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Full Length Research Paper

Genotypic variability, heritability and path analysis of yield components of determinate lablab *(Lablab purpureus* (L.) Sweet*)* inbred lines in Kenya

Eliezah M. Kamau[1*], Miriam G. Kinyua[2], Charles N. Waturu[1] and David R. Karanja[1]

[1]Kenya Agriculture and Livestock Research Organization, P. O. Box 57811-00200, Nairobi, Kenya.
[2]School of Agriculture and Biotechnology, University of Eldoret, P. O. Box 1125, Eldoret, Kenya.

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Lablab is a leguminous crop that offers great potential as food and cash crop in Kenya. However, high yielding early maturing determinate varieties suitable for short season environments and for intercropping systems are lacking. This study was conducted to estimate heritability, genetic advance and correlation between grain yields and yield attributing traits of advanced inbred determinate lines. Thirty nine lablab F_5 inbred lines and a local determinate accession were evaluated at KALRO Katumani and Thika using randomized complete block design (RCBD) with two replications in 2017. Significant differences (P< 0.05) were observed among the genotypes for all the characters. Phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were highest for seed weight per plant and the lowest for maturity traits. Broad heritability for the 11 characters was moderate to high ranging from 0.40 - 0.86. The highest genetic gain (48.53%) was recorded on seed weight per plant and lowest on the maturity related traits. Pods number (r = +0.87) and raceme number (r = +0.81) had the highest positive and significant (P> 0.05) correlation with seed yield per plant. Path analysis revealed that pods per plant (0.68), racemes per plant (0.25) and pods per raceme (0.13) had the largest direct effect on seed yield. The study identified, moderate to high heritability and genetic advance estimates and significant positive correlations of pods per plant, raceme per plant, plant height, pod width, pods per raceme and number of flower nodes. The same traits also had high direct and indirect effects on seed yield and therefore suitable for phenotypic selection of improved determinate lablab genotypes. The results of the study are discussed in light of crop improvement of this leguminous crop.

Key words: Lablab, heritability, genetic gain, path analysis, determinate, yield.

INTRODUCTION

Lablab (*Lablab purpureus* (L.) Sweet) is a multipurpose leguminous crop commonly used for food, feed, soil conservation, weed management and medicine (Kamau et al., 2021; Kimani et al., 2012). In Kenya, the annual demand for this commodity is higher than the availability leading to importation from neighbouring countries (AFFA, 2016). The shortage is due to low productivity at farmer's field, which is attributed to cultivation of

*Corresponding author. E-mail: eliezahngware@yahoo.com.

genotypes with low yield potential and long maturity duration (Kamotho et al., 2016). The crop is predominantly grown by small holder farmers in semi-arid environments characterized by dwindling seasonal rainfall (Bosire et al., 2019). Production of late maturing cultivars in semi-arid areas under rain-fed conditions subjects the crop to the end of season drought stress which leads to further yield loss (Sennhenn, 2015). There is need to develop higher yielding varieties that are early maturing to cushion farmers from complete crop failure due to end of season moisture stress.

Majority of the lablab landraces and varieties frequently used by Kenyan farmers are not only late maturing but also have indeterminate growth habit thereby limiting their utilization especially under intercropping system (Kamotho, 2015). Cereal/lablab intercropping system is very common among lablab small holder farmers with limited arable land (Kamotho et al., 2010). Intercropping enables the farmers to produce diverse crop species within the same field and season thus minimizing risks associated with crop failure (Bonginkosi et al., 2018). The current practice is where the farmers intercrop the cereals with indeterminate lablab cultivars. Under the cereal/lablab intercropping system, the indeterminate and aggressive lablab varieties become very vegetative and climb on, pull down and lodge the intercrop cereal resulting in yield reduction of both the cereal and lablab crop (Kamotho, 2015; Kgasago, 2006). In lablab, the determinate growth habit is characterized by the main axis terminating into inflorescence. This type of growth habit has been associated with reduction of flowering and maturity period (Keerthi et al., 2014; Keerthi et al., 2016). Varieties with determinate bush growth habit are also suitable for production under cereal legume intercropping system which dominates most of lablab growing areas in Kenya. Therefore, development of higher yielding varieties that combine both early maturity and determinate growth habit can enhance lablab production and productivity in marginal areas and under cereal legume intercropping system.

Progress of selecting genotypes with high potential in crop improvement program rests on availability of phenotypic and genotypic variability of targeted agronomic traits in the population (Lagat et al., 2019). In addition, the understanding of other genetic parameters such as genetic advance estimates and heritability are important to predict the gains from selection (Holland et al., 2010) . A breeder expects to increase the population mean of the traits in the next generation through the selection of those individuals with high genetic potential. The response to selection (genetic gain or genetic advance) is the change of population mean between generations following selection (Acquaah, 2012). The genetic gain attained through selection depends on the available phenotypic variation, heritability of the trait being selected and the selection pressure imposed by the breeder. Heritability is the proportion of the phenotypic variance that is due to genetic effects. A high heritability is likely to contribute to high response to selection and thereby advancing the population in the desired direction of change (Acquaah, 2012). However, better information is obtained when these parameters are considered together rather than individually (Asfaw et al., 2017). For example, a trait which combines high genetic coefficient of variation, genetic gain and heritability estimates are desirable because it indicates the trait is under additive gene action and therefore simple selection for the trait would be effective (Hailu et al., 2016).

Broad heritability and genetic gain estimates of yield contributing attributes in lablab has been reported by several authors (Venkatesha et al., 2007; Parmar et al., 2013; Singh et al., 2015; Salim et al., 2014; Sadak et al., 2018). However, the information on genetic parameters of important agronomic traits of local lablab populations under Kenyan conditions is still lacking, hence the need to generate the information. Holland et al. (2010) reported that heritability and genetic advance of crop traits are affected by the genetic composition of the population and the growing environment.

Grain yield is a complex quantitative trait that is influenced by a number of yield contributing characters (Ashebr et al., 2020). Identification of characters that correlate with yield and understanding their relationships will allow an indirect selection of yield based on those characters. Correlation coefficient estimates the magnitude and direction of components influencing the main character such as yield. Path coefficient analysis (PCA) gives more information than simple correlations coefficient by partitioning both direct and indirect effects, thereby revealing the importance of each component in determining the trait of interest (Gelalcha and Hanchinal, 2013).

The use of correlation coefficients jointly with path coefficient analysis to understand trait associations has been widely reported (Hassan et al., 2013; Machikowa and Laosuwan, 2011; Vu et al., 2019; Sayo et al., 2017; Salim et al., 2014). For instance, Salim et al. (2014) found that days to flowering, number of pods/plant, pod yield/plant, pod length, number of seeds/pod, number of seeds/plant, 100-seed weight influenced lablab seed yield/plant directly in positive direction. Pramod et al. (2011) reported that number of pods per plant, pod length, pod width and seed length had positive effect on pod yield per plant while days to first flowering had negative effect. However, through path coefficient analysis, they found highest indirect effect on pod yield/plant was through days to first flower, days to first picking and per cent fruit set/cluster. However, there is limited information on association of yield related traits of local genotypes of lablab in Kenya. Therefore, this study was carried out to estimate the genetic parameters of advanced inbred lablab lines, assess relationship between their yield and yield components and determine the direct and indirect effects of different yield-related

traits on grain yield.

MATERIALS AND METHODS

Plant materials

Five local lablab indeterminate genotypes (Njoro, GBK 028663, DL1002, Kagio and Kahuro) and a determinate accession (KDD) were used to generate the population used in this study. Njoro, Kagio and Kahuro are landraces with indeterminate growth habit, moderate maturity duration and with large black seeds. Njoro is commonly grown in rift valley region while Kagio and Kahuro are grown in central region of Kenya. Genotype GBK 028663 is an accession from gene bank of Kenya (GBK) which has indeterminate growth habit, moderate maturity and with brown spotted seeds. DL1002 is a released variety in Kenya and has indeterminate growth habit, moderate maturity with black seeds. The accession KDD was collected from a market in Nairobi, Kenya, has determinate growth habit, early maturity and with small sized cream coloured seeds. However, this accession is not reported to be grown in any region of Kenya and could be an introduction from outside the country.

Population generation

The six parental genotypes were planted in plastic pots in a screen house at KALRO Thika in April 2014. The parents were planted three times at one week interval in order to synchronise the flowering of the genotypes. Crosses were made between the determinate parent and all the other indeterminate parents using the technique described by Rangaswami and Kunhi (1935). The F_1 seeds from all the five crosses were harvested and bulked together to form a composite bulk. The F_1 seeds were planted in a screen house in October of 2014 and allowed to self-pollinate to generate F_2. All the F_2 seeds were then space planted in the field during the long rains of 2015 to raise F_2 plants. All the F_2 plants with determinate growth habit were selected and F_3 seeds harvested and bulked. A sample of determinate F_3 seeds was planted during the short rains of 2015 to raise F_3 plants. About 400 F_3 determinate plants were selected and their seeds harvested individually. Four hundred progeny rows from the $F_{3\text{-}4}$ seeds were raised in the field during the long rains of 2016. A spacing of 50 cm between rows and 20 cm within rows was used. Each progeny row was 2 m long with about 10 plants. At maturity, a total of 39 progeny rows were selected based on maturity period, number of pods per plant, plant height and seed colour. The selection tried to capture as much variability of these traits as possible. The F_5 seeds of the selected rows were harvested separately. These seeds were used to study the relationship between grain yield and its related traits.

Experimental design

The study was carried out at two locations in Kenya Agricultural and Livestock Organization (KALRO) centres at Katumani in Machakos and at Thika in Kenya during the April to June rainy season of 2017. KALRO Katumani and Thika are located at coordinates 1° 35' S and 37° 14'E and 0° 59' S and 37° 04'E respectively. In each site, 39 F_5 inbred lines together with their determinate parent (KDD) were planted using randomized complete block design (RCBD) with two replications. The plot size was two rows of 2 m long each. A basal application of Di-ammonium phosphate (DAP) fertilizer at a rate of 150 kg ha^{-1} was done in the planting furrows during planting. One seed was planted in the furrow at a spacing of 50 × 25 cm between and within rows respectively giving a population of 8 plants per m^2. Hand weeding was done two times at the first trifoliate and pre-flowering growth stages. The crop was sprayed with recommended insecticides to control insect pests.

Data collection

For each trial, plant height at physiological maturity stage, number of pods per plant at maturity, number of racemes per plant at maturity, pod width and length at pod filling stage, number of primary branches per plant, number of pods per raceme (main raceme) at maturity, number of flowering nodes at 50% flowering, days to 50% flowering, days to 75% pod maturity, 100 seed weight and grain yield per plant were recorded. The data on days to 50% flowering, days to 75% pod maturity and 100 seed weight was on plot basis while the other traits were taken from six randomly selected plants per plot. The grain yield weight was obtained at approximately 12% moisture content.

Data analysis

Data for each trait was subjected to analyses of variance (ANOVA) using a GENSTAT ed. 15 statistical program to estimate the genetic variability of the selected genotypes and to partition the phenotypic variability into components due to genetic and environmental factors. Measures of variability such as genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), broad sense heritability (h^2), and genetic advance (GA) based on percentage of the mean were estimated. The genetic parameters were estimated using formulas adopted from Allard (1960) and Singh and Chadhary, (1985) as follows:

σ^2G = (Mean Square Genotype - Mean Square Error)/r
σ^2P = (Mean Square Genotype)/*r*
σ^2e = Mean Square Error/*r*

r is the number of replications. σ^2P is the phenotypic variance, σ^2e is environmental variance while σ^2G is the genotypic variance. The Mean Square Genotype (MSG) and Mean Square Error (MSE) are variance components estimated as functions of the mean square estimates from ANOVA table. Mean square genotype (MSG), estimates genotypic variance and is the observed variance among the line mean. Mean square error (MSE) measures variance from plot residuals. Phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) are estimated using the following formulas:

PCV% = $(\sqrt{\sigma 2P})/x * 100$
GCV% = $(\sqrt{\sigma 2G})/x * 100$

σ^2P represents the phenotypic variance: σ^2G represents the genotypic variance, while x represents the grand mean. Heritability (h^2B) expressed as the percentage of the ratio of the genotypic variance (σ^2G) to the phenotypic variance (σ^2P) was estimated based on the genotypic grand mean. Expected genetic advance (GA) was estimated using a formula of Allard (1960).

GA = K (Sp) h^2B,
GA (as % of mean) = (GA/$\bar{x}$) x100

Where h^2B and Sp is the heritability ratio and the phenotypic standard deviation respectively. K is a selection differential that varies depending on the selection intensity. In the present analysis 2.06 was considered for K.

Correlation coefficient (*r*) was used in the study to determine inter-relations between 11 quantitative characters. Pearson correlation coefficients between traits were generated using the

Table 1. Analysis of variance of 9 yield and yield related traits of 39 F_5 inbred genotypes and their determinate parent evaluated at Thika and Katumani sites in Kenya during the March to May season of 2017.

			Mean square								
Site	**S.O.V.**	**D.F**	**SWPP**	**100Sw**	**PPP**	**RPP**	**PL**	**PW**	**PH**	**DTF**	**DTM**
Thika	Rep	1	211.25	0.45	781.20	22.76	0.27	0.003	92.02	1.51	1.80
	Geno	39	111.54***	13.15**	239.20*	5.60*	0.27***	0.06***	187.61*	20.91*	14.33**
	Error	39	41.14	6.50	125.70	3.14	0.08	0.009		12.54	5.56
	Total	79									
Katumani	Rep	1	337.57	1.80	147.60	13.41	1.61	0.14	18.24	0.05	36.45
	Geno	39	105.89***	19.91***	268.8**	4.42*	0.32***	0.09***	325.52***	7.15***	85.5***
	Error	39	36.46	3.44	106.1	2.53	0.12	0.018	50.33	1.43	16.17
	Total	79									

SWPP= seed weight per plant, 100SW=100 seed weight, PPP=pods per plant, RPP= raceme per plant, PL=pod length, PW= pod width, PH=plant height, DTF= days to flowering, DTM= days to maturity; ***, **, * is significant at the 0.001, 0.01, 0.05 level respectively.

IBM SPSS statistics version 20 procedure. Correlations were based on two locations averages. The significance for correlation coefficient was tested on a two-tailed test on the same program.

Using the same software, a linear regression analysis was carried out to estimate the relationship between seed yield per plant (dependent variable) and the other 10 independent variables. Validity of P values for the t-test was determined by testing the normality of residuals. A test on multicollinearity among the various predictors was also done. Path coefficient analysis for seed yield per plant was carried out as demonstrated by Dewey and Lu (1959). The ten characters, as in the linear regression analysis were included in the path coefficient analysis for single plant yield.

RESULTS

Genotypic and phenotypic variance of determinate lablab characters

Significant differences were observed among the genotypes for all the characters suggesting presence of high amount of variability for the characters studied. The mean sum of squares for 9 characters in 39 genotypes and one check accession of lablab are presented in Table 1. The estimates of genotypic variance (σ^2G), phenotypic variance (σ^2P), phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV), heritability (in a broad sense), and genetic advance as a percentage of the mean were analysed for Thika site (Table 2) and Katumani site (Table 3).

High range of variation in Thika site was recorded for seed weight per plant (5- 42 g), pods per plant (9-68), plant height (26-82 cm) and for 100 seed weight (14- 30 g), while in the Katumani site the ranges for seed weight per plant was 13-51 g, pods per plant (20- 88), plant height (46 - 143 cm) and for 100 seed weight was 14 - 30 g. Low range of variation was observed for days to flowering and days to maturity in both sites.

In the present investigation, the σ^2P was higher than the corresponding σ^2G for all the characters evaluated at both sites. For most of the characters studied, the two values differed moderately suggesting that the expression of these characters was reasonably influenced by the environment. PCV and GCV was high for number of racemes per plant at 33.5% (PCV) compared to 22.3% (GCV) in Thika and 21.24% (PCV) compared to 14% (GCV) at Katumani.

Heritability (H^2) expressed as the percentage of the ratio of the genotypic variance (σ^2G) to the phenotypic variance (σ^2P) was estimated for each character in the two sites (Tables 2 and 3). At Thika site, broad sense heritability estimates ranged from 0.86 for pod width to 0.4 for days to flowering, whereas heritability was highest for plant height at 0.85 and lowest for number of racemes per plant at 0.43 at Katumani site. Most of the characters recorded broad sense heritability of more than 0.5 at Thika while the values were more than 0.6 for most of the characters at Katumani site. There was higher broad sense heritability estimates at Katumani site for days to flowering (0.81), days to flowering (0.80), plant height (0.85) and 100SW (0.83) compared to 0.61, 0.40, 0.49 and 0.51 respectively for the same characters at Thika site.

The genetic advance (GA) shows the extent of gain in a trait which is attained under a particular selection pressure. In this study, selection pressure of 5% was considered. The genetic advance was expressed as percentage of the mean (GAM) of the trait for easier comparison amongst traits with different measurements units. The results showed highest GAM for seed weight per plant of 48.53 and 37.80% at Thika and Katumani respectively whereas the lowest GAM was recorded for days to maturity (3.37%) at Thika and days to flowering (5.55%) at Katumani. In addition, pods per plant and raceme per plant showed relatively high estimates of genetic advance of 33.4% and 30.57% respectively, at Thika site. The other traits that displayed higher estimates GAM at Katumani experiment were pods per

Table 2. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variations and genetic advance as percent of mean for characters of 39 F_5 inbred lines and their determinate parent studied at Thika site in Kenya.

Traits	σ²G	σ²P	σ²E	Mean (g)	Range (g)	PCV	GCV	ECV	H^2	GA	GAM (%)
Seed weight per plant	35.18	55.75	20.57	20.00 ± 1.00	5 - 42	37.33	29.66	22.68	0.63	9.71	48.53
100 SW	3.32	6.57	3.25	20.88 ± 0.35	14 - 30	12.28	8.73	8.63	0.51	2.67	12.78
Pods per plant	56.75	119.60	62.85	32.00 ± 1.62	9 - 68	34.18	23.54	24.77	0.47	10.69	33.41
Raceme per plant	1.25	2.82	1.57	5.00 ± 0.24	1 -10	33.56	22.32	25.06	0.44	1.53	30.57
Pod length	0.10	0.14	0.04	5.10 ± 0.05	3.9 – 6.9	7.20	6.04	3.92	0.70	0.53	10.44
Pod width	0.030	0.034	0.00	1.70 ± 0.02	1.3 – 2.0	10.60	9.84	3.95	0.86	0.32	18.82
Plant height	45.92	93.81	47.89	51.00 ± 1.32	26 - 82	18.99	13.29	13.57	0.49	9.77	19.15
Days to flowering	4.19	10.46	6.27	50.54 ± 0.45	46 -59	6.40	4.05	4.95	0.40	2.67	5.28
Days to maturity	4.38	7.16	2.79	100.00± 0.35	94 - 104	2.68	2.09	1.67	0.61	3.37	3.37

S.E Mean= Standard error of the mean, σ²G = Genotypic variance, σ²E = Environmental variance, σ²P = Phenotypic variance, H^2 (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation, (%) GA= Genetic advance, GAM= Genetic advance as percent of mean.

Table 3. Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variations and genetic advance as percent of mean for characters of 39 F_5 inbred lines and their determinate parent studied at Katumani site in Kenya.

Traits	σ²G	σ²P	σ²E	Mean(g)	Range (g)	PCV	GCV	ECV	H^2	GA	GAM (%)
Seed weight per plant	34.72	52.95	18.23	26 ± 0.97	13 - 51	27.99	22.66	16.42	0.66	9.83	37.80
100 SW	8.23	9.95	1.72	21.30 ± 0.38	14 - 30	14.81	13.47	6.16	0.83	5.37	25.23
Pods per plant	81.35	134.40	53.05	42 ± 1.53	20 - 88	27.60	21.47	17.34	0.61	14.46	34.42
Raceme per plant	0.96	2.21	1.25	7.00 ± 0.21	4 - 13	21.24	14.00	15.97	0.43	1.33	19.00
Pod length	0.10	0.16	0.06	5.1 ± 0.05	4 – 6.3	7.84	6.20	4.80	0.63	0.52	10.10
Pod width	0.04	0.05	0.01	1.7 ± 0.03	1.3 – 2.1	12.89	11.62	5.58	0.81	0.37	21.57
Plant height	137.6	162.7	25.17	70.4 ± 1.52	46 - 143	18.12	16.66	7.13	0.85	22.22	31.56
Days to flowering	2.85	3.58	0.73	55.8 ± 0.23	53 - 62	3.39	3.02	1.53	0.80	3.10	5.55
Days to maturity	34.6	42.75	8.09	99.08 ± 0.80	90 - 120	6.60	5.94	2.87	0.81	10.92	11.02

S.E Mean= Standard error of the mean, σ²G = Genotypic variance, σ²E = Environmental variance, σ²P = Phenotypic variance, H^2 (%) = Broad sense heritability, GCV (%) = Genotypic coefficient of variation, PCV (%) = Phenotypic coefficient of variation, (%) ECV= Environmental coefficient of variation, (%) GA= Genetic advance, GAM= Genetic advance as percent of mean.

plant (34.42%), 100 seed weight (25.23%) and plant height (31.56%). The maturity related traits (days to 50% flowering and days to maturity) and pod length consistently showed lowest GAM of less than 12% in both sites.

Correlation coefficients among traits

The Pearson correlations coefficients calculated among the 11 traits averaged over the sites are presented in Table 4. The correlations were based on the calculated means of the genotypes for Thika and Katumani experiments. The study showed that all the characters were positively and significantly ($P< 0.05$) correlated to seed weight per plant with exception of 100 seed weight and

Table 4. Correlation coefficients among 11 characters estimated from 39 F_5 inbred lines and their determinate parent.

Traits	SWPP	100 SW	PPP	RPP	PL	PW	PPR	NFN	PH	DTF	DTM
Seed weight per plant (SWPP)	1	0.086	0.869**	0.811**	0.025	0.223**	0.203**	0.461**	0.515**	0.254**	0.182*
100 SW		1	-0.13	0.056	-0.038	0.102	-0.279**	-0.068	0.128	0.061	0.087
Pods per plant (PPP)			1	0.752**	0.019	0.059	.411**	0.487**	0.435**	0.208**	0.079
Raceme per plant (RPP)				1	-0.024	0.12	0.13	0.429**	0.593**	0.386**	0.072
Pod length (PL)					1	0.019	-0.085	0.013	0.021	0.065	0.072
Pod width (PW)						1	-0.058	-0.019	0.086	0.127	0.275**
Pods per raceme (PPR)							1	0.584**	0.124	-0.06	-0.165*
No. flower nodes (NFN)								1	0.410**	0.086	-0.061
Average plant height (PH)									1	0.500**	0.138*
Days to flowering (DTF)										1	0.426**
Days to maturity (DTM)											1

***, **, * Correlation is significant at the 0.001, 0.01, 0.05 level respectively.

pod length. Pods number (r = +0.87) and raceme number (r = +0.81) seems to contribute significantly to seed weight per plant which suggests that indirect selection for seed weight per plant can be effectively realized by selecting for the higher number of pods and raceme per plant.

In addition, moderate significant correlations was observed for seed weight per plant and number of flowering nodes per raceme (r=+0.46) and plant height (r=+0.52). The genotypes that produced many pods per plant also had many racemes per plant as shown by the high positive correlations (r=+0.75) between the two traits. Similarly, tall plants tended to produce many racemes as indicated by relatively high positive corrections (r=+0.60) between the two traits. Moderate positive correlations were recorded between pods per plant and pods per raceme (r=+0.41), number of nodes per raceme (r=+0.49) and plant height (r=+0.44). Genotypes with many racemes per plant, pods per raceme and big plant height tended to have many flowering nodes per raceme as indicated by their positive moderate correlation of 0.43, 0.58 and 0.41 respectively. The days to flowering exhibited some moderate positive correlations of r=+0.50 and r=+0.43 for plant height and days to maturity respectively. Low but significantly negative correlations was recorded for 100 seed weight and the number of pods per raceme (r= -0.28).

Path analysis

The analysis of variance (ANOVA) indicated that the regression model of the 10 independent variable on seed weight of the lablab genotypes was significant at P< 0.001 (Table 5). The regression coefficients from the model were therefore used for undertaking the path analysis. The adjusted R square was also high at 0.860.

The regression coefficients and collinearity statistics of the causal factors on seed weight per plant of lablab genotypes are presented in Table 6. The beta standardized coefficients ranged from 0.68 for pods per plant to -0.08 for days to flowering. The regression coefficients for all the independent variables were significant at P< 0.05 except for pod length and plant height. Collinearity implies that two variables are linear combinations of each other. As the collinearity increases, the regression coefficient estimates become unstable. Collinearity statistics consists of tolerance and variance inflation factors (VIF). The tolerance and VIF statistics for the independent variables considered in this study were within the acceptable range of > 0.10 for tolerance and < 10 for VIF (Hair et al., 2010).

A path coefficient analysis which gives indirect effects for each independent variable on the dependent variable is presented in Table 7. Among the 10 independent traits (causal), eight of them had positive direct effect on seed yield per plant (dependent). These were 100 seed weight, pods per plant, racemes per plant, pod length and pod width, number of flowering nodes, plant height and days to maturity. Pods per raceme and days to maturity had negative direct effect on seed

Table 5. ANOVA and summary of regression model of 10 independent variables on seed weight per plant of 39 F_5 inbred lines and their determinate parent.

ANOVA of Seed weight per plant				Regression Model summary			
Model	**Sum of Squares**	**DF**	**Mean Square**	**R**	**R Square**	**Adj. R Square**	**Std. Error of the Estimate**
Regression	14286.209	10	1428.621***	0.932	0.869	0.860	3.803
Residual	2155.485	149	14.466				
Total	**16441.694**	**159**	-	-	-	-	-

*** is significant at the 0.001 level .

Table 6. Regression coefficients and collinearity statistics of 10 independent variables on seed weight per plant of 39 F_5 inbred lines and their determinate parent.

Model	Unstandardized coefficient		Standardized coefficient	T	Collinearity statistics	
	B	**Std. err**	**Beta**		**Tolerance**	**VIF**
Constant	-23.494	7.284	-	-3.225***	-	-
100 SW	0.337	0.100	0.108	3.380***	0.863	1.159
Pods per plant	.442	0.035	0.681	12.745***	0.309	3.241
Raceme per plant	1.027	0.234	0.248	4.392***	0.276	3.626
Pod length	0.145	0.674	0.007	.216ns	0.961	1.041
Pod width	5.561	1.446	0.120	3.846***	0.903	1.108
Pod per raceme	-.346	0.117	-0.126	-2.948***	0.482	2.076
No of flower nodes	0.395	0.174	0.096	2.272*	0.490	2.041
Plant height	0.034	0.026	0.054	1.299ns	0.509	1.963
Days to flowering	-0.201	0.096	-0.082	-2.094*	0.574	1.743
Days to maturity	0.148	0.065	0.080	2.270*	0.709	1.410

***, **, * regression coefficients is significant at the 0.001, 0.01, 0.05 level respectively.

yield per plant. Pods per plant, racemes per plant, pod width and 100 seed weight had the largest direct effect on seed weight yield respectively. Raceme per plant, pods per raceme, number of flowering nodes per raceme and plant height had fairly high indirect positive effects through pods per plant (0.51, 0.28, 0.33 and 0.30) respectively. The effects of these four traits on seed weight through pods per plant were larger than their respective direct effects. Even though the direct effect of days to flowering is negative, its indirect effects through pods per plant is positive and substantial. Pods per plant and number of flowering nodes had small indirect negative effect of -0.05 and -0.07 respectively through pods per raceme. Small negative indirect effect of pods per plant through 100 seed weight (-0.085 was recorded)

DISCUSSION

Genotypic variability is prerequisite for progress of any breeding program. In conventional plant breeding, variability is created through crossing (hybridization) of plants which carry the desired genes followed by discrimination among the variability (selection) to identify the most desirable recombinant (Acquaah, 2012). Success in improvement of the desired traits requires presence of many recombinants with wide range of targeted character from which selection can be done (Odouri, 2008). In this study, the variability of some determinate recombinant lablab lines derived from crossing early maturing determinate accession with the local indeterminate landraces were evaluated. The highly significant difference in mean squares implied that there is distinguishable evidence of inherent genetic variability among the lablab lines with respect to seed weight per plant, 100 seed weight, number of pods per plant, raceme per plant, plant height, days to 50% flowering and days to maturity. Wide range of variation was shown for most of the traits except for days to 50% flowering and maturity. The presence of variability for most traits offers adequate variation upon which to establish a breeding program. The narrow range of variation observed on maturity traits could be explained by the fact that all the lines evaluated in this study were of determinate growth habit. Selection of genotypes with determinate growth habit at early generation population could also have resulted in selection of early flowering and maturing genotypes. The mean number of days to flowering (50-

Table 7. Path coefficient analysis showing direct effect (bold) and indirect effects of 10 characters on seed yield per plant in lablab bean based on 39 F_5 inbred lines and their determinate parent.

Character	100SW	PPP	RPP	PL	PW	PPR	NFN	PH	DTF	DTM
100 seed weight (100SW)	**0.108**	-0.085	0.014	-0.001	0.012	0.035	-0.007	0.007	-0.005	0.007
Pods per plant (PPP)	-0.085	**0.681**	0.187	0.000	0.007	-0.052	0.047	0.023	-0.017	0.006
Raceme per plant (RPP)	0.006	0.512	**0.248**	0.000	0.014	-0.016	0.041	0.032	-0.032	0.006
Pod length (PL)	-0.004	0.013	-0.006	**0.007**	0.002	0.011	0.001	0.001	-0.005	0.006
Pod width (PW)	0.011	0.040	0.030	0.000	**0.120**	0.007	-0.002	0.005	-0.010	0.022
Pod per raceme (PPR)	-0.030	0.280	0.032	-0.001	-0.007	**-0.126**	0.056	0.007	0.005	-0.013
No. of flower nodes (NFN)	-0.007	0.331	0.106	0.000	-0.002	-0.074	**0.096**	0.022	-0.007	-0.005
Plant height (PH)	0.014	0.296	0.147	0.000	0.010	-0.016	0.039	**0.054**	-0.041	0.011
Days to flowering (DTF)	0.007	0.142	0.096	0.000	0.015	0.008	0.008	0.027	**-0.082**	0.034
Days to maturity (DTM)	0.009	0.054	0.018	0.000	0.033	0.021	-0.006	0.007	-0.035	**0.080**
Total effects	**0.085**	**0.797**	**0.811**	**0.026**	**0.223**	**0.203**	**0.461**	**0.515**	**0.254**	**0.182**

Bold and diagonal figures indicate direct effect; Residual effect: 0.14.

55) and maturity (99-100) of the determinate lines tested in this study (Tables 2 and 3) are lower than those reported on indeterminate local landraces by Kamotho (2015). This indicates that selection of determinate growth habit in lablab can result in selection for early flowering and maturing genotypes. Earliness to flowering and maturity has been reported to be linked to determinate growth habit in some legumes (Keerthi et al., 2014; Repinski et al., 2012; González et al., 2016).

The study showed that the phenotypic variance was higher than the genotypic variance in all the traits studied across the sites. Progress from selection depends on the availability of genetic variability in the population and selection is more effective when there is high genetic variation in relation to environmental variation. In this study, the magnitude of the genotypic variance for seed weight per plant, 100 seed weight, pod length, pod width and days to maturity yield components were consistently higher than their respective environmental variance in both sites. This implies that significant improvement for these traits can be achieved through phenotypic selection (Manggoel et al., 2012). Variability in quantitative characters of lablab was also reported by Verma et al. (2015) and Salim et al. (2014).

The genotypic and phenotypic variance estimates and the range of mean values of traits can give a rough estimate about the magnitude of variation present among different genotypes. However, genotypic coefficient of variation is better in revealing the extent of variability present within the genetic materials and its estimate gives good implication for genetic potential in crop improvement through selection (Burse et al., 2015). According to Hailu et al. (2016) PCV and GCV values > 20% are regarded as high, while values between 10 and 20% medium and values < 10% are considered low. In this study, high PCV and GCV values of > 20% were observed for seed weight per plant and pods per plant in all the sites. In addition to this, these characters recorded medium to high heritability (Tables 2 and 3) suggesting the presence of additive gene effects and therefore possibility of improvement through phenotypic selection of these traits. Singh et al. (2015) and Parmar et al. (2013) in lablab and Asante et al. (2009) in mung bean have reported high PCV and GCV and moderate heritability for number of pods per plant. However, heritability values reported for pods per plant in this study (0.49 for Thika and 0.61 for Katumani) is lower than those reported by Pramod et al. (2011), Verma et al. (2015) and Salim et al. (2014) in lablab but was higher than that of Chaitanya et al. (2014). The discrepancies of heritability values could be due to nature of test materials and environment where experiments were conducted. The low PCV and GCV values and moderate to high heritability observed in this study agrees with that of Singh et al. (2015) in lablab. Generally, the differences between PCV and their corresponding GCV values for all characters with exception of racemes per plant was small to moderate indicating that these characters were less influenced by the environment. The high difference between GCV and PCV for raceme per plant and its corresponding moderate heritability in both sites suggest that selection for this trait using observed variation may be less effective since the proportion of additive gene effect is low.

Successful selection based on phenotype is possible in characters with large heritability estimates, however use of heritability together with genetic advance estimates is more reliable in guiding selection (Ayalew et al., 2011). Genetic advance (GA) is the gain of genotypic value of a new population compared with the base population resulting from one cycle of selection in a given selection intensity (Hailu et al., 2016). In this study, high heritability coupled with relatively high genetic advance as percent of mean was observed for seed weight per plant, pods per plant, pod width and plant height (Tables 2 and 3). This suggests that these traits are under additive gene

action and selection based on the phenotypes will be effective. Our results were similar with the findings of Chaitanya et al. (2014), Veerendra et al. (2014) and Singh et al. (2013) for pods per plant, Pramod et al. (2011) and Parmar et al. (2013) for pod width, Singh et al. (2015) and Verma et al. (2015) for plant height, Salim et al. (2014) and Singh et al. (2013) for seed yield per plant. Moderate to high heritability coupled by low genetic advance as percentage of mean was observed for days to 50% flowering and maturity (Tables 2 and 3). The low genetic advance of these two maturity related traits could be as a result of the small phenotypic variance of the test materials. This is because genetic advance has direct relationship with standard deviation of the population and heritability. In this study, all the test materials are of determinate growth habit, a trait that is associated with earliness to maturity (Keerthi et al., 2014) and this could have contributed to narrow phenotypic variability for these maturity traits and consequently low genetic advance. However, the moderate to high heritability and low genetic advance of these two traits could also be as a result of influence of non- additive gene action and considerable influence of the environment. This suggests that based on the evaluated determinate lablab lines in this study, days to flowering and maturity characters can only be partially improved through phenotypic selection. Simmilar results of moderate to high heritability coulped by low genetic advance for days to 50% flowering and maturity has been reported by Singh et al. (2015) and Verma et al. (2015) in lablab and Veerendra et al. (2014) in pigeon peas.

Plant breeders are rarely interested with one character and therefore there is need to study the association between various characters and especially between yield and other traits (Tadele et al., 2014). A good understanding of the relationship of plant characters and the yield is essential because the final yield is the sum total of effects of all its related traits (Verma et al., 2015). The knowledge of the association of grain yield and its related traits of the determinate lablab genotypes will allow an indirect selection of yield based on those characters. In the present study, correlation coefficient (*r*) was used to determine associations of yield related traits of the determinate lablab genotypes. Correlation coefficient ranges between -1 and 1 with correlation of 0 implying that there is no linear relationship between the variables while -1 or 1 suggests total linear relationship.

This study identified that the number of pods and racemes had high significant correlation with seed weight per plant. The results are in agreement with those of Salim et al. (2014) in lablab, Tadele et al. (2014) in lentil and Manggoel et al. (2012) in cowpeas. In determinate lablab genotypes, seeds are contained in pods borne on the axillary or terminal racemes and therefore genotypes with many pods and racemes are likely to contain many seeds and therefore high seed yield. This suggests that in breeding programs, selection for high grain yield can be effectively realized through the indirect selection for traits that are visually easy to score like high number of pods and racemes. Other traits with moderate to low significant positive correlation with grain yield per plant include days to 50% flowering, maturity pod width, plant height and flowering nodes per raceme. This suggests that those lines which, flowered and matured late, with longer stem height, many flowering nodes and many racemes and pods produced high grain yield. Generally, in absence of production constraints such as moisture stress, late flowering and maturing varieties are likely to have an advantage in gaining more plant height and grain productivity since the total amount of photosynthates received from the leaves is greater than for early maturing varieties (Yamada et al., 2012).

Through path coefficient analysis, the total correlation between traits is partitioned into direct and indirect effect which forms a better basis for selection to improve yield (Manggoel et al., 2012). Direct effects measure the sensitivity of the dependent variable to changes in the independent variable by one unit while all other factors are held constant. In contrast, the indirect effect quantify the changes on dependent variable when the independent variable is held constant and the intermediary variable changes by the amount it would have changed had the independent variable increased by one unit (Pearl, 2001). In this study, the number of pods per plant had the highest direct positive effect on seed yield per plant. High direct effects of number of pods per plant on seed yield has been reported by Salim et al. (2014), Singh et al. (2011), Singh et al. (2015) and Verma et al. (2015) in lablab, Veerendra et al. (2014) in French beans and Machikowa and Laosuwan (2011) in Soybean. Moderate positive indirect effect on seed yield through pods per plant was detected for raceme per plant, pods per raceme, flowering nodes per plant and plant height. This suggests that selection of high number of units of these characters can be effective in selection of high seed yield in determinate lablab genotypes. The negative direct effect of days to flowering and 100 seed weight on grain yield per plant observed in the current study is in agreement with the findings of Singh et al. (2011) in lablab. However, the negative effect of these two traits is cancelled by positive indirect effects through other traits. The overall positive association (sum of direct and indirect effects) of plant height, days to flowering and maturity and yield suggests that there will be a problem when combining dwarfness, earliness to flowering and maturity with high seed yield. Development of early maturing lines is suitable for drought prone areas or where early cessation of rainfall is prevalent while short determinate lablab lines are essential in maize-lablab intercropping system. Our results therefore imply that a compromise on the seed yield has to be made in selection program of suitable lablab varieties for areas with early cessation of rainfall and under intercropping system.

Conclusion

In the foregoing discussion, it can be concluded that the materials used in this study had substantial genetic variability. The level of genetic variability observed for various traits would be beneficial for breeding varieties of lablab that are high yielding and with determinate growth habit. The characters studied also showed some considerable heritability which can warrant selection of improved genotypes. This study identified, moderate to high heritability and genetic advance estimates and significant positive correlations of pods per plant, raceme per plant, plant height, pod width, pods per raceme and number of flower nodes. The same traits also had high direct and indirect effects on seed yield. These traits could therefore be used as suitable selection criteria for effective improvement in yield of determinate lablab genotypes.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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