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Research Article
Genetic Variability, Heritability and Genetic Advance of Some Haricot Bean (*Phaseolus vulgaris* L.) Varieties at Bench-Maji Zone, Southwest Ethiopia

Wondwosen Wondimu and Abebe Bogale

Department of Plant Science, College of Agriculture and Natural Resources, Mizan-Tepi University, P.O. Box 260 Mizan Teferi, Ethiopia

Abstract

Background and Objective: Assessing variability is fundamental to identify the most important traits in haricot bean improvement program. The objective of the present study was to estimate variability, heritability and genetic advance based on twelve morphological characters of haricot bean (*Phaseolus vulgaris* L.). **Methodology:** The experiment was conducted in 2015 and 2016 in main cropping season at 2 locations of Bench-Maji Zone by using randomized complete block design with 3 replications. The data were subjected to one way analysis of variance using SAS. **Results:** The results revealed significant differences ($p<0.05$) among genotypes for most characters at both locations. The maximum value between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was recorded for number of primary branches (12.6-4.9%) at South bench and plant height (11.6-6.8%) at Menit Shasha. High PCV was recorded for grain yield at both locations and hundred seed weight at South Bench and stand count and number of pod/plant at Menit Shasha. The GCV of high order was observed only for grain yield (20.6%) at South Bench. While, high order of GCV was observed for stand count (20.1%) and number of pod/plant (23.06%) at Menit Shasha. High heritability values were observed on most characters considered at both locations. High heritability coupled high genetic advance (as percentage of the mean) was observed for number of pods/plant, hundred seed weight and grain yield at both locations. Similarly biomass and harvest index at South Bench and primary brunch, stand count at harvest and number of seeds/pod at Menit Shasha were recorded. **Conclusion:** Therefore, any improvement of these characters would result in a substantial increment on grain yield. Evaluation for variability of haricot bean using conventional approach still could provide vital information but using contemporary molecular genetic analysis approaches such as mapping of quantitative trait loci using molecular markers is helpful to understand variability at molecular level, improve selection knowledge and arrive at more comprehensive conclusions.

Competing Interest: The authors have declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Phaseolus vulgaris L. belongs to the family *Fabaceae* usually called bean, common bean, haricot bean and kidney bean and field beans. In common, it is an annual crop, which thrives, in warm climate. It grows optimally at temperature of 18-24°C[1]. The crop grows well between 1400 and 2000 m above sea level[2]. In East African countries of Burundi, DR. Congo, Ethiopia, Kenya, Rwanda, Tanzania and Uganda, making this the most important region for the crop within the African continent[3].

Haricot bean is the most economically important pulse crop grown in Ethiopia. The crop is usually grown by subsistence farmers as a sole crop and/or intercropped with other crops. Considering the production volume and importance, it was noticed as a major pulse crop in many parts of the country. Accordingly, a continuous increase in area and volume of production has been registered. The national production of haricot bean in 2015 cropping season is estimated at over 540.24 thousand t, with a production area of 357.29 thousand hectares and average yield/hectare was about 1.48 t[3].

The average yield/hectare of haricot bean in Bench-Maji Zone is 1.796 t ha^{-1} which was far greater than the national annual average yield[3]. In reality, the area has possibly the highest potential for haricot bean production than any region in Ethiopia, its productivity has never reached full potential of production that has rated in research center (2.6-3.6 t ha^{-1})[4]. Several factors are accountable for this, in which infertility caused by moisture stress, soil reaction, lack improved varieties and biotic factors (disease and pest) are put in the top list[5].

Shortage of the improved varieties of common bean was the main problem that aggravates yield reduction in common bean in the study area. For this reason, assessing variability is fundamental to identify important traits for haricot bean improvement. Knowledge of genetic variability, heritability and genetic advance provide more reliable information on variability, heritable trait, nature and level of interrelation ship of haricot bean yield and yield components. Therefore, the present study was conducted to understand the nature and extent of genetic variability, heritability and genetic advance in some important traits of haricot bean genotypes.

MATERIALS AND METHODS

Description of the study areas: The experiments were conducted at two locations in Bench-Maji Zone during the 2015 and 2016 main cropping seasons. Lists of the testing locations in this study with their soil type, altitude, latitude and longitude of locations are presented in Table 1.

Experimental materials: A total, nine haricot bean genotype from Melkasa Agriculture Research Center and one local check were used in this study. List of nine haricot bean genotypes, code and origin are given in Table 2.

Experimental design and procedures: The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replication and the plot size was 2.1 m×4.8 m. The spacing was 0.4 and 0.1 m intra row and inter- row spacing, respectively and 1.5 m between adjacent blocks and 1 m between plots were left for easy of movement and management activities. Each genotype was sown at seed rate

Table 1: Descriptions of soil type, altitude, latitude and longitude of testing locations

Location	Altitude (m.a.s.l)	Temperature	Global positions	
			Latitude	Longitude
South Bench	1385	17-29°C	6°49′47″N	35°29′12″E
Menit Shasha	1150	20-32°C	6°52′N	35°21′E

Source: Bench Maji zone Agriculture and Natural resource office, 2015 and 2016

Table 2: Description of haricot bean genotypes origin, commercial value and color

Genotypes	Origin	Commercial value	Color
Local	Farmers of the districts	Food	Black
Awash Melka	MARC/MARI	Canning	White
Chercher	Haramaya University	Canning	White
Awash 1	HARC/HARI	Canning	White
Roba	MARC/MARI	Canning	White
Red Wolayita	HARC/HARI	Food	Red
Nasir	MARC/MARI	Food	Red
Gofta	Haramaya University	Canning	Grey
Mexican 142	MARC/MARI	Food	Creamy

of 85 kg ha^{-1}. The national recommended rates of fertilizer, 46 kg P_2O_5 ha^{-1} was used in the form of DAP. The whole dose was applied at planting. All crop management practices was carried out as per the time schedule and existing conditions of the study area.

Statistical analysis: The data were subjected to one way analysis of variance using SAS Version 9.1 software[6]. The significant difference among genotypes was tested by 'F' test at 1 and 5% levels of probability.

$$\text{Coefficient of variation (CV \%)} = \frac{\sqrt{\text{Error MS}}}{\text{Grand mean}} \times 100$$

The significance was tested by referring the table given by Snecedor[7].

Components of variance: The genotypic and phenotypic components of variance were computed according to formulae given by Burton and Devane[8] for the observed characters.

$$V_g = \frac{\text{MST} - \text{MSE}}{r}$$

Where:
$V_g (\sigma^2 g)$ = Genetic variance
MST = Mean square of treatment
MSE (Ve) = Error variance
r = Number of replications

Genotypic and phenotypic variance:

$$\sigma^2 g = \sigma^2 p - \sigma^2 e$$
$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where:
$\sigma^2 g$ = Genetic variance
$\sigma^2 p$ = Phenotypic variance
$\sigma^2 e$ = Error variance

Genotypic and phenotypic coefficient of variability: Genotypic and phenotypic coefficients of variability were computed according to the formula stated by Burton and Devane[8].

$$\text{Genotypic coefficient of variability (GCV)} = \frac{\sqrt{\sigma^2 g}}{X} \times 100$$

$$\text{Phenotypic coefficient of variability (PCV)} = \frac{\sqrt{\sigma^2 p}}{X} \times 100$$

$$\text{Environmental coefficient of variability (ECV)} = \frac{\sqrt{\sigma^2 e}}{X} \times 100$$

Where:
$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance
$\sigma^2 e$ = Environmental variance
X = General mean of character

The PCV and GCV values are ranked as low, medium and high by Shivasubramanian and Menon[9] as follows: 0-10%-Low, 10-20%-Moderate, >20%-High.

Heritability: Broad sense heritability was estimated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage[10].

$$h^2_B = \frac{V_g}{V_p} \times 100$$

Where:
h^2_B = Heritability in broad sense
V_g = Genotypic variance
V_p = Phenotypic variance

Heritability values were categorized as low, moderate and high by Robinson *et al.*[11] as follows: 0-30%: Low, 30-60%: Moderate, 60% and above, High.

Genetic advance: The extent of genetic advance is expected by selecting certain proportion of the superior progeny was calculated by using the following formula suggested by Robinson *et al.*[11].

$$\text{Genetic advance (GA)} = k \sigma_p h^2$$

Where:
k = Intensity of selection at 5% (k-2.06)
σ_p = Phenotypic standard deviation
h^2 = Heritability in broad sense

The value of 'k' was taken as 2.06 assuming 5% are selected.

Genetic advance expressed as percentage over mean (GAM):

$$GAM = \frac{GA}{X} \times 100$$

Where:
GA = Genetic advance
X = General mean of the character

The GAM was categorized as suggested by Johanson *et al.*[12] as: 0-10% = Low, 11-20% = Moderate, >20% and above, High.

RESULTS AND DISCUSSION

The analysis of variance for different characters at South Bench and Menit Shasha locations are presented in Table 3. The results revealed significant differences (p<0.05) among genotypes for most characters at both locations with the exception of day to emergency, days to flowering, day to maturity and number of primary branches at South Bench and day to emergency at Menit Shasha.

Phenotypic and genotypic variations: The effectiveness of selection in any crop depends on the extent and nature of phenotypic and genotypic variability present in different agronomic traits of the population[13]. Generally, genetic parameters including genotypic coefficient of variation, heritability and genetic advance are prerequisite for genetic improvement of crops[14]. High genotypic coefficient of variation indicates availability of high genetic variation. The lower value of variation indicates that selection is not effective for particular character because of the narrow genetic variability[15].

According to Burton and Devane[8], PCV and GCV values great 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be moderate. Estimated variance components, PCV and GCV for the characters studied are presented in Table 4 and 5. In this study, PCV ranged from 3.8% for days to maturity to 24.43% for grain yield and the GCV ranged from 3.3% for days to maturity to 12.9% for grain yield at South Bench but at Menit Shasha districts PCV ranged from 4.77% for days to maturity to 24.4% for number of pod/plant and the GCV

Table 3: Analysis of variance for different characters of haricot bean genotypes at South Bench and Menit Shasha in 2015-16 main cropping season

Sours of variation	df	DE	DF	DM	PH	PPB	SCH	NPP	NSPP	BMTH	HI	HSW	GY
South Bench													
MSR	2	5.81	6.48	69.6	443.43	0.44	177.7	13.86	0.25	0.58	0.0065	8.07	0.019
MST	8	0.28ⁿˢ	19.70ⁿˢ	4.2ⁿˢ	117.7**	0.44ⁿˢ	544.3**	44.2**	0.46**	1.33*	0.007**	59.16**	0.6**
MSE	16	0.89	7.31	12.2	43.72	0.28	108.11	5.68	0.11	0.48	0.0008	6.39	0.07
'F'value		0.32	2.69	0.35	2.69	1.54	5.04	7.79	4.25	2.77	8.87	9.25	7.99
CV%		10.11	6.64	4.32	9.12	11.78	5.55	9.67	5.89	15.71	6.39	11.01	13.5
Menit Shasha													
MSR	2	1.148	3.44	18.2	443.4	0.1	85.2	5.01	1.27	22.5	0.0199	6.04	19.27
MST	8	0.34ⁿˢ	13.9**	34.2**	117.7*	1.35**	3207**	68.4**	1.86**	54.9*	0.007*	47.03*	41.0**
MSE	16	0.15	3.27	4.3	43.72	0.12	45.5	2.63	0.33	14.1	0.0019	8.67	4.18
'F'value		2.31	4.25	7.9	2.69	10.9	70.5	8	5.61	3.9	4.1	5.43	9.79
CV%		4.72	4.25	2.6	9.12	7.6	4.17	25.9	12.2	10.2	9.02	12.3	11.13

*Significant at 5% level of probability, **highly significant at 1% level of probability, ns: Not significant, DE: Day to emergency, DF: Days to flowering, DM: Day to maturity, PH: Plant height, PPB: Number of primary branches, SCH: Stand count, NPP: Number of pod/plant, NSPP: Number of seed/pod, BM: Biomass, HI: Harvesting index, HSW: Hundred seed weight and GY: Grain yield

Table 4: Genotypic, phenotypic and environmental variance genotypic, phenotypic and environmental coefficient of variation, heritability and genetic advance (GA as % of mean) of quantitative traits of 9 genotypes of haricot bean at South Bench in 2015-16 main cropping season

Characters	V_p	V_g	V_e	PCV	GCV	ECV	$h^2\%$	GA	GAM
DE	0.69	0.20	0.89	8.9	4.77	10.1	53.6	0.92	10
DF	11.44	4.13	7.31	8.3	5.1	6.6	61.4	4.28	10.37
DM	9.55	2.65	12.2	3.8	3.3	4.4	86.8	5.53	6.8
PH	68.4	24.68	43.72	11.4	6.8	9.1	59.6	10.16	14.03
PPB	0.333	0.053	0.28	12.6	4.9	11.65	38.9	0.46	10.13
SCH	253.51	145.4	108.11	8.5	6.4	5.5	75.3	24.7	13.18
NPP	18.52	12.84	5.68	17.5	14.6	9.68	83.4	7.4	30.08
NSPP	0.227	0.117	0.11	8.5	6.1	5.9	72.8	0.72.	12.7
BMTH	0.48	0.28	0.48	15.0	12	15.6	80.0	1.14	25.79
HI	0.0028	0.002	0.0008	11.5	10	6.1	86.9	0.095	20.65
HSW	23.98	17.59	6.39	21.4	18.3	11	85.5	8.63	37.7
GY	0.246	0.176	0.07	24.43	20.6	13	84.3	0.86	42.2

DE: Days to emergency, DF: Days to flowering, DM: Days to maturity, PH: Plant height, PPB: Primary brunch, SCH: Stand count at harvest, NPP: Number of pods per plant, NSPP: Number of seeds per plant, HSW: Hundred seed weight, GY: Grain yield, BMY: Biomass yield, HI: harvest index, GV: Genotypic variance, GCV: Genotypic coefficient of variation, h^2: Heritability, PV: Phenotypic variance, PCV: Phenotypic coefficient of variation GAM: Genetic advance as per cent of mean and GA: Genetic advance

ranged from 3.13% for days to emergency to 23.06% for number of pod/plant. The maximum value between PCV and GCV was recorded for number of primary branch (12.6-4.9%) followed by plant height (11.4-6.8%) at South Bench and plant height (11.6-6.8%) at Menit Shasha. It indicates that the expression of character relatively more influenced by environments. In agreement with the present study. Gutu[16] reported that the maximum value between PCV and GCV for number of primary branches in French bean.

Generally, the GCV and PCV were similar in magnitude and direction in both locations which indicated that the genotypes were able to express their genetic potential for various traits. GCV of high order was observed only grain yield (20.6%). This result agrees with the findings of More and Borkar[17] reported that high genotypic coefficients of variations for grain yield in common beans genotypes. On the other hand, hundred seed weight (18.3%), harvest index (10%), biomass (12%), number of pods/plant (14.6%) had moderate GCV. Earlier researchers also reported relatively moderate for biological yield[18] and for hundred seed weight at South Bench, however in Menit Shasha, high order of GCV was observed for stand count (20.1%) and number of pod per plant (23.06%). This result disagrees with the findings[18]. On the other hand, number of primary branches, number of seed/pod, hundred seed weight, biomass and grain yield had moderate GCV. Earlier researchers also reported relatively moderate for number of seed per pod, biological yield and hundred seed weight[18].

Other traits such as days to 50% emergence, days to 50% flowering, days to maturity and plant height, had shown low GCV at both location in addition number of primary branch, stand count at harvest, number of seeds/pod at South Bench and harvesting index at Menit Shasha district had low GCV. Similar results of lower GCV in plant height, days to 50% flowering, days to 90% maturity were also reported by Narayan[18]. Similarly Plant height, days to maturity and days to flowering low GCV was recorded by Gutu[16].

Relatively higher PCV was observed in grain yield at both locations and hundred seed weight at South Bench and stand count and number of pod/plant at Menit Shasha. These findings are in conformity with earlier reports of Narayan[18] in number of pod/plant and grain yield and hundred seed weight[17]. Traits such as biomass, number of primary branch, harvest index and plant height at both locations and number of pods/plant at South Bench and number of seed-pod and hundred seed weight at Menit Shasha had moderate PCV. The moderate value of PCV for the above mentioned characters was reported by Narayan[18].

Lower PCV was observed for phonological parameters (days to 50% emergence, days to 50% flowering and days to 90% maturity) at both locations. In the same way, stand count at harvest and number of seeds/pod revealed lower PCV value at South Bench. This result was supported by previous findings by Narayan[18] and Negash[19] who reported lower PCV for days to maturity and days to 50% flowering.

Among all traits, high GCV and PCV values (>20%) were observed for grain yield at South Bench and number of pod/plant and stand count Menit Shasha. Moderate GCV and PCV values (>10%) were observed for hundred seed weight, harvest index, biomass and number of pods/plant at South Bench and number of primary branches, number of seed/pod, biomass and hundred seed weight at Menit Shasha, therefore further selection of these traits could improve the genotype. Similarly, high GCV and PCV value for grain yield reported by Negash[19] and on number of pod/plant reported by Prakash *et al.*[20].

On the other hand, low PCV and GCV (<10%) were observed for days to maturity, days to flowering and days to maturity. This traits offered less scope of selection as they under the influence of environments. The current results were supported by previous foundlings reported by More and Borkar[17].

Generally, the PCV values were greater than GCV values although the differences were not large suggesting that there was influence of the environment. The environmental coefficients of variation (ECV) of traits were lower than both genotypic and phenotypic coefficient of variations. This implies that the environmental role was less for the expression of such characters. This implies that the environmental role was less for the expression of such characters.

Estimates of heritability (H$_2$B) in broad sense: Information on heritability in broad sense (h$_2$B) and genetic advance of yield attributing traits and their association helps plant breeder to identify characters for effective selection. The concept of heritability explains whether differences observed among individuals rose as a result of differences in genetic makeup or due to environmental forces. According to Robinson *et al.*[11], heritability values are categorized as low from 0-30%, moderate from 30-60% and 60% and above are high. Considering this benchmark, heritability estimate of this study are described as follows.

In this study, heritability (h$_2$B) estimate ranged from 38.9% for primary branch to 86.9% for harvest index (Table 4) at South Bench and from 30.5% for day to emergency to 95.86% for stand count (Table 5) at Menit Shasha. Based on

Table 5: Genotypic, phenotypic and environmental variance, genotypic, phenotypic and environmental coefficient of variation, heritability and genetic advance
(GA as % of mean) of quantitative traits of 9 genotypes of haricot bean at Menit Shasha in 2015-16 main cropping season

Characters	V_p	V_g	V_e	PCV	GCV	ECV	$h^2\%$	GA	GAM
DE	0.213	0.065	0.148	5.6	3.13	4.7	30.5	0.42	5.1
DF	6.817	3.547	3.27	8.9	4.43	4.25	52.03	2.8	6.5
DM	14.27	9.97	4.3	4.77	3.94	2.59	70.0	5.45	6.8
PH	68.35	24.63	43.72	11.4	6.8	9.1	36.03	6.13	8.5
PPB	0.53	0.41	0.12	16.7	13.95	7.54	77.36	1.16	25.3
SCH	1099.29	1053.8	45.49	20.5	20.1	4.17	95.86	65.47	40.5
NPP	24.55	21.92	2.63	24.4	23.06	7.99	89.29	9.78	48.17
NSPP	0.84	0.51	0.33	19.37	15.09	12.14	60.7	1.14	24.1
BM	27.72	13.62	14.1	14.25	10.0	10.16	49.13	5.33	14.42
HI	0.0036	0.0017	0.0019	12.5	8.59	9.08	47.2	0.058	12.08
HSW	21.45	12.78	8.67	19.35	14.93	12.3	60	5.72	23.89
GY	16.45	12.27	4.18	22.04	19.05	11.12	74.58	6.22	33.86

DE: Days to emergency, DF: Days to flowering, DM: Days to maturity, PH: Plant height, PPB: Primary brunch, SCH: Stand count at harvest, NPP: Number of pods per plant, NSPP: Number of seeds per plant, HSW: Hundred seed weight GY: Grain yield, BMY: Biomass yield, HI: Harvest index, GV: Genotypic variance, GCV: Genotypic coefficient of variation, h^2: Heritability, PV: Phenotypic variance, PCV: Phenotypic coefficient of variation, GAM: Genetic advance as per cent of mean and GA: Genetic advance

the above bench mark days to 90% maturity, stand count at harvest, number of pods/plant, number of seeds/plant, biomass, harvest index, hundred seed weight and grain yield exhibited relatively higher H_2B values at both location. Likewise, days to flowering at South Bench and number of primary branches at Menit Shasha showed very high heritability estimates in the broad sense. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. This may be attributed due to uniform environmental conditions during the conduct of the experiment. Indicating that the possibility of success in selection. Earlier workers also reported relatively higher broad sense heritability values for days to 90% maturity, days to 50% flowering, plant height, number of seeds/plant and hundred seed weight[19]. Similarly, Narayan[18] reported that number of seeds per pod, harvest index, seed yield/plot and biological yield had high broad sense heritability. Moderately high heritability estimates were obtained from traits like primary branch, plant height and days to 50% emergence at South Bench and day to emergency, days to flowering, plant height and biomass and harvesting index Menit Shasha.

Expected genetic advance (GAM %): The expected genetic advance (GA) values for twelve characters of the genotypes evaluated are presented in Table 4 and 5. These values are also expressed as percentage of the genotypes mean for each character so that comparison could be made among various characters, which had different units of measurement. High H_2B along with high GAM is an important factor for predicting the resultant effect of selecting the best individuals.

Percentage of mean genetic advance (GAM) estimates varied from for days to 6.8% maturity to 42.2% for grain yield and from 5.1% days to emergency to 48.17% number of pods/plant at South bench and Menit Shasha conditions, respectively. In this study, higher GAM (>20 percent) was recorded for grain yield (42.2%), hundred seed weight (37.7%), number of pods/plant (30.08%), biomass (25.79%) and harvest index (20.65%) at South Bench and number of primary branch/plant (25.3%), stand count (40.5%),number of pod/plant (48.17%), number of seed/pod (24.1%), hundred seed weight (23.89%), grain yield (33.86%)at Menit Shasha. This finding is in agreement with Negash[19] where 100-seed weight (56.6%) and number of seed/pod 23.71% with Gutu B. 2015 showed a high genetic advance as percent of mean. Similarly the same result was reported by Narayan[18] hundred seed weight (57.57%), grain yield (38.56%) and number of pod/plant (24.15%).

The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action[21]. Accordingly, Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates[12]. High heritability coupled high genetic advance (as percentage of the mean) was observed for number of pods per plant, hundred seed weight and grain yield at both locations, likewise biomass and harvest index at South Bench and number of primary brunch, stand count at harvest and number of seeds per pod at Menit Shasha were exhibited. This reflected that the involvement of additive gene action for the inheritance of these traits and selection would be effective.

This finding was similar with the result of Negash[19] and Narayan[18], respectively opposite to the above mentioned traits, day to 90% maturity at South Bench and Menit Shasha locations showed.

High heritability coupled with low genetic advance as percent of mean compare to the other traits. The traits processing low genetic advance with high heritability which indicates the presence of non additive gene thus, simply selection procedures in early segregating generation will not be effective for screening of desirable traits. Further explanation by Sardana *et al.*[22] suggested that high heritability might not necessarily lead to increased genetic gain, unless sufficient genetic variability existed in the germplasm. In agreement with the current finding, high heritability with low genetic advance were detected by Negash[19] for day to maturity in French bean.

Therefore, any improvement of these characters would result in a substantial increment on grain yield. Thus, evaluation for variability of haricot bean using conventional approach still could provide vital information but using contemporary molecular genetic analysis approaches such as mapping of quantitative trait loci using molecular markers is helpful to understand variability at molecular level, improve selection knowledge and arrive at more comprehensive conclusions. Repeating the experiment is advisable to better estimate environmental effects.

CONCLUSION

This study generally indicated that there was genetic variability among the genotypes. Thus, there is enormous opportunity in the improvement of haricot bean genotypes. Therefore, the information generated from this study needs to be used by breeders who are interested both in commercial and food type haricot bean genotypes. Besides, these haricot bean materials need to be tested in similar agro ecologies for their stability.

SIGNIFICANCE STATEMENTS

This study discovers the genetic variability, heritability and genetic of the tested haricot bean varieties. It also indicates yield attribute traits of the haricot bean varieties considered and further selection of this trait could improve the genotypes. Thus, direct selection of these characters and incorporation of selected individuals in breading programs would bring improvement in the genotypes.

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