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Correlation and Path Coefficient Analysis of Grain Yield and It's Contributing Traits in Faba Bean (*Vicia faba* L.) Genotypes

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Abstract

Understanding the degree of association between agronomic traits is very important as it provides the base for effective selection. Hence, this research was conducted to study the associations among yield, and yield related traits in faba bean at three locations: Holetta, Watebecha Minjaro and Jeldu with and without lime application in 2017. The experiment comprised 50 faba bean genotypes arranged in randomized complete block design with three replications. Grain yield was positive and significantly associated with plant height and hundred seeds weight both at phenotypic and genotypic levels. These two traits were found as important yield components suggesting that they will have practical importance in selection of genotypes for high grain yield. Therefore, positive and significant association of pairs of traits at phenotypic and genotypic level validates the possibility of correlated response to selection whereas negatively correlated traits prohibit their improvement. The magnitudes of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients except for some traits, which indicate the presence of inherent or genetic association among various traits. The phenotypic expression of the correlation gets modified under the influence of environment and genotypic correlation provides measures of genetic association between traits and more reliable than phenotypic correlation and this helps to identify the traits to be utilized in breeding program. Genotypic path coefficient analysis indicated that hundred seeds weight and plant height exerted positive direct effect on grain yield. In conclusion, this investigation indicated that there is large scope of simultaneous improvement in grain yield as well as other yield components through direct and indirect selection.

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Introduction

Faba bean is the leading pulse crops in Ethiopa, sharing 30% of area coverage and 34% of the total production of pulses [1]. It is a major source of protein rich foods in the developing countries like Ethiopia for subsistence farmers [2]. It can substitute meat where there is demand for non-animal protein sources [3].

Genotype selection is fundamental in breeding program in order to get high productivity in a given environment. Yield per unit area is the cumulative effects of many traits hence direct selection for high yield is not easy as it is highly influenced by environment and indirect selection through yield components found more effective [4]. Indirect selection takes into account the information on association among agronomic traits, their association with grain yield as well as their direct influence on grain yield. However, selection for yield via highly correlated characters becomes easy if the contribution of different traits to yield is quantified using path coefficient analysis [5].

Awareness on the extent and nature of interrelationship among traits helps in formulating efficient system of multiple trait selection. Besides this, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be used for hybridization. In Ethiopia, the information on these aspects in faba bean is rare. Therefore, there is a need to generate information on interrelationships of grain yield and related agronomic traits among faba bean genotypes. Hence, this study was initiated with the objective to study associations among yield, and yield related traits in faba bean.

Materials and methods

The experiment was carried out with and without lime at three locations (Holetta Agricultural Research Center, Jeldu subsite, and Watebecha Minjaro farmer training center) in the central highlands of Ethiopia. The experiment was under rain fed conditions during the main cropping season (June to December) of 2017 on Nitosol at each location.

Fifty faba bean genotypes were used for this study (Table 1). The genotypes were arranged in randomized complete block design with three replications. Each experimental plot consisted of one rows 4 m long with inter-row spacing of 40 cm continuously and intra-row spacing of 10 cm. Fertilizer were applied at the rate of 121 kg/ha in the form of NPS. Recommended agronomic practices were applied to each plot alike.

Table 1: List of 50 faba bean genotypes used.

Genotypes			
Ashebeka	EH06027-2	EK 05037-4	Holetta-2
Bulga 70	EH06070-3	EK05001-1	Kasa
Cool-0018	EH06088-6	EK05006-3	KUSE2-27-33
Cool-0024	EH07015-7	EK05037-5	Mesay
Cool-0025	EH07023-3	EKLS/CSR02010-4-3	Moti
Cool-0030	EH08035-1	EKLS/CSR02012-2-3	NC58
Cool-0031	EH09002-1	EKLS/CSR02014-2-4	Numan
Cool-0034	EH09004-2	EKLS/CSR02017-3-4	Obse
Cool-0035	EH09007-4	EKLS/CSR02019-2-4	Selale
CS20DK	EH09031-4	EKLS/CSR02023-2-1	Tesfa
Degaga	Gebelcho	EKLS/CSR02028-1-1	Tumsa
Didi'a	Gora		Wayu
Dosha	Hachalu		Wolki

Data collection

Data recorded on plot basis: Days to 50% flowering: Number of days from planting to the date on which 50% of plants in the plot produce at least their first flower. Days to 90% physiological maturity: Number of days from the date of planting to the date on which 90% of the pods reach physiological maturity. Grain filling period: The number of days between days to 50% flowering and days to 90% physiological maturity. Hundred Seeds Weight: The weight in gram of one hundred randomly taken seeds from each experimental plot adjusted to standard moisture content for pluses (10%). Chocolate spot disease: The severity of chocolate spot disease was recorded using 1-9 scale [6].

Data recorded on plant basis

Plant height: The average height of five plants in each plot measured in centimeter from the ground surface to the top of the main stem at maturity. Number of poding nodes per plant: The average number of poding nodes of five plants in each plot. Number of pods per poding node: The average number of pods per poding nodes of five plants in each plot. Number of pods per plant: The average number of pods of five plants in each plot. Grain yield: Grain yield in gram from five random plants at the middle of the row adjusted to standard moisture content for pluses. Economic growth rate: Grain yield (g/5 plant) divided by grain filling duration and then multiplied by 100. Grain production efficiency: Grain filling duration divided by duration of vegetative period and then multiplied by grain yield (g/5 plant).

Data analysis

Association of traits

Phenotypic and genotypic correlation coefficient analysis

Phenotypic (r_p) and genotypic (r_g) correlations between two traits were estimated using the formula suggested by Johnson et al. [7] and [8].

$$r_p = \frac{P\,\mathrm{cov}_{xy}}{\sqrt{(V_p x . V_p y}} \;\; ; \;\; r_g = \frac{G\,\mathrm{cov}_{xy}}{\sqrt{(V_g x . V_g y}}$$

Where, r_p = Phenotypic correlation coefficient, r_g = Genotypic correlation coefficient, $Pcov_{xy}$ = Phenotypic covariance between variables x and y, $Gcov_{xy}$ = Genotypic covariance between variables x and y, V_{px} = Phenotypic variance of variable x, V_{gx} = Genotypic variance of variable x, V_{py} = Phenotypic variance of variable y and V_{gy} = Genotypic variance of variable y.

The calculated phenotypic correlation value was tested for its significance using t-test:

$$t = \frac{r_p}{SE(r_p)}$$

Where, r_p = Phenotypic correlation; SE (r_p) = Standard error of phenotypic correlation obtained using the following formula [9].

$$SE(r_p) = \sqrt{\frac{1 - r^2 ph}{n-2}}$$

Where, n is the number of genotypes tested, r^2p is phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels were tested for their significance by the formula described by Robertson [10] as indicated below:

$$t = \frac{r_p}{SE(r_p)}$$

The calculated ''t'' value was compared with the tabulated ''t'' value at (n-2) degree of freedom at 5% level of significance. Where, n is number of genotypes.

$$SEr_{gxy} = \sqrt{\frac{1 - r^2 g_{xy}}{h^2 x} .\, h^2 y}$$

Where, r^2g_{xy} = genotypic correlation coefficient, h^2x = Heritability of trait x and h^2y = Heritability of trait y.

Path coefficient analysis

Path coefficient analysis was conducted as suggested by Wright [11] and worked out by Dewey and Lu [5] using the phenotypic as well as genotypic correlation coefficients to determine the direct and indirect effects of yield components on seed yield based on the following relationship.

$$r_{ij} = p_{ij} + \sum r_{ik} p_{kj}$$

Where, r_{ij} = Mutual association between the independent trait (i) and dependent trait, seed yield (j) as measured by the correlation coefficients, p_{ij} = Components of direct effects of the independent trait (i) as measured by the path coefficients and $t = \frac{r_p}{SE(r_p)}$ = summation of components of indirect effect of a given independent trait (i) on a given dependent trait (j) via all other independent traits (k).

The contribution of the remaining unknown factor will be measured as the residual effect. Residual effect (h) will be calculated using the formula given by [5].

$$h = \sqrt{1 - R^2}$$

Where, h = residual effect and $R^2 = \sum r_{ij} p_{ij}$

Results and discussion

Association of traits

Phenotypic and genotypic correlations of grain yield with other traits

Grain yield showed positive and significant phenotypic association with plant height, number of poding node per plant, pod per plant and pod per poding node and hundred seeds weight over locations and soil managements (Table 2). Inferring that, any improvement of traits with significant positive correlation would result in a substantial increment on grain yield. Similar results were reported that significant positive correlation of grain yield with hundred seeds weight [12], with pods per plant [13].

Grain yield had positive and significant genotypic correlation with plant height, hundred seeds weight, grain production efficiency and economic growth rate across environments (Table 2). The result indicated any improvement of traits with significant positive correlation would result in a substantial increment on grain yield. Similar results were reported that seed yield strongly correlated with plant height [14-17]. Likewise, recent reports on faba bean also indicated significant and positive association of yield with plant height and hundred seeds weight at genotypic level [12, 18]. In contradict to this result previously reported nonsignificant and positive correlation of plant height with seed yield per plant [19] and negative but significant association of plant height and number of pods per plant with seed yield per plot [20].

Positive and significant association of pairs of traits at phenotypic and genotypic level validates the possibility of correlated response to selection whereas negative correlations prohibit the simultaneous improvements of those traits. This correlation analysis, allowed concluding that, plant height and hundred seeds weight were found an important yield components of faba bean. Similar findings have been reported that effective yield improvement would be achieved through the traits, which have significant and positive correlation with yield, and other economic traits [12,13,21]. Likewise, significant positive correlation was reported between seed yield with plant height, number of pod per plant and hundred seeds weight [22].

The magnitudes of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients except for some traits, which indicate the presence of inherent or genetic association among various traits. The phenotypic expression of the correlation gets modified under the influence of environment and genotypic correlation provides measures of genetic association between traits and is more reliable than phenotypic correlation and this helps to identify the traits to be utilized in breeding program. In agreement with this finding, it was reported higher genotypic correlation coefficients than phenotypic correlations, which revealed that there was a strong inherent association between various traits [12].

Phenotypic and genotypic correlations among other traits

Days to 90% maturity was significant and positively correlated with days to 50% flowering, grain filling period, number of pod per poding node, hundred seeds weight and chocolate spot at phenotypic level and with plant height, grain filling period and hundred seeds weight at genotypic level. It had significant and negative genotypic correlation with number of poding node per plant, pod per plant and pod per poding node over locations and soil managements (Table 2). The improvement of traits that have positive and significant relation indirectly leads to improvement of days to 90% maturity whereas improvements of negatively correlated traits oppose improvement days to 90% maturity. Similar results were reported that days to maturity significant and positively correlated with hundred seeds weight [18].

Hundred seeds weight significant and positively correlated with days to 90% maturity, grain filling period and grain production efficiency whereas significant and negatively correlated with days to 50% flowering, number of poding node per plant, number of pod per plant, number of pod per poding node and chocolate spot both at phenotypic and genotypic level (Table 2). There were similar trends for association of hundred seeds weight with other traits under lime and without lime applications over locations at both phenotypic and genotypic levels (data not shown). The result indicated any improvement of traits with significant positive correlation with would result in a substantial increment on hundred seeds weight. Previously, positive and significant genotypic correlation of hundred seeds weight with days to 90% maturity was reported by different authors [15,18,19].

Phenotypic direct and indirect effects of traits on grain yield

The phenotypic path analysis result indicated that economic growth rate followed by grain production efficiency and days to 90% maturity had maximum positive direct effects on grain yield over locations and soil managements. However, plant height and number of pod per plant had negative direct effect on grain yield. The contribution of plant height and number of pod per plant on grain yield took mainly through their highest and positive indirect effect with number of poding node per plant for both and number of pod per poding node for number of pod per plant (Table 3). At phenotypic level selection based on days to 50% flowering, days to 90% maturity and number of poding node per plant helps for the improvement of seed yield in faba bean. Similar results were reported that negative direct effect of plant height on grain yield [12] and in contradict number of pod per plant and plant height had high positive direct effect at phenotypic level on seed yield per plant [16,23].

Traits like days to 50% flowering, days to 90% maturity and number of poding node per plant ultimately affects grain yield were the components that exerted a substantial direct effect on grain yield. The residual effect determines unaccounted variability of the dependent factor (grain yield). The magnitude 0.031 indicates that the traits included in the path analysis explained 96.9% of the variation in grain yield. As suggested by Singh et al. [12] path analysis at the phenotypic level may not provide a true picture of direct and indirect causes and therefore, it would be advisable to understand the contribution of different traits at genotypic level.

Table 2: Phenotypic correlation coefficients (rp) (above) and genotypic (rg) (below) diagonal of 12 agronomic traits with grain yield in 50 faba bean genotypes tested with and without lime over three locations in 2017.

Trait	DF	DM	GFP	PH	PNPP	PPP	PPPN	HSW	GY	CS	GPE	EGR
DF	1	0.38**	-0.55**	-0.50**	0.02	0.17**	0.27**	-0.22**	-0.11**	-0.07*	-0.51**	0.02
DM	0.27	1	0.56**	-0.80**	-0.46**	-0.21**	0.24**	0.16**	-0.10**	0.17**	-0.10**	-0.22**
GFP	-0.51**	0.69**	1	-0.27**	-0.43**	-0.34**	-0.03	0.33**	0.01	0.21**	0.37**	-0.22**
PH	0.05	0.30*	0.23	1	0.51**	0.27**	-0.21**	0.11**	0.38**	-0.25**	0.43**	0.43**
PNPP	0.15	-0.61**	-0.65**	0.18	1	0.83**	0.15**	-0.32**	0.54**	-0.17**	0.36**	0.62**
PPP	0.33*	-0.56**	-0.74**	0.09	0.95**	1	0.65**	-0.48**	0.56**	-0.09**	0.35**	0.63**
PPPN	0.55**	-0.38**	-0.75**	-0.01	0.72**	0.90**	1	-0.42**	0.29**	0.07*	0.14**	0.28**
HSW	-0.30*	0.62**	0.77**	0.24	-0.80**	-0.88**	-0.85**	1	0.21**	-0.17**	0.31**	0.13**
GY	-0.08	0.21	0.25	0.70**	0.13	0.04	-0.09	0.37**	1	-0.17**	0.89**	0.97**
CS	-0.18	-0.28*	-0.12	0.12	0.31*	0.30*	0.25	-0.38**	-0.11	1	-0.09**	-0.22**
GPE	-0.36*	0.25	0.49**	0.64**	-0.04	-0.17	-0.33*	0.53**	0.94**	-0.07	1	0.78**
EGR	0.01	0.08	0.07	0.67**	0.25	0.19	0.04	0.23	0.98**	-0.1	0.88**	1

*, **: significant at $P < 0.05$ and $P < 0.01$, respectively; DF: Days to 50% Flowering; DM: Days to 90% Maturity; GFP: Grain Filling Period; PH: Plant Height; PNPP: Number of Poding Node Per Plant; PPP: Number of Pod Per Plant; PPPN: Number of Pod Per Poding Node; HSW: Hundred Seeds Weight; GY: Grain Yield; CS: Chocolate Spot; GPE: Grain Production Efficiency; EGR: Economic Growth Rate.

Table 3: Phenotypic direct (bold diagonal) and indirect (off diagonal) effects of traits on grain yield of 50 faba bean genotypes tested over locations and soil managements.

Trait	DF	DM	PH	PNPP	PPP	PPPN	HSW	CS	GPE	EGR	r_p
DF	**0.011**	0.036	0.002	0.000	-0.002	0.003	0.000	0.000	-0.174	0.015	-0.110
DM	0.004	**0.094**	0.003	-0.007	0.002	0.003	0.000	0.001	-0.034	-0.161	-0.096
PH	-0.005	-0.075	**-0.004**	0.008	-0.003	-0.002	0.000	-0.001	0.147	0.312	0.378
PNPP	0.000	-0.043	-0.002	**0.016**	-0.009	0.002	-0.001	-0.001	0.124	0.451	0.537
PPP	0.002	-0.02	-0.001	0.013	**-0.011**	0.007	-0.001	0.000	0.120	0.455	0.564
PPPN	0.003	0.023	0.001	0.002	-0.007	**0.011**	-0.001	0.000	0.049	0.206	0.286
HSW	-0.002	0.015	0	-0.005	0.005	-0.005	**0.002**	-0.001	0.106	0.091	0.206
CS	-0.001	0.016	0.001	-0.003	0.001	0.001	0.000	**0.004**	-0.030	-0.160	-0.171
GPE	-0.005	-0.009	-0.002	0.006	-0.004	0.002	0.001	0.000	**0.342**	0.562	0.891**
EGR	0.000	-0.021	-0.002	0.01	-0.007	0.003	0.000	-0.001	0.266	**0.722**	0.971**

Residual effect: 0.031; DF: Days to 50% Flowering; DM: Days to 90% Maturity; PH: Plant Height; PNPP: Number of Poding Node Per Plant; PPP: Number of Pod Per Plant; PPPN: Number of Pod Per Poding Node; HSW: Hundred seeds weight; CS: Chocolate Spot; GPE: Grain Production Efficiency; EGR: Economic Growth Rate.

Genotypic direct and indirect effects of traits on grain yield

The genotypic path coefficient analysis was done on the basis significance correlation at genotypic levels. Therefore, based on their correlation coefficient, at genotypic level 4 traits that have significant relationship with grain yield were included in the path analysis. The genotypic correlations were partitioned in to direct and indirect effects using grain yield as a dependent variable (Table 4). The genotypic path analysis indicated that economic growth rate followed by grain production efficiency, hundred seeds weight and plant height exerted positive direct effect on grain yield over locations and soil managements. These traits showed positive genotypic correlation with grain yield and exerted considerable direct effect on grain yield. Similar results were reported that plant height had high positive direct effect on seed yield per plant while in contradict high and negative direct effect of hundred seeds weight on seed yield per plant at genotypic level [16,23].

The residual effect 0.058 indicates that traits which were included in the genotypic path analysis explained 94% of the total variation in grain yield. The path analysis indicated that hundred seeds weight and plant height should be used as direct selection criteria for better grain yield. Therefore, selecting genotypes having high hundred seeds weight should be used to improve seed yield in faba bean. In harmony with this result, different authors reported that hundred seeds weight had positive and direct effects on seed yield and suggested that selection based on hundred seeds weight helps for improvement of grain yield in faba bean [18,20,21,24].

Table 4: Genotypic direct (bold diagonal) and indirect effect (off diagonal) of four traits on grain yield of 50 faba bean genotypes tested with and without lime over locations.

Trait	PH	HSW	GPE	EGR	r_g
PH	**0.036**	0.013	0.173	0.474	0.696
HSW	0.009	**0.054**	0.141	0.164	0.368
GPE	0.024	0.028	**0.268**	0.625	0.945**
EGR	0.024	0.012	0.236	**0.71**	0.983**

Residual effect: 0.058; PH: Plant Height; HSW: Hundred seeds weight; GPE: Grain Production Efficiency; EGR: Economic Growth Rate.

Conclusion

Understanding the degree of association between the different agronomic traits is very important as it provides the base for effective selection. Grain yield was found to be positive and significantly associated with plant height, number of poding node per plant, pod per plant and pod per poding node and hundred seeds weight at phenotypic level. Likewise, positive and significantly associated with plant height, hundred seeds weight, grain production efficiency and economic growth rate at genotypic level. Positive and significant association of pairs of traits at phenotypic and genotypic level validates the possibility of correlated response to selection whereas negative correlations prohibit the simultaneous improvements of those traits. This result allowed concluding that, plant height and hundred seeds weight were found as important yield components of faba bean suggesting that these traits will have practical importance in selection of faba bean genotypes for high grain yield.

The magnitudes of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients except for some traits, which indicate the presence of inherent or genetic association among various traits. The phenotypic expression of the correlation gets modified under the influence of environment and genotypic correlation provides measures of genetic association between traits and more reliable than phenotypic correlation and this helps to identify the traits to be utilized in breeding program.

Path analysis for grain yield at genotypic level indicated that economic growth rate followed by grain production efficiency, hundred seeds weight and plant height exerted positive direct effect on grain yield.

In conclusion, the present investigation indicated that there is large scope of simultaneous improvement in grain yield as well as other yield components through selection. It dictates to study more genotypes over years to confirm the importance of traits identified as yield predictors in faba bean.

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