seed yield. In contradict to the present finding, Kumar *etal.* (2017) andDewangan *etal.*(2019) have been observed positive and highly significant association of seed yield with days to 50% flowering, days to maturity, plant height and hundred seed weight.

Days to 90 % maturity had positive and highly significant genotypic correlation with days to 50% flowering, grain filling period, plant height and thousand seed weight.However, it had negative and highly significant association with number of pods per plant, number of seeds per pod and rust.This implies genotypes with early flowering would tend to mature early and genotypes taking longer to mature also have taller plant height, susceptible to rust and produce low number of pods per plant and seeds per pod and tend to give high thousand seed weight.In line with the present finding, Dewangan *etal*.(2019)reported similar association of days to maturity with days to 50% flowering, plant height, hundredseed weight and pods per plant.

Table 6.Correlation coefficients at genotypic (above diagonal) and phenotypic level (below diagonal) among traits combined over location.

Traits	DF	DM	GFP	PLH	NPPL	NSPP	TSW	Rust	SYH
DF	**1**	0.437^{**}	-0.391^{**}	0.335^{*}	-0.356^{*}	-0.272^{*}	0.394^{**}	-0.109	-0.212
DM	0.286^{*}	**1**	0.657^{**}	0.456^{**}	-0.670^{**}	-0.388^{**}	0.520^{**}	-0.441^{**}	-0.368^{**}
GFP	-0.378^{**}	0.779^{**}	**1**	0.185	-0.387^{**}	-0.169	0.202	-0.360^{**}	-0.199
PLH	0.279^{*}	0.249	0.058	**1**	-0.198	-0.160	-0.026	0.139	-0.015
NPPL	-0.233	-0.190	-0.031	0.080	**1**	0.005	-0.843^{**}	0.166	0.626^{**}
NSPP	-0.109	-0.160	-0.083	0.015	0.015	**1**	-0.021	0.034	0.338^{*}
TSW	0.361^{**}	0.377^{**}	0.128	-0.008	-0.493^{**}	-0.131	**1**	-0.408^{**}	0.018
Rust	-0.096	-0.310^{*}	-0.237	0.072	0.008	0.158	-0.392^{**}	**1**	-0.474^{**}
SYH	-0.196	-0.186	-0.052	0.115	0.267	0.083	0.059	-0.444^{**}	**1**

Where: DF= Days to 50% Flowering, GFP = Grain Filling Period, DM =Days to 90% Maturity, PH= Plant Height, NPPL= Number of Pods per Plant, NSPP= Number of Seeds per Pod, TSW= Thousand Seed Weight, SYH = Seed Yield (kg ha^{-1}).

3.4.Genotypic Path Coefficient Analysis

In the present study, for genotypic path analysis, seven traits were used as casual (independent) variables (DF, DM, PH, NPPL, NSPP, TSW and Rust) and partitioned into direct and indirect effects using seed yield (SYH) as a dependent variable.The genotypic direct and indirect effects of different trait on seed yield are described in (Table 7).The genotypic path analysis showed that number of pod per plantexerted positive direct effect on seed yield followed by thousand seed weight, plant height and number of seeds per pod.The direct effect of these traits on seed yield indicates that, improvement on these traits will increase seed yield.The positive and direct effects of number of pod per plant, thousand seed weight and number of seeds per pod on seed yield were in accordance with the finding of Kumar *etal*. (2017) andDewangan *etal*.(2019).

Whereas rust followed by days to maturity and days to 50% flowering exhibited negative direct effect on seed yield. Days to maturity had high positive indirect effect on seed yield through thousand seed weight, rust and plant height. The strong and positive correlation along with positive direct effect of traits on seed yield is considered as an important component of yield. Hence ,number of pods per plant and number of seeds per pod had both positive direct effects and significant positive correlation with seed yield and are the most preferred traits for selection.

Table 7. Genotypic direct (bold diagonal) and in direct effect of seven traits on seed yield of faba bean

Traits	DF	DM	PLH	NPPL	NSPP	TSW	Rust
DF	**-0.151**	-0.180	0.138	-0.293	-0.020	0.269	0.055
DM	-0.066	**-0.413**	0.187	-0.561	-0.012	0.354	0.222
PLH	-0.051	-0.188	**0.410**	-0.171	-0.003	-0.015	-0.068
NPPL	0.052	0.273	-0.083	**0.849**	0.022	-0.565	-0.083
NSPP	0.036	0.061	-0.013	0.221	**0.083**	-0.084	-0.045
TSW	-0.060	-0.215	-0.009	-0.704	-0.010	**0.681**	0.205
Rust	0.016	0.182	0.056	0.141	0.007	-0.278	**-0.503**

Where: DF= Days to 50% Flowering, DM = Days to 90% Maturity, PH= Plant Height, NPPL= Number of Pods per Plant, NSPP= Number of Seeds per Pod, TSW= Thousand Seed Weight

The cause of the positive association of number of podsper plant with seed yield was mainly due to their direct effect. Although, the number of seedsper pod had positive direct effect on seed yield, their high indirect effect mainly via number of pods per plant counterbalances the low direct effect on seed yield. The causes of the positive association of number of seedsper pod with seed yield were mainly due to their indirect effects through number of pods per plant and its positive direct effect.

4. CONCLUSIONS

The analysis of variance (ANOVA) revealed highly significant differences among tested genotypes for all traits. The presence of highly significant difference was an indication of the existence of considerable genetic variability among the genotypes for the studied traits. The highest grain yield was recorded in genotype G-1(8216.69) followed by G-31(7983.89), G-53(7926.23), G-22(7909.36) and G-28(7803.56 kg ha^{-1}).

The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits although the differences were not large for most of traits.However, days to 50 % flowering, grain filling period, days to maturity, plant height and number of seeds per pod showed lower phenotypic and genotypic coefficient of variation.The highest estimates of heritability were recorded fordays to 50% flowering, rust and thousand seed weight. Thousand seed weight and rust exhibited high heritability and genetic advance as percent of mean. This indicated that those traits are controlled by genetic factor and higher chance to improve through phenotypic direct selection.

The present study showed, the magnitudes of genotypic correlation coefficients are higher than the phenotypic correlation coefficients.Seed yield showed negative and highly significant correlation with days to maturity and rust at genotypic, and both at genotypic and phenotypic levels, respectively.Seed yield was positively andsignificantlyassociated withnumber of pods per plant and number of seeds per pod at genotypic level. This indicated that the possibility of simultaneously improving seed yield through indirect selection of these traits.Number of pods per plant and number of seeds per pod had both positive direct effects and significant positive correlation with seed yield. Therefore, important consideration should be given for these traits while practicing selection aimed at the improvement of seed yield.

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