Evaluating the Genetic Variations Among Improved Haricot Bean Varieties (*Phaseolus vulgaris* L.) Based on Their Agronomic Traits and Performing Their Half Diallel Cross

Getahun Bekana[*], Endashaw Girma, Abenezer Abebe, Alemnesh Sisay, Desalegn Alemayehu, Kidane Maryam Wagaw, Awol Beshir, Desalegn Chalchisa, Fassil Hailu, Deressa Tesfaye

Department of Horticulture and Plant Science, College of Agriculture and Veterinary Medicine, Jimma University, Jimma, Ethiopia

Email address:
getahunbekana2006@gmail.com (G. Bekana), endashaw.girma11@gmail.com (E. Girma)
[*]Corresponding author

Abstract: Haricot bean, often known as Boleqe in Ethiopia. It is a major legume crop produced widely all over the world. Depending on the variety, it may adapt to a wide range of environmental conditions, from sea level to almost 3000 meters above sea level. It thrives commonly in warm climates with temperatures ranging from 18 to 24°C. Despite its importance for nutrition and export, haricot bean production in Ethiopia is limited to small regions and small-scale growers, with little or no fertilizer or soil amendments being employed. The responses of the haricot bean varieties to each limitation varied, although they are mostly determined by the environmental conditions. The main bottle neck of haricot bean production is the lack of improved high producing cultivars that suit to each agroecology. The current experiment was carried out on six released haricot bean varieties with half diallel without reciprocal crosses on the field to make F1 hybrids in all possible combinations and with the objective of evaluation of agronomic traits of haricot bean varieties and performing their half diallel cross by using complete block design. An analysis of variance revealed a highly significant difference in yield contributing components among these released varieties at 5% probability level for most of the traits. This suggests that the released haricot bean varieties have a high genetic variation.

Keywords: Common Bean, Crop, Diallel Cross, Genetic Variation, Legume, Traits, Variety

1. Introduction

Haricot bean (*Phaseolus vulagris L*), known as dry bean, common bean, kidney bean and field bean, also known as boleqe locally in Ethiopia. It is a major legume crop grown all over the world and belongs to Fabaceae family crop that grows annually. It thrives in a warm region with temperatures ranging from 18 to 24°C [1]. Despite its nutritional and export value, it is only cultivated in a few areas of our country. Common bean, like many other pulse crops, has a short cycle. This feature of the crop makes it a valuable technology in locations where moisture stress is a result of late onset or early termination of rainfall.

Haricot bean is typically a small-scale producer's crop, with few or no inputs, such as fertilizer or soil amendments [2]. Depending on the variety, the crop can be grown in a wide range of climatic conditions, from sea level to nearly 3000 meters above sea level (m.a.s.l.). However, due to poor pod set caused by high temperatures, it does not grow well below 600 meters [3].

Haricot bean is primarily farmed by smallholder farmers in Ethiopia as a food crop and a source of income. It is one of the rapidly expanding legume crops that offer an important part of most Ethiopians' daily nutrition as well as foreign profits [4]. The crop is frequently produced in elevations ranging from 1400-2000 meters above sea level. East Hararghe, West Wellega, East shewa, West Arsi, Sidama, Wolayita, Wollo, and East Gojam are the key production

areas [5].

Between 1400 and 2000 meters above sea level, the crop grows best [6]. In 2011/12, the country's total Haricot bean production was around 3,978,023.01 quintals (1.78 percent of grain production) on about 341,708.15 hectares of land (2.84 percent of grain crop area) [7]. Haricot bean varieties have a wide range of growth behaviors, allowing the crop to adapt to a wide range of growing conditions [8]. Early maturity and a reasonable level of drought tolerance contributed to the crop's importance in farmers' risk-aversion techniques in drought-prone lowland sections of the country [6]. But, as the official statistics of the country, CSA report [7], the average haricot bean productivity was about 15.89 quintal per hectare during 2014/15. However, results from experimental plots show that 25-30 quintal per hectare can be achieved [5].

Moisture stress, the lack of improved high producing cultivars, low soil fertility, and losses due to insect pests and disease are all factors that contribute to the low yield [9, 10, 4]. Varieties differ in their responses to these restrictions, although environmental factors have a big influence [2]. Haricot bean productivity in these locations could be improved by selecting cultivars that are well adapted to local agro-ecological conditions, soil fertility, and moisture levels. However, little study has been done in this area at the Jimma University Experimental Site, and despite its importance, the crop has been introduced in this portion of the country in an insufficient manner. Furthermore, finding acceptable alternative N-fixing crops such as haricot bean is critical for improving soil fertility as well as increasing crop productivity and farmer livelihoods.

Breeders fully intend long in advance and serve a range of mating designs to estimate genetic variants in any crop population. The genetic material analyzed differs across mating schemes, determining the amount to which additive, dominance, and epistatic variations can be assessed [11]. Diallel cross [12] is a mating method used by plant and animal breeders as well as geneticists to examine the genetic basis of qualitative and quantitative traits. According to Obi [13], there are 4 main kinds of diallel mating designs: (i), Full diallel- which involves both parents and reciprocal crosses as well as F1 and F2. (ii), Full diallel without parents. (iii), Half diallel with parents but no reciprocal. (iv), Half diallel without both parents as well as reciprocal crosses. But, all of them are different from one other based on parents involved in crosses to generate hybrids in all conceivable pairings.

Objective:

Estimating the variations among the varieties based on their agronomic traits and performing their half diallel cross.

2. Literature Review

2.1. Phenotypic and Genotypic Coefficients of Variation

Crop genetic relationships are an important part of crop improvement programs because they provide information about genetic diversity and can be used to stratify breeding populations [14]. Accurate assessment of genetic diversity levels and patterns can be extremely useful in crop breeding for a variety of purposes, including (i) analyzing genetic variability in cultivars, (ii) identifying diverse parental combinations to produce segregating progenies with maximum genetic variability for further selection, and (iii) introgressing desirable genes from diverse germplasm into the available germplasm. Assessing the genetic links between inbred or pure lines can be very useful when planning crosses and assigning lines to different genotypes categories. Genetic variation analysis in germplasms can help with accession classification and identification of subsets of core accessions that may be useful for specific breeding purposes.

In any plant breeding program, naturally occurring genetic variation is beneficial. The amount of overall genotypic and phenotypic variability in a crop germplasm determines when crop improvement programs are started and new varieties are developed. The genetic component of population variability is the most relevant to the breeder since it can be passed on to the offspring. Furthermore, appropriate management of this type of variability might result in a long-term improvement in the crop's performance [15]. The observable traits of variation existing in a population are phenotypic variability, which is a combined impact of genotypic value and environmental deviation. Genotypic variations, on the other hand, are the component of variation caused by genetic differences between individuals within a population and are the primary concern of plant breeding [16].

2.2. Heritability and Genetic Advance

One of the criteria for a successful breeding program in selecting genotypes with desirable features is knowledge of the nature and extent of variability and inheritance in a population [17]. It is consequently critical for breeders to understand the heredity of agronomical traits in order to efficiently boost crop output. Heritability is defined as the measure of the correlation between breeding values and phenotypic values, according to Falconer and Mackay [18]. As a result, heritability serves a predictive function in breeding, reflecting the phenotype's dependability as a pointer to its breeding value. The breeding value affects how much of the trait is passed down to subsequent generations [19]. Heritability in the broad sense expresses the extent to which phenotypes are determined by the genes transmitted from the parents, and it gives an idea of the total variation accounted to genotypic effect [20], whereas heritability in the narrow sense expresses the extent to which phenotypes are determined by the genes transmitted from the parents.

The term "genetic advance" refers to the connection between heredity and selective response. The most successful selection condition is a strong genetic progress combined with a high heritability estimate [21]. When heredity is used to compute genetic progress, which shows the degree of character gain achieved under a given selection pressure, the utility of heritability rises.

If the component characteristics are highly heritable and favorably linked with yield, the most effective yield

component breeding to improve yield may be accomplished. Due to the polygenic character of quantitative traits, it is difficult to determine whether observed variability is substantially heritable or not. Heritability is also important for selection-based improvement since it reflects the amount to which a feature may be passed down over generations [22, 23].

The majority of essential agronomic characteristics are quantitative in nature and expressed in degrees rather than kinds. Plant breeders need knowledge that will enable them to quickly discover superior genotypes, select them, and concentrate their genes in a commercially viable line or variety. To do so, you must first determine whether the characteristic is heritable, then determine the kind and amount of the genetic components of the variance.

Under one cycle of selection at a particular selection intensity, the anticipated genetic advance from selection refers to the improvement in genotypic value of characteristics for the new population relative to the base population [16]. Because high heritability does not necessarily imply strong genetic gain, combining heritability and genetic advance to forecast the final impact for choosing superior varieties [24] should be utilized to predict the ultimate effect for selecting superior variations. For potential selection, genetic advancement provides a clear picture and accurate vision of segregating generations. The breadth of selection in creating new genotypes with favorable traits is confirmed by higher heritability estimates combined with superior genetic progress [25].

2.3. Correlation Analysis

The correlation coefficient is a measure of how closely characteristics are related. Breeders must comprehend the amount of variation, correlation, and inheritance of critical agronomic characteristics. Without a cause-and-effect link, the correlation coefficient merely measures mutual association [26]. A positive correlation value indicates that two variables are changing in the same direction, i.e., a high value of one variable is linked with a high value of the other and vice versa. Depending on the sign of genetic connections between two features, selection progress might be aided or hampered. The correlation value (r = 1) denotes complete (100%) correlation, in which both qualities vary in the same direction, (r = -1) denotes 100 percent relationship between the two characters but in the opposite direction, and (r = 0) denotes no correlation at all [18].

Days to flowering are strongly linked with days to maturity in Haricot bean [27]. Dry seed yield is strongly associated with days to maturity [15]. The number of pods per plant and the number of seeds per pod are positively associated with seed yield, which is also correlated with plant height and seed size [28]. Seed output was also strongly associated with the number of pods per plant, the number of seeds per pod, and all architectural characteristics except branches per plant, according to Murut [29]. Seed yield, number of nodes per plant, and number of nodes on the main stem were all inversely linked with seed weight, whereas

main stem internode length was favorably correlated. Vasic [30] discovered that plant height and productive height were related to yield, as determined by the quantity of pods per plant and seeds per plant. Seed length and seed height were shown to be positively and highly associated with hundred seed weight [31].

2.4. Path Coefficient Analysis

The path coefficient analysis has been proposed as an effective measure of direct and indirect causes of association, since it depicts the relative significance of each component involved in contributing to the end result, yield [26].

Path coefficient analysis is defined as "the ratio of the overall effect's standard deviation" [18]. Rather from simple correlation coefficients, path coefficient analysis would give a better indicator for selection by revealing the source and impact of various yield components. Because of the significant genetic link, there was a large positive direct influence on yield. In plant breeding programs, path coefficient analysis is used to identify the nature of the relations between yield and yield components that may be utilized as selection criterion to increase crop output. The objective of path analysis is to accept explanations of the relationship between characteristics based on a cause-and-effect model and to assess the relevance of influencing traits on a given attribute.

The quantity of pods per plant has a preponderant direct influence on yield, according to a path coefficient analysis of various yield component interactions in common bean [32]. These factors also had a key impact in predicting yield in divergent parents in terms of seed quantity per pod and seed weight. Leaf number was strongly linked to the number of pods per plant, but leaf size was strongly linked to seed size. Days to flowering had a favorable and substantial direct influence on seed yield in the parameter's selection for yield enhancement in French bean, whereas days to maturity and plant height had negative direct effects [33].

2.5. Diallel Cross

A diallel cross is a mating technique used by geneticists and plant breeders to explore the genetic basis of quantitative characteristics. All parents are crossed in a complete diallel to create hybrids in all conceivable combinations. Half diallels with and without parents, as well as diallels without reciprocal crossings, are examples of variations. Full diallels need twice as many crossings and entries in studies, but they enable for paternal and maternal effects to be tested. A half diallel without reciprocals can be successful if such "reciprocal" effects are believed to be insignificant [34].

To identify heterotic groups, estimate general or particular combining ability, interactions with testing locations and years, or estimations of additive, dominant, and epistatic genetic effects and genetic correlations, common analytic techniques use general linear models. The mating design is diallel when the same parents are employed as females and males in breeding. The collection of all potential mating

between various genotypes is known as a diallel cross. Individuals, clones, homozygous lines, and other genotypes can be identified, and if there are n of them, there are n square mating combinations, counting reciprocals separately.

The partitioning of the sum of squares of the treatment Griffing [34], Method 2 (parents and F1 hybrids) Model 1 should be used to split the sum of squares of the treatment means in sum of squares for general and particular combining abilities (fixed effects).

3. Material and Methods

3.1. Description of the Study Area

The experiment was conducted during the rainy season at Jimma University College of agriculture experimental site. The mean annual rainfall for this site is 1460 mm with a bimodal pattern, which extends from March to September. The peak rainy months are April, July, August and September. The mean minimum and maximum temperatures are 15 and 26°C, respectively.

3.2. Experimental Materials and Procedures

Six released haricot bean varieties were tested by randomized complete block design with three replications and half diallel mating design was used for crossing. The other materials used for the experiments were as follows: - Peg, spade, pencil, meter, scissors, strings and plastic bags were used during the experiment. The plot size of 4m x 1.6m was used with a spacing of 40cm and 10cm between rows and plants respectively. Spacing between plots and replications were 1m and 1m respectively.

3.3. Data Collected

All agronomic practices were done as per the recommendation for haricot bean. Data on agronomic traits such as number of leaves per plant, leaf area, number of primary branches per plant and plant height were collected from the average value of randomly selected five plants per plot. Whereas 50% flowering and emergence date were collected on plot basis.

Number of leaves per plant (NL): The total number of leaves recorded on a plant.

Leaf area (LA): The average area of three leaf (top, middle and bottom) on one plant per plot and five plant per plot.

Plant height (PHT): The distance from the soil surface to the top of the canopy of a plant in centimeter.

Number of primary branches per plant (BN): The numbers of branches originated from the main stem.

Days to emergence (DTE): The number of days from date of planting to the stage 50% of seedlings emergence.

Days to 50% flowering (DTF): Number of days from date of sowing to the date on which 50% of the plants in each plot had one or more flowers.

3.4. Statistical Analysis

The data collected were checked for meeting all the ANOVA assumptions and subjected to analysis of variance was performed using randomized complete block design of Statistical Analysis Software (SAS. Inc., Version 9.3). Least Significant Difference test at 5% probability level was used for mean comparison. and genotypic variance, phenotypic variance, heritability, phenotypic correlation, genotypic correlation and path coefficient analysis was included.

Genotypic, environmental and phenotypic variances calculated as follows: genotypic variance- $\sigma^2 g$ = (msg-mse)/r, environmental variance- $\sigma^2 e$ =mse/r, phenotypic variance- $\sigma^2 p = \sigma^2 g + \sigma^2 e$, heritability- $H_b = \sigma^2 g$ over $\sigma^2 p$ *100. Where, $\sigma^2 g$ - Genotypic variance; *msg* - Mean square of genotype; *mse* - Mean square of error; $\sigma^2 p$ – phenotypic variance; $\sigma^2 e$ – Error variance; r - Number of replications which is three (3) and H_b - Heritibility in broad sense.

Both genotypic and phenotypic Correlation coefficients were computed from the components of variance and covariance based on the method described by Singh and Chaudhary [40], using the CANDISC procedure of SAS [41]; whereas path coefficient calculated from correlation coefficient to determine the magnitudes and direction one trait effect showed over the other.

4. Result and Discussion

4.1. Results

Table 1. Analysis of Variance (ANOVA).

Genotype	DTE	DTF	PHT-cm	LN	BN	LA
Red Wolaita	5.7bc	45.3b	85.7c	61.9ac	7.8a	72.6c
BC4-4	5.3c	42.0cd	62.3d	39.6bc	6.4a	114.7a
Atndaba	6.0ab	44.3bc	88.0a	53.7ac	8.4a	59.3f
Dimtu	6.3a	47.3a	60.7d	54.9ac	6.9a	70.6d
Nasir	5.3c	44.0bc	86.4b	68.3ac	8.6a	66.4e
Gobe Rasha-1	6.0ab	43.0c	62.0d	47.0ac	6.9a	139.6a
Mean	5.8	44.3	74.2	54.2	7.5	87.2
CV (%)	6.1	1.4	19.7	18.1	28.0	14.4
LSD	0.9	1.6	3.2	25.4	5.4	32.5

*DTE=days to emergency, DTF=days to flowering, PHT=plant height, LN=leaf number, BN=primary branch number, LA=leaf area.

Table 2. *Genetic, phenotypic variance and heritability.*

Variance	DTE	DTF	PHT	LN	BN	LA
MS	0.5	10.4	566.0	314.6	2.5	3122.1
MSE	0.1	0.4	213.9	96.5	4.4	157.4
δ_g^2	0.1	3.3	117.4	72.7	-0.6	988.3
δ_p^2	0.2	3.7	331.3	169.2	3.7	1145.6
H^2	0.5	0.9	0.4	0.4	-0.2	0.9

*DTE=days to emergency, DTF=days to flowering, PHT=plant height, LN=leaf number, BN=primary branch number, LA=leaf area, MS-mean square of treatments, MSE-mean square of error, δ_g^2- genotypic Variance, δ_p^2 phenotypic Variance and H^2- Heritability in broad sense

Table 3. *Phenotypic correlation (above diagonal) and genotypic correlation (below diagonal).*

Variable	DTE	DTF	PHT	LN	BN	LA
DTE	1.00000	0.24745	-0.09255	0.10482	0.12685	-0.02347
DTF	0.65044	1.00000	0.01584	0.25758	-0.01603	-0.60194**
PHT	-0.30725	0.08689	1.00000	0.72375**	0.80919**	-0.48224*
LN	-0.09390	0.51215	0.71964	1.00000	0.12685	-0.49276*
BN	-0.17785	0.17090	0.94077*	0.80856*	1.00000	-0.35931
LA	-0.07895	-0.63801	-0.69923	-0.71676	-0.71871	1.00000

*DTE=days to emergency, DTF=days to flowering, PHT=plant height, LN=leaf number, BN=primary branch number, LA=leaf area.

Table 4. *Direct effect (bold diagonal) and indirect effect for phenotype path-coefficient analysis.*

Traits	PHT	DTE	DTF	LN	BN	LA
PHT	**0.736911**	-0.0682	0.011673	0.533339	0.596301	-0.35537
DTE	-0.04219	**0.455837**	0.112797	0.047781	0.057823	-0.08522
DTF	0.002243	0.035034	**0.14158**	0.036468	-0.00227	-0.35537
LN	0.224617	0.032531	0.079941	**0.310352**	0.16417	-0.15293
BN	0.091819	0.014394	-0.00182	0.060024	**0.113471**	-0.04077
LA	-0.10322	-0.00502	-0.10322	-0.10548	-0.07691	**0.214051**

*DTE=days to emergency, DTF=days to flowering, PHT=plant height, LN=leaf number, BN=primary branch number, LA=leaf area.

Table 5. *Direct effect (bold diagonal) and indirect effect for genotype path-coefficient.*

Traits	PHT	LN	BN
PHT	**0.682416**	0.491094	0.641997
LN	0.57694	**0.801706**	0.648228
BN	0.098243	0.084437	**0.104429**

*PHT=plant height, LN=leaf number, BN=primary branch number.

4.2. Discussions

4.2.1. Varieties Mean Comparison

Based on days to emergence varieties Dimtu, Atndaba and Gobe Rasha-1 were statically the same, but they late emerger than the rest of the varieties. Similarly, Dimtu variety was flowered later than the five varieties and followed by Red Wolaita. Regarding to plant height Gobe Rasha-1, Dimtu and BC4-4 varieties were statistically not significantly different and short in length comparing to the rest whereas Red Wolaita, Nasir and Atndaba are significantly different and tall in height. This result contradicts with Tadesse's [35] finding in case of Dimtu. According to leaf number parameter BC4-4 and Nasir varieties were significantly different whereas the remains varieties non-significant. All the varieties non-significant based on number of branches. Finally, the leaf area for BC4-4 and Gobe Rasha-1 varieties were not significantly different whereas the remains significant. This result also similar to Tadesse [35] for plant height (table 1).

4.2.2. Genetic, Phenotypic Variance and Heritability

Genetic and phenotypic variance values for traits such as days to emergency, days to flowering and leaf area have no large difference, but their heritability fall in the range of maximum heritability; which similar with Kefelegn and Wondimu findings [36, 37]. Particularly, heritability for DTE=50%, DTF=90%, LA=90%) and the rest traits fall in the range from medium to low according to Robinson [38]. Even though genotype and phenotype variance values are not differed largely, the phenotypic variance for some studied traits shown great value and this referees the varieties differ phenotypically rather than genotypically; Similar results also reported by these scholars [35-37] (table 2).

4.2.3. Phenotypic Correlation, Genotypic Correlation and Path Coefficient Analysis

Date of flowering show negative highly significant phenotypic correlation with leaf area. Plant height has positive significant phenotypic correlation with leaf number, primary branch and leaf area, but has positive genotypic correlation only with branch number. Leaf number has negative significant phenotypic correlation with leaf area. Branch number and leaf number indicate positive genotypic correlation. Most of the traits concerned showed significant phenotypic correlation rather than genotypic correlation [39]. As a result, improving or selecting these traits depending on their phenotype is difficult because the environmental variation greatly influenced the traits. However, traits like

plant height, primary branch and leaf number can be improved together by selecting superior phenotype because the genotype correlation was significant (table 3).

Phenotypic path coefficient analysis shows all traits have direct effect on plant height with greater effect from date of emergency, leaf number and leaf area and low effect from primary branch and date of flowering [30, 39]. Path coefficient analysis for genotype correlation indicate that primary branch contributes more indirectly through leaf number and leaf number effect directly than indirect (tables 4 and 5).

5. Half Diallel Crossing

The half diallel crossing was conducted on six haricot bean varieties following the appropriate steps and using crossing materials. The procedure followed: (1) Five Vigorous plant Selected from each variety nearly at flowering stage, (2) flowers were selected (3) Emasculated (4) The male parent (pollen) collected (5) Dust the pollen on female parent (6) Bagging and labeling. Then after harvesting F1 generation and continue breeding stage to get best variety.
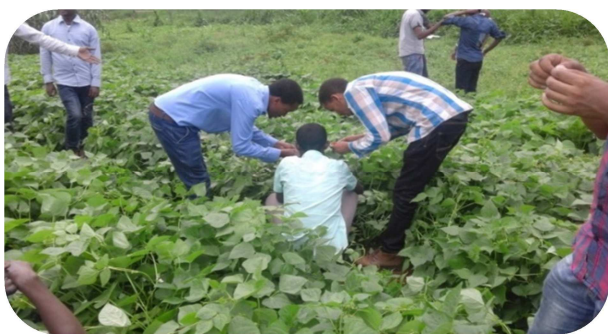

Figure 1. Diallel crossing practice.

6. Conclusion

Haricot bean in Ethiopia is grown predominantly under smallholder producers as an important food crop and source of cash. The current experiment was carried out on six released haricot bean varieties with half diallel without reciprocal crosses on the field to make F1 hybrids in all possible combinations and with the objective of evaluation of agronomic traits of haricot bean varieties and performing their half diallel cross. They were tested by randomized complete block design with three replications. Some of the data were collected on agronomic traits such as number of leaves per plant, leaf area; number of primary branches per plant and plant height average value of randomly selected five plants per plot. Whereas 50% flowering and emergence date were collected on plot basis. The data collected were checked for meeting all the ANOVA assumptions and subjected to analysis of variance was performed using randomized complete block design of Statistical Analysis Software. Finally, the variability among varieties were significant at 5% for most of the traits, but this report could not address the yield and some yield components traits due to

limitation of time. Generally, it is recommended to start the laboratory session on time to accommodating all parameter in analysis for assessment of viabilities.

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