

# Inheritance of Primary Yield Component Traits of Common Beans (*Phaseolus vulgaris* L.): Number of Seeds per Pod and 1000 Seed Weight in an 8X8 Diallel Cross Population

Atnaf Tiruneh Mulugeta, Mohammed Ali Hussein, Zelleke Habtamu

**Abstract**—Thirty six genotypes (8 parents and 28 F<sub>1</sub> diallel crosses) were grown in randomized complete block design during 2006 at Mandura, North western Ethiopia. The experiment was executed to study the inheritance of two primary yield component traits: number of seeds per pod and 1000 seed weight. Statistical significant difference was observed between genotypes, parents, and crosses for these traits. The mean square due to GCA was significant for the two traits. However, SCA mean square was significant only for number of seeds per pod. Thus both additive and non-additive types of gene actions were important in the inheritance of number of seeds per pod. Significant b<sub>1</sub> component was obtained for this trait. The b<sub>2</sub> and b<sub>3</sub> components, however, were not significant, suggesting the absence of gene asymmetry. From Wr/Vr graph, inheritance of seeds per pod was governed by partial dominance with additive gene action.

**Keywords**—Diallel crosses, General combining ability, *Phaseolus vulgaris* L., Specific combining ability.

## I. INTRODUCTION

COMMON beans are rich in protein (20-28%), especially the amino acids lysine and tryptophan, are an important source of minerals such as iron and zinc [15], [11]. It therefore supplements the cereal-based diet in many parts of the world. It is an important food crop in eastern and southern Africa and known as the second most important source of human dietary protein and the third most important source of calorie of all the agricultural commodities produced in eastern and southern Africa [8]. Due to its relative early maturity, it is one of the major crops produced in areas with short rainy season and is suitable in intercropping and double-cropping [21].

The seed yield of a food legume is usually expressed as a function of number of pods per plant, number of seeds per pod and average seed weight [18]. These traits have often been considered in a breeding program of beans aiming to enhance seed yield because of their meaningful and consistent correlation with seed yield [13].

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The choice of promising genotypes from diverse genetic base, and their subsequent utilization for hybridization is one of the strategies for improving the productivity of crops including beans. Effective selection for seed yield and its components requires information on the magnitude of useful genetic variance present in the population and earlier studies in common bean showed considerable genetic variation for seed yield and its components [4], [13]. The Ethiopian bean improvement program has focused on screening of introductions and could not generate basic genetic information. Hence it is necessary to systematically test the performance of parental lines and their F<sub>1</sub> hybrids. A suitable genetic design for beans is, the use of diallel mating system [9], [16]. It is a method where the progeny performance can be statistically separated in to components relating to general combining ability (GCA) and specific combining ability (SCA) [3], [6]. GCA and SCA are a measure of additive and non-additive genetic variation of parents, and crosses, respectively [19].

Inheritance studies have been conducted on many crops, in various parts of the world. However, little information is documented on the inheritance of important traits of common beans in Ethiopia. The study was, therefore, executed to generate basic genetic information on the inheritance of two important primary yield component traits of common beans: number of seeds per pod and 1000 seed weight.

## II. MATERIALS AND METHODS

The experiment was conducted at Mandura, Metekel zone, Benishangul Gumuz regional state, North-western Ethiopia. Thirty six genotypes (8 parents and their 28 F<sub>1</sub> diallel crosses) were studied in two replications of Randomized Complete Block Design (RCBD) in 2006. Diallel crosses were made by hand and Plants were hybridized using emasculation with protected stigma method: the flower bud of the female parent is emasculated, sepals are kept intact to protect the bud, and pollination quickly follows [2], at Melkassa Agricultural Research Center in the central rift valley of Ethiopia during the dry season (March to June, 2005) under furrow irrigation and during the rainy season (July to September, 2005) to ensure enough F<sub>1</sub> seed for planting. Six of the parents were released varieties and being under production in different agro ecologies of Ethiopia and two CIAT lines (BELDAKMI RR5

and SK93263) were screened at Awassa College of Agriculture for good performance. Description of the eight parents used in the diallel cross study are given in Table I.

TABLE I  
DESCRIPTION OF THE PARENTAL LINES FOR THE 8X8 DIALLEL CROSSES OF COMMON BEANS

N <sup>o</sup>	Parent	Status/Origin	Seed color	Seed shape	Seed size	Growth H
1.	Roba-1	Released-1990	Cream	Elongated	Small	Ind. bush
2.	Dimtu	Released-2003	Red	Round	Small	Ind. bush
3.	Zebra	Released-1999	Carioca	Round	Medium	Ind. bush
4.	MAM-41	Released-2003	Cream	Round	Medium	Ind. Prost
5.	BELDAK	CIAT	Cr. Pinto	Round	Medium	Ind. Prost
6.	SK 93263	CIAT	White	Round	Medium	Ind. Prost
7.	Tabor	Released-1999	Cream	Elongated	Medium	Ind. Bush
8.	Red wolaita	Released-1974	Red	Elongated	Medium	Ind. bush

Cr. pinto = Cream pinto, Ind. bush = Indeterminate bush, Ind. prost = Indeterminate prostrate, Growth H= Growth habit, BELDAK = BELDAKMI RR 5.

A plot consisting of two 1m long rows spaced 60cm apart was used to facilitate furrow supplemental irrigation when needed. Intra-row plant-to-plant spacing was 10cm. Two seeds were hand planted per hill and the stand thinned to one plant per hill 10 days after emergence to maintain optimum plants per plot. Standard agronomic and plant protection treatments were used uniformly across the plots for the duration of the experiment. A random sample of five plants from each plot and a random sample of five pods from each of the five plants were considered to collect data on number of seeds per pod, whereas 1000 seed weight was measured on plot bases.

The data were subjected to the Analysis of Variance (ANOVA) using SAS statistical software [14]. Existence of significant difference among genotypes justifies further analysis. Diallel analysis was carried out according to [6] Method II, Model I (Fixed Model), which involves parents and one-way F<sub>1</sub> hybrids. Griffing's diallel analysis [6] was supplemented by [7] analysis. Combining ability analyses were carried out using a SAS program developed by [23].

The W<sub>r</sub>/V<sub>r</sub> ANOVA and graphs are the other powerful tools in Hayman's analysis with an inbuilt test for epistasis. In the absence of epistasis, the regression of W<sub>r</sub> on V<sub>r</sub> gives a linear regression line of unit slope. Therefore, the deviation of this regression line from unity is an indication of the existence of epistasis. Direct ANOVA of (W<sub>r</sub>-V<sub>r</sub>) also tests the absence/presence of epistasis. Significance of the difference (W<sub>r</sub>-V<sub>r</sub>) is an indication of the existence of epistasis. The intercept of the W<sub>r</sub>/V<sub>r</sub> regression line also shows the degree of dominance. If the regression line intercepts the W<sub>r</sub> axis above the point of origin, this indicates incomplete dominance. If the regression line passes through the origin, then there is complete dominance. If the intercept is negative (the regression line passes below the point of origin), then over dominance contributes to the expression of the trait. Finally the correlation between parental means and the covariance (W<sub>r</sub>) is used to judge the direction of dominance. If the correlation coefficient (r) is negative, dominance tends to increase the trait. If r is positive then dominance decreases the trait.

### III. RESULTS AND DISCUSSION

Ordinary Analysis of Variance for the 36 genotypes carried out according to [20], and there was significant difference between the genotypes for the traits studied: number of seeds per pod and 1000 seed weight. Parents also differed in these traits which show that there is enough additive genetic variance to be exploited. Similarly, statistical significant difference was observed between crosses for these traits (Table II).

TABLE II  
ANALYSIS OF VARIANCE FOR NUMBER OF SEEDS PER POD AND 1000 SEED WEIGHT

Number of seeds per pod					
Source	DF	Sum of squares	Mean square	F-value	Probability
Replication	1	6.902	6.902	31.36	0.0001
Genotype	35	42.139	1.204	5.47	0.0001
Parents	7	16.914	2.416	8.53	0.0056
Crosses	27	23.959	0.887	5.79	0.0001
AVHET	1	1.265	1.265	5.75	0.022
Error	35	7.703	0.22		
Total	71	56.744			

1000-seed weight					
Source	DF	Sum of squares	Mean square	F-value	Probability
Replication	1	34.7222	34.7222	0.07	0.7938
Genotype	35	153548.6111	4387.1103	8.77	0.0001
Parents	7	38743.7500	5534.8214	5.39	0.0205
Crosses	27	113050.0000	4187.0370	15.83	0.0001
AVHET	1	1754.8600	1754.8600	3.5067	0.06950
Error	35	17515.2778	500.4365		
Total	71	1710.986			

AVHET= Average heterosis, when significant it indicates directional dominance

Griffing's method II model I and Hayman's approach Analysis of Variance of diallel analysis are merged in to one table without changing the essence of both the models. The mean square due to GCA was significant for the traits considered: number of seeds per pod and 1000-seed weight. However, SCA mean square was significant only for number of seeds per pod. Thus both additive and non-additive types of gene actions were important in the inheritance of number of seeds per pod although additive gene action was more important as the variance component due to GCA was greater than the variance component due to SCA (the ratio of GCA:

SCA variance component was more than unity and is 2.5, as indicated in Table III). Significant  $b_1$  (average heterosis) component was obtained for number of seeds per pod indicating the presence of directional dominance in the expression of the trait. The  $b_2$  and  $b_3$  components, however, were not significant, suggesting the absence of gene asymmetry in the parents and SCA effects in the crosses, respectively. Only additive type of gene action was important in the inheritance of 1000-seed weight.

The GCA and SCA effects of the traits are presented in Table IV. Parents, Roba-1, Zebra, BELDAKMI RR 5, SK 93263 and Tabor had significant GCA effects for number of seeds per pod. Roba-1 was good general combiner for this trait as it had showed the maximum GCA effect for the trait. Moreover it had the highest per se performance.

TABLE III  
GRIFFING'S METHOD II MODEL I AND HAYMAN'S DIALLEL ANALYSIS FOR  
NUMBER OF SEEDS PER POD AND 1000 SEED WEIGHT

Number of seeds per pod					
Source	DF	Sum of squares	Mean square	F-value	Probability
Genotype	35	42.1390	1.2040	5.4700	0.00010
GCA (a)	7	31.1461	4.4495	20.2156	0.00000
SCA (b)	28	10.9927	0.3926	1.7837	0.05256
b1	1	1.2650	1.2650	5.7500	0.02200
b2	7	2.0432	0.2919	1.3261	0.26744
b3	20	7.6842	0.3842	1.7456	0.07276
Error	35	7.7035	0.2201		
Ratio of GCA:SCA variance components				2.497	
1000-seed weight					
Genotype	35	153548.6111	4387.1031	8.7700	0.00010
GCA (a)	7	141637.5000	20233.9286	40.4323	0.0001
SCA (b)	28	11911.1111	425.3968	0.8501	0.6681
b1	1	1754.8600	1754.8600	3.5067	0.06950
b2	7	3622.9200	517.5600	1.0342	0.42540
b3	20	6533.3300	326.6700	0.6528	0.84281
Error	35	17515.2778	500.4365		
Ratio of GCA:SCA variance components				26.40	

GCA (a) = General combining ability, SCA= Specific combining ability,  $b_1$ = tests overall difference between parental and  $F_1$  means,  $b_2$ = measures consistency of mean dominance deviation over arrays (gene asymmetry), and  $b_3$ = measures non-additive deviations unique to each  $F_{1s}$  (SCA effects)

TABLE IV  
ESTIMATION OF GCA AND SCA EFFECTS AND ACTUAL PARENT AND CROSS VALUES FOR NUMBER OF SEEDS PER POD AND 1000 SEED WEIGHT

Number of seeds per pod										
	1	2	3	4	5	6	7	8	Cr.M	GCA
1	<b>-0.075</b>	5.400	5.390	4.800	5.080	5.420	5.720	5.070	5.270	0.78**
2	-0.100	<b>0.021</b>	4.770	4.980	4.640	3.870	4.330	4.870	4.692	0.14
3	0.311	0.331	<b>-0.033</b>	4.120	3.600	3.520	4.540	4.480	4.345	-0.28*
4	-0.370	0.445	0.014	<b>-0.078</b>	3.760	3.880	5.230	4.300	4.437	-0.19
5	0.182	0.383	-0.234	-0.169	<b>-0.874</b>	4.000	5.180	4.760	4.432	-0.46**
6	0.63*	-0.281	-0.209	0.056	0.451	<b>-0.407</b>	5.210	3.550	4.208	-0.57**
7	-0.159	-0.9**	-0.278	0.323	0.55*	0.68*	<b>-0.362</b>	5.680	5.129	0.52**
8	-0.340	0.095	0.130	-0.142	0.59*	-0.510	0.53*	<b>-0.175</b>	4.674	0.05
P.M	6.070	4.880	3.980	4.120	2.780	3.040	5.260	4.510		
1000-seed weight (gm)										
	1	2	3	4	5	6	7	8	Cr.M	GCA
1	<b>0.889</b>	225.00	245.00	270.00	265.00	265.00	205.00	200.00	239.28	-35.4**
2	17.389	<b>-1.111</b>	240.00	260.00	270.00	300.00	235.00	200.00	247.14	-26.9**
3	4.889	-8.611	<b>-16.11</b>	310.00	335.00	330.00	260.00	235.00	279.28	5.625
4	7.889	-10.61	6.889	<b>-20.11</b>	330.00	375.00	270.00	280.00	299.28	27.6**
5	0.389	-3.111	29.39*	2.389	<b>-25.11</b>	360.00	290.00	270.00	302.85	30.1**
6	-16.61	9.889	7.389	30.39*	12.889	<b>-19.11</b>	285.00	295.00	315.71	47.1**
7	-8.611	12.889	5.389	-6.611	10.889	-11.11	<b>-3.111</b>	225.00	252.85	-20.9**
8	-7.111	-15.61	-13.11	9.889	-2.611	5.389	3.389	<b>9.889</b>	243.57	-27.4**
P.M	200.00	215.00	265.00	305.00	305.00	345.00	225.00	225.00		

Diagonals and below the diagonals represent SCA effects and above the diagonals represent the actual values of the crosses. GCA = General combining ability effects of the parents, P, M is the per se of the parents, Cr. Mis cross mean of every parent. \*, \*\* represent significant of GCA and SCA effects from zero at  $P \leq 0.05$  and  $P \leq 0.01$ , respectively. 1 = Roba-1, 2 = Dimtu, 3 = Zebra, 4 = MAM-41, 5 = BELDAKMI RR 5, 6 = SK93263, 7 = Tabor, 8 = Red wolaita.

Number of seeds per pod is one of the principal yield components in common beans. As a result, Roba-1 could be considered as good parent for future hybridization program with a major aim of improving yield. Positive and significant GCA effect was observed by Tabor for the same trait. Foolad

and Bassiri [5] have found good general combiner parents for number of seeds per plant. Parents, SK 93263 and BELDAKMI RR 5 on the other hand exhibited the minimum GCA effects for the trait, suggesting that these two parents

were poor combiners for number of seeds per pod in their progenies.

All parents except Zebra exhibited highly significant GCA effects for 1000-seed weight. SK 93263 followed by BELDAKMI RR 5 were good general combiners for this trait. These two parents were poor general combiners for number of seeds per pod. Similarly, Roba-1 which was a good general combiner for number of seeds per pod here exhibited the minimum GCA effects. Such situations could possibly be explained by the phenomenon of component compensation in beans [1]. This result is in agreement with the findings of [10], [12], and [5]. However, several other authors showed that there were parents which had positive or negative GCA effects for the traits considered [17], [12], and [22].

Information on SCA estimates of crosses are important to know the hybrid performance based on the per se performance of parental lines. Only eight crosses exhibited significant SCA effects for number of seeds per pod, among which four crosses (Roba-1 x SK 93263, BELDAKMI RR 5 x Tabor, SK 93263 x Tabor, and BELDAKMI RR 5 x Red wolaita) showed positive SCA effects for the trait, indicating that these crosses produced larger number of seeds per pod than it would be expected from the per se performance of the parents.

Different statistics and their significance tests of the Hayman's graphical approach for number of seeds per pod are presented in Table V. The  $(W_r - V_r)$  was not significant, indicating the absence of epistasis in the expression of the trait. The  $W_r/V_r$  graph (Fig. 1) revealed that the estimated regression line intercepted the  $W_r$ -axis above the point of origin. This suggested that inheritance of number of seeds per pod was governed by partial dominance with additive type of gene action. The regression line did not significantly deviate from unit slope, indicating the absence of epistasis. The distribution of array points on the regression line revealed that, Tabor possessed the maximum number of dominant gene, being closest to the origin. BELDAKMI RR 5 on the other hand contained the maximum recessive genes, being farthest from the point of origin. Array points scattered along the regression line on the graph, showing the genetic diversity among parents for the trait considered.

#### IV. CONCLUSION AND RECOMMENDATION

In the 8 x 8 diallel crosses of elite common bean genotypes (6 released varieties and 2 promising genotypes); there was significant difference between genotypes, parents, and crosses for the traits considered. Presences of significant statistical difference between parents show that there is sufficient additive genetic variance to be exploited. The crosses were in general superior in performance than parents, indicating presence of directional dominance which increases these traits.

TABLE V  
DIFFERENT STATISTICS FOR THE HAYMAN'S GRAPHICAL APPROACH OF  
DIALLEL ANALYSIS

Parents	Number of seeds per pod			
	$V_r$	$W_r$	$(W_r + V_r)^*$	$(W_r - V_r)^{**}$
Roba-1	0.244	0.286	0.530	0.041
Dimtu	0.303	0.363	0.666	0.060
Zebra	0.594	0.773	1.367	0.179
MAM-41	0.365	0.479	0.844	0.113
BELDAKMI RR 5	0.800	0.759	1.559	0.042
SK 93263	0.729	0.692	1.421	0.037
Tabor	0.275	0.110	0.385	0.165
Red wolaita	0.550	0.400	0.950	0.150

$$b_{W_r, V_r} = 0.96^{**} \text{ Intercept} = 0.11^{**}$$

$V_r$  = Variance of all the progenies in each parental array (an array is a group of crosses involving a particular parents),  $W_r$  = Covariance between parents and their offspring's in each array and  $b_{W_r, V_r}$  = Regression of  $W_r$  on  $V_r$  and test for  $b_{W_r, V_r} = 1$ , and Intercept = The point where the regression line intercepted the  $W_r$ -axis test for Intercept = 0. Significance of  $(W_r + V_r)$  and  $(W_r - V_r)$  is from the direct ANOVA of the parameters.

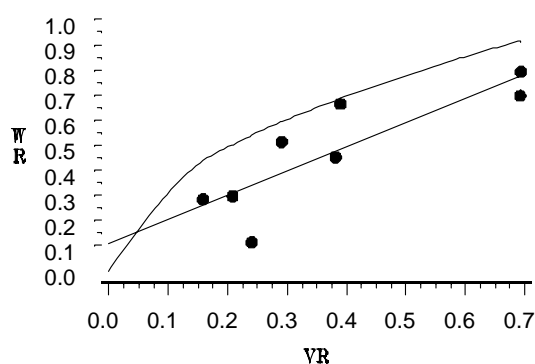


Fig. 1  $W_r/V_r$  graph for number of seeds per pod

The study showed that only additive type of gene action was important in governing the inheritance of 1000 seed weight. However, both additive and non-additive types of gene actions were important in the inheritance of number of seeds per pod. Additive gene action was more important as the variance component due to GCA was greater than the variance component due to SCA. The preponderance of additive genetic variation in the  $F_1$  generation would indicate higher heritability and the possibility of identifying transgressive methods like recurrent selection and pedigree selection can be employed to improve such traits. Similarly, from the graphical approach of Hayman, the inheritance of number of seeds per pod was governed by partial dominance with additive type of gene action. Traits governed by such type of gene action can be improved in the early generations in a breeding program.

Roba-1 proved to be good general combiner and possessed more number of dominant genes for number of seeds per pod. Moreover, Roba-1 has got the maximum per se performance for the trait. Similarly, Tabor was good general combiner and possessed more number of dominant genes for the same trait and also it has been involved as one parent for the crosses that exhibited the maximum SCA effects for number of seeds per

pod and 1000-seed weight. Thus these varieties can be considered as a good parent for future hybridization program.

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