
COMBINING ABILITY AND HERITABILITY ESTIMATES OF TRAITS RELATED TO BIOLOGICAL NITROGEN FIXATION AND YIELDS IN COMMON BEAN (*Phaseolus vulgaris* L.) CULTIVARS

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ABSTRACT

Improvement of common bean lines for their ability to fix more nitrogen may improve yields of common bean. The success of a breeding program depends on the choice of the populations capable of producing progeny with desired trait combinations. The aim of this study was to estimate the general and specific combining abilities and discriminate superior parents and hybrid combinations among six different common bean cultivars and their diallel hybrids. The values for heritability in a broad sense (h^2_b) and narrow sense (h^2_n) were high for all traits indicating reliability in the transmission of traits to offspring. Genotypes Kijivu, Msolini and G51137A with good general combining ability have potential for obtaining superior lineages, which may be used in breeding programs. Among hybrids evaluated, the promising combinations for further utilization in hybrid development were G51137A x Kijivu, G51137A x Msolini and G51495A x Msolini with good specific combining ability.

Keywords: Combining ability, *Phaseolus vulgaris*, Heritability.

Introduction

Biological Nitrogen Fixation (BNF) can be considered as one of the sources of crop nutrient supply for poor and small-scale farmers who cannot afford the use of costly inorganic fertilizers (Wunnaet *al.*, 2009). Common bean yields, like those of other legumes that fix nitrogen, are dependent on nitrogen derived from the symbiotic relationship between common bean plants and rhizobia (Wunnaet *al.*, 2009). According to Mmbaga and Friesen (2003), Tanzania is among the countries where a lot of research has been done on types, quantities and methods of fertilizer application. However, with the poor farmers' scarce resources there has been minimal adoption of these types of technologies. Many farmers use nitrogen fixing legumes in their farming systems (Chivengeet *al.*, 1998). Nitrogen-fixing legumes like common bean can be used to provide nitrogen to the soil. Improvement of common bean varieties for their ability to fix more

nitrogen for improving the yields of common bean is of paramount need. There is genotypic variability for nitrogen fixation and related traits in common bean germplasm, and several traits (such as nodule dry weight, biomass production, shoot dry weight, harvest index, pod yield and nitrogenase activity) which have been identified and used as selection criteria for increased N₂ fixation (Pimratchet *et al.*, 2004).

The success of a breeding program depends on the choice of the populations capable of producing progeny with desired trait combinations (Getachew, 2014). Segregating populations make it possible to select lines with superior performance to that of the parents. Diallel analysis method provides a systematic approach for identifying appropriate parents and crosses to be used for improvement of crop varieties. It also aids in choosing the most efficient method for parental selection by allowing them to estimate several genetic parameters (Ramalho *et al.*, 1993). The diallel analysis method has been widely used by plant breeders to select appropriate parents and crosses and to determine the combining abilities of parents in the early generations (Gonçalves-Vidigale *et al.*, 2008). The most commonly used diallel analysis methods are those proposed by Griffing (1956) and Gardner and Eberhart (1966). Griffing's (1956) methodology is centered on the estimation of the general combining ability (GCA) of possible parents and the specific combining ability (SCA) of the respective hybrid combinations (Cruz *et al.*, 2004). Combining ability analysis is one of the powerful tools in identifying the best combiners, which may be hybridized to exploit transgressive segregants that help in identifying superior recombinant inbred lines.

The limitation to N₂ fixation imposed by the plant genotype can now be alleviated through breeding (Bliss, 1993). There has been considerable investment in improving the capacity of common bean to fix atmospheric nitrogen (Devi *et al.*, 2013). Some studies have indicated that selection to increase nitrogen fixation will be successful if variability in germplasm is heritable and selected parents are agronomically suitable (Bliss, 1993). In plant breeding programs, selecting genotypes for development of new cultivars is one of the main objectives, and the efficiency is increased following careful evaluation of the parents to compose the crossings (Machado *et al.*, 2002).

Genotypes with high nodulation ability sometimes lack desirable characters and are not of the preferred seed types. In such cases, hybridization is required between the preferred types. When doing hybridization, information about heritability of traits is required in order to predict the success of selection from populations created from such crosses. It is essential to know how much of the variation in a crop is genetic, and to what extent this variation is heritable, because

efficiency of selection depends mainly on additive genetic variance, influence of the environment and interaction between genotype and environment (Hinkossa *et al.*, 2013).

Choices of parents should be based both on GCA and SCA (Griffing, 1956). The diallel crossing was used because it can produce all possible single crosses among a set of inbred lines and has been widely utilized to provide information on the potential of parents involved in hybrid combinations as well as implications on genetic control of the traits under investigation (Gonçalves-Vidiga *et al.*, 2008). Diallel analysis provides a systematic approach for the detection of appropriate parents and crosses. Hence, the aim of this study was to estimate the general combining ability (GCA) and specific combining abilities (SCA) and to discriminate the superior parents and hybrid combinations among six different common bean cultivars in order to determine the most appropriate parents and crosses for improved N₂ fixation, plant growth and yields.

2. Materials and Methods

2.1 Parental genotypes

Six common bean genotypes were crossed in a half diallel method. Three cultivars with high nodulation ability used were Kijivu, Yellow and Msolini and three lines with low nodulating potential were G51137A, G51495A and G19696.

2.2 Crossing of the parents

The study was conducted in a screen house at Sokoine University of Agriculture, Morogoro, Tanzania. The minimum and maximum temperatures for the area were 19.9°C and 29.3°C, respectively, while the relative humidity was 81.4%. Parents were grown in four-litre plastic pots. Pots were filled with 4 kg of field soils, incorporated with TSP fertilizer at the rate of 2.67 mg/kg. Four seeds were sown per pot later thinned to 2 seedlings per pot. At flowering crosses were made. The parents included Kijivu, Msolini, Yellow (nodulated genotypes) and G 51137 A, G 51495 A and G 19696 (non-nodulated). Emasculation and pollination were performed by hand, using the methodology proposed by Veira (1967). This method consists of mechanical emasculation of the female parent, by removing the flower buds before flowering. Emasculation was followed by cross pollination, for which ripe pollen grains from open flowers of male parents were used to perform the crosses. A total of 50 crosses were conducted for each hybrid combination to guarantee a sufficient quantity of seeds to form F1 populations.

The experiment composed of six generations, 2 parents P1, P2 and F1, F2, BC1 and BC2 generations derived from the cross between G51137A x Kijivu (non-nodulated and high nodulated). The experiment was done in a screen house, seeds sown in pots consisted of 15 plants for G51137A, 15 plants for Kijivu, 15 plants for F1, 14 plants for F2, 20 plants for BC1

and 24 plants for BC2 generations. The genetic parameters were estimated from the variances of the parents and in the F₁, F₂, BCP₁ and BCP₂ generations. Evaluation of parents and F₁ generation was done in a screen house. Seeds were sown in four litre pots, 2 plants per pot and two pots per line and laid out in the completely randomised design with three replications. The plants were harvested individually and the grain yield recorded as g/plant. The broad sense heritability, narrow sense heritability and average degree of dominance were calculated for the crossing between parents G51137 x Kijivu. These estimates were based on variances obtained from the parents and investigated generations calculated with formulas described by Mather and Jinks 1982;

$$h^2b \% = (\sigma_g^2 / \sigma_p^2) \times 100$$

$$h^2n \% = (\sigma_a^2 / \sigma_p^2) \times 100$$

$$\delta^2a = (2 \delta^2F2) - [\delta^2BC1 + \delta^2 BC2]$$

$$\delta^2p = \delta^2F2 - \delta^2e$$

$$\delta^2e = (\delta^2P1 + \delta^2a + (2\delta^2F1))/4$$

Whereby: h²b = heritability in broad sense, h²n = heritability in narrow sense, σ_a^2 = Component of additive variance, σ_p^2 = Component of phenotypic variance, δ^2_e = Component of environmental variance

2.3 Data Collected

The following characteristics were assessed: number of nodules/plant, shoot dry weight and root dry weight, root length, plant height and grain yields per plant as in Chapter 3.

2.4 Data Analysis

The data were subjected to analysis of variance by the R software package. Treatment means, sum of square partitioning for general and specific combining ability, were performed according to Griffing (1956), mean comparison was run based on Duncan's Multiple Range Test at 5% probability level.

3. Results and Discussion

3.1 Combining abilities of parents for N₂ fixation variables: Mean squares for GCA and SCA analyses for studied variables

The analysis of variance showed significant ($P \leq 0.05$) GCA and SCA effects for all the studied variables (Table 1). Significant GCA indicates additive genetic effect and reliability of response to selection while significant SCA indicates dominance genetic effect and reliability of hybrid development.

Table 1: Analysis of variance (Mean squares) for combining ability in the studied variables

Source	df	Plant height (cm)	Number of nodule/plant	Root length (cm)	Root dry weight (g)	Shoot dry weight (g)	Yield (g/plant)	% N
GCA	5	327.4***	273.6***	302.9***	11.8***	56.9***	403.2***	65.2***
SCA	9	20.2***	14.4***	14.9***	8.4***	13.7***	14.4***	12.4***
Error	28	2.2	2.4	2.9	0.02	0.5	2.4	0.4

3.2 The general combining ability (GCA) effects of parental genotypes for the studied variables

Significant GCA ($P \leq 0.05$) effects were observed among the cultivars, indicating that additive effects were involved in the control of the tested characteristics (Table 2). Therefore, new cultivars could be obtained from these parents. Genotype Msolini and G 19696 had the highest positive GCA for plant height (Table 2). In plant breeding these parents can be used to increase this characteristic as plant height has positive correlation with number of nodules per plant; hence taller bean genotypes have more nodules (Fening, 2009). Genotypes Kijivu and G51137A showed positive GCA for number of nodules/plant. Genotypes G51495A and Yellow (Table 2) had negative GCA estimates for number of nodules per plant, hence should not be used as parents in a breeding program designed to improve this characteristic. Msolini, G51495A and G51137A had positive GCA values for shoot dry weight hence these parents can be used in a breeding program to improve this trait. Improving shoot dry weight improves number of nodules per plant (Fening, 2009). Genotypes G51495A, Kijivu and Msolini for root length and genotypes G51495A, Msolini and G51137A for root dry weight have positive GCA; hence, to improve these traits these genotypes could be used as parents. Msolini, G51137A and G51495A having a positive GCA for % N, hence can be used in a breeding program to increase % N. For grain yield, genotype Msolini, G51495A and G51137A have positive GCA for yield; hence, these genotypes could be used in a breeding program for yield improvement.

High estimates of the general combining ability indicate parental superiority in the magnitude of the mean of a given trait, as compared to other parental crosses (Griffing, 1956). High GCA also means that the parent can combine well with a number of other parents to give good hybrids and that additive gene effects account for variation in the trait. Thus, performance in subsequent generations after a cross can be highly predictable. The inbred lines that revealed strong GCA effects could be utilized further as sources for population improvement towards the accumulation

of favorable additive genes for common bean variety improvement (Franco *et al.*, 2001). Vencovsky and Barriga (1992) mentioned that a high (or low) estimate of GCA for a particular parent indicates a higher (or lower) concentration of favorable alleles in it as compared to the others used in the same diallel crossing. Negative GCA was observed for some traits such as number of nodules/plant, shoots dry weight, yield, plant height and estimated %N. The negative values of GCA reveal the inferiority of these genotypes in relation to others regarding these traits. Hence, reduced yield could be obtained by using G19696 as parent (Machado *et al.*, 2002).

Table 2: Estimation of general combining ability (GCA) of parental lines for the studied variables

Genotype	Plant height (cm)	Nodules/plant (no)	Root length (cm)	Root dry weight (gm)	Shoot dry weight (cm)	% N	Grain yield (g/plant)
G 51137 A	-18.9	3.81	-1.25	0.02	0.81	0.27	1.20
G 51495 A	5.9	-0.74	2.03	0.04	0.62	0.29	0.20
G 19696	12.9	-3.07	-0.80	-0.05	-1.42	-0.55	-1.30
Kijivu	2.3	3.15	0.89	-0.01	0.24	-0.05	0.30
Msolini	14.2	-0.07	0.14	0.03	-0.32	0.13	0.50
Yellow	-16.6	-0.74	-1.02	0.00	-0.55	-0.07	-0.70
SE	0.7	1.3	0.6	0.02	0.4	0.3	0.4

3.3 Specific combining ability (SCA) effects for the studied variables

The best genotype combinations for plant height were G51137A x Kijivu and G51495A x Yellow (Table 3), which presented high positive SCA values, followed by G51137A x Msolini (12.7) and G19696 x Kijivu (9.3). These combinations could be recommended for intrapopulational breeding because at least one of the parents (G51495A or Kijivu) had positive GCA. Results showed that these hybrid combinations present a high potential for obtaining superior lineages with regard to plant height. Alghamdi *et al.* (2009) also reported significant SCA effects for plant height in faba bean crossing. Combination G51137A x Yellow (-32.7) and G51495A x Kijivu (-29.2) had high negative SCA values which could reduce plant height. With regard to number of nodules per plant, combinations of G51137A x Kijivu and G 51495A x Kijivu showed positive SCA values. The results suggest that the specific combinations can be used in a breeding program to obtain hybrids with increased number of nodules per plant. For root length, combinations of G51495A x Yellow and G51495A x Msolini had the highest SCA values. These combinations could be used for improvement of this trait in hybrid combinations.

Crosses of G51137A x Msolini and G19696 x Kijivu had the highest SCA values for shoot dry weight while for grain yield, combinations of G19696 x Msolini, G51495A x Yellow and G51137A x Msolini presented positive and high SCA effects. Crosses G19696 x Kijivu and G51137A x Yellow have higher and positive SCA effects for root length, while for root dry weight cross G51137A x Kijivu, G51495A x Msolini and G19696 x Msolini had positive SCA though it was too low. Alghamdi, (2009) reported significant SCA effects for yield in faba bean crosses. Hybrid combinations with high means, favorable SCA estimates and including at least one of the parents with high GCA, would tend to raise the concentration of favorable alleles (Cruz and Regazzi, 1994). SCA effects are the deviations in the performance of a hybrid compared with what would be expected based on the GCA of the parents.

Table 3: Specific combining ability (SCA) effects for characters measured in the common bean hybrids

Genotype	Plant height (cm)	Nodules/plant (no)	Root length (cm)	Root dry weight (gm)	Shoot dry weight (cm)	% N	Grain yield (g/plant)
G51137A x Kijivu	20.1	1.41	0.17	0.02	-0.48	-0.16	0.10
G51137A x Msolini	12.7	-0.51	-1.08	-0.04	1.52	0.00	0.30
G51137A x Yellow	-32.7	-1.03	0.91	0.00	-0.42	0.16	-0.40
G51495A x Kijivu	-29.2	1.63	0.89	-0.01	-0.09	-0.04	0.10
G51495A x Msolini	-10.6	0.18	3.09	0.01	0.27	0.01	-0.70
G51495A x Yellow	16.6	0.52	2.58	-0.01	0.44	0.01	0.40
G19696 x Kijivu	9.3	-3.04	-1.11	-0.03	0.55	0.20	-0.30
G19696 x Msolini	-1.9	0.80	1.3	0.01	0.11	-0.02	0.40
G19696 x Yellow	-7.3	0.51	-0.2	0.00	-0.02	0.07	1.3
SE	11.4	1.5	0.6	0.02	0.4	0.3	0.2

3.4 Number of evaluated plants, means and variances of traits obtained in six generations (P1, P2, F1, F2, BC1 and BC2) for the cross G51135A x Kijivu

High values of % N (6.5), grain yield (12.3 g/plant), plant height (120.4 cm) and root length (21.6 cm) in the F2 and BC1 generations (Tables 4 and 5) revealed presence of transgressive segregants because the F2 values were greater than those observed in G 51137A

and Kijivu, the parental genotypes, except for root length. The best performances that were generally observed for the segregating generations for number of nodules/plant, % N, yield, plant height, root length and shoot and root dry weight were observed in F2 generation (Tables 4 and 5). This may imply greater heterogeneity, suggesting great variability within this population, in turn signifying higher rate of transmission of these characteristics to future generations. High variances suggest a high rate of transmission of this characteristic to generations from crosses. Smaller variances were observed in the parents, confirming homozygosis and homogeneity in these populations. Genetic variability aids as the basis for selection (Pimratchet *al.*, 2004).

Table 4: Number of evaluated plants, means and variances of traits obtained in six populations (P1, P2, F1, F2, BC1 and BC2) derived from crosses G51135A x Kijivu

Generation	Number of nodules/plant			% N		Grain yield (g/plant)	
	n	m	δ^2	m	δ^2	m	δ^2
G51137A	15	0	0.0	3.4	0.2	4.7	1.5
Kijivu	15	43.5	2.4	6.3	0.4	10.4	1.6
F1	15	7.4	3.5	4.5	0.5	7.2	3.3
F2	14	14.5	7.7	6.5	1.5	12.3	10.1
BC1	20	5.3	3.1	3.8	0.8	6.8	5.1
BC2	24	18.2	6.9	6.3	1.1	11.2	7.0

n = number of evaluated plants, m = mean and δ^2 = variance,

Table 5: Number of evaluated plants, means and variances of some traits obtained in six populations (P1, P2, F1, F2, BC1 and BC2) derived from cross G51135A x Kijivu

Generation	Plant height			Root length		Shoot dry weight		Root dry weight	
	n	m	δ^2	m	δ^2	m	δ^2	m	δ^2
G51137A	15	118.3	1.6	21.1	1.8	5.5	0.4	0.5	0.04
Kijivu	15	106.6	1.7	15.4	1.7	6.5	0.3	0.4	0.01
F1	15	117.6	2.7	18.4	4.0	6.4	0.7	0.4	0.02
F2	14	120.4	11.6	20.4	8.6	6.7	1.5	0.6	0.05
BC1	20	118.4	7.8	21.6	5.1	6.3	1.2	0.5	0.01

BC2	24	109.8	9.0	18.1	6.1	6.9	0.9	0.5	0.02
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n = number of evaluated plants, m = mean and δ^2 = variance

3.5 Heritability and component of variances for the studied variables

Heritability in the broad sense ranged from 0.50 (root dry weight) to 0.81 (plant height) while the narrow sense ranged from 0.55 for plant height to 0.80 for yield (Table 6). The heritability in the broad sense and narrow sense were both high, hence most of the gene effects are due to additive gene action. Thus, it is possible to improve these traits genetically with high predictability. Higher heritability may also imply lower environmental variance or minor interaction between genotype and environment (Acquaah, 2007). Wunna *et al.* (2009) reported high heritability for biomass production (0.73 - 0.89) in peanut. According to the present study, additive variance was higher than dominance variance for all traits (Table 6). The existence of high additive variance suggests possible identification of superior genotypes (Cruz *et al.*, 2012). Environmental variance was less than additive and dominance variances for all traits.

Table 6: Broad and narrow sense heritability and component of variances for studied variables in cross G51135A x Kijivu

Genetic parameters	Plant height (cm)	Nodules/plant (no)	Root length (cm)	Root dry weight (gm)	Shoot dry weight (cm)	% N	Grain yield (g/plant)
H² b	0.81	0.69	0.66	0.50	0.67	0.73	0.76
h²n	0.55	0.70	0.70	0.70	0.60	0.73	0.80
δ^2a	6.4	5.4	6.0	0.07	0.9	1.1	8.1
δ^2p	11.6	7.7	8.6	0.10	1.5	1.5	10.1
δ^2g	9.4	5.3	5.7	0.05	1.0	1.1	7.7
δ^2e	2.2	2.4	2.9	0.02	0.5	0.4	2.4
δ^2d	1.5	1.0	1.0	0.7	1.1	1.0	1.0

H² b = Heritability in broad sense, H²n = Heritability in narrow sense, δ^2 a = additive variance, δ^2 p = phenotypic variance, δ^2 g = genetic variance, δ^2 e = environmental variance, δ^2 d = dominance variance,

3.6 Mean performance of parents and their hybrids

The mean performance of the six parents and their respective crosses are presented in Table 7. The parental genotypes G19696 and Msolini had taller plants (223.5 and 213.5 cm, respectively) while genotype Yellow was the shortest (95.7 cm). Crosses G51495A x Yellow (214.3 cm), G19696 x Msolini (210.2 cm) and G19696 x Kijivu (209.5 cm) revealed higher values for this

trait. The parents Kijivu and Msolini showed higher values for number of nodules per plant (43.7 and 35.7 respectively), while for the crosses, higher values were on G51137 A x Kijivu (14.4), G51495A x Kijivu (9.7) and G51137A x Msolini (9.0) for this trait. The parental genotypes G51495A and G51137A showed higher values for root length (25.7 and 21.3 cm respectively) while for the crosses the higher values were for G51495A x Msolini (20.17 cm) and G51495A x Kijivu (22.0 cm) for this trait. However, for shoot dry weight, parents Msolini and Yellow had higher values (10.1 and 7.4 g), while among the crosses G51137A x Msolini had a higher value (7.6 g). Among crosses, the lowest values for shoot dry weight were observed from crosses G19696 x Msolini (3.9 g) and G19696 x Yellow (3.6 g). The parents Msolini and Kijivu had highest values for grain yield (11.2 and 10.3 g/plant, respectively) while among the crosses higher grain yield values were from G51137A x Msolini (8.2 g/plant) and G51137A x Kijivu (7.8 g/plant).

On the other hand, crosses with lowest grain yields were G19696 x Kijivu (4.8 g/plant) and G19696 x Yellow (4.1 g/plant). The highest %N was from the parental genotype Msolini (6.6) and Yellow (6.5). Crosses G51495A x Msolini and G51495A x Yellow recorded higher values for % N (5.3 and 5.2, respectively). Parents with high performance are likely to give progenies with high performance. For example with plant height, parents G19696 and Msolini which were tall resulted in tall crosses like G19696 x Kijivu and G19696 x Msolini. This indicates the importance of evaluating parents before selecting them for crossing. Parent Kijivu showed high performance for number of nodules per plant. Parents Kijivu and G51137A, with high GCA for number of nodules per plant, resulted in good performance of cross G51137A x Kijivu. Differences among parental lines indicated sufficient diversity for most traits under study, and thus genetic variability would be expected in the progenies in segregating generations following crossing (Ibrahim, 2010). Furthermore, it allows plant breeders to build future breeding programmes for high potential yield in common bean.

Table 7: Mean performance of parents and their F1 hybrids for the studied traits

Genotype	PH (cm)	Nodules/plant (no)	RL (cm)	RDW (gm)	SDW (cm)	% N	Grain yield (g/plant)
G51137A	117.5a	0.0a	21.3bcd	0.3c	5.5bc	4.4bc	4.7ab
G51495A	185.0bc	0.0a	25.7d	0.4cd	4.9abc	4.1ab	3.9a
G19696	223.5d	0.0a	17.8abc	0.2a	3.3a	3.4a	5.2abc
Kijivu	104.0a	43.7g	15.0a	0.3cd	6.4cd	6.1de	10.3f
Msolini	213.5cd	35.7f	17.5abc	0.4d	10.1e	6.6e	11.2f

Yellow		95.7a	26.3e	14.3a	0.3cd	7.4d	6.5e	7.9de
G51137A	x	188.5bc	14.4d	18.0abc	0.3cd	6.1cd	4.9bc	7.8de
Kijivu								
G51137A	x	193.0bcd	9.0cd	16.0ab	0.3c	7.6d	5.3cd	8.2e
Msolini								
G51137A	x	116.8a	7.7bc	16.8abc	0.3c	5.4bc	5.2cd	6.6b-e
Yellow								
G51495A	x	164.0b	9.7cd	22.0cd	0.3c	6.3cd	5.1c	6.8cde
Kijivu								
G51495A	x	194.5bcd	5.0abc	20.2abc	0.4d	6.1cd	5.3cd	6.1bcd
Msolini								
G51495A	x	214.3cd	4.7abc	18.5abc	0.3cd	4.9abc	5.1c	6.1bcd
Yellow								
G19696 x Kijivu		209.5cd	2.7ab	17.2abc	0.2a	4.1ab	4.5bc	4.8abc
G19696 x Msolini		210.2cd	2.6ab	18.8abc	0.3bc	3.9ab	4.4bc	5.8abc
G19696 x Yellow		174.0b	2.3ab	16.2abc	0.3ab	3.6a	4.1ab	4.1a
CV%		9.9	30.5	16.3	9.4	15.7	9.7	15.5
SE		9.9	1.9	1.7	0.02	0.5	0.3	0.6

Different letters within each column indicate significant difference at 5% level

4 Conclusions

Based on heritability estimates, the present study revealed that there is high heritability, which indicates that traits can be transferred successfully and hence there would be a possibility to improve nitrogen fixation and agronomic traits using these parents. Genotypes Kijivu, Msolini and G51137A have potential for obtaining superior lineages, which may be used in intrapopulation breeding programs. Among the nine hybrids evaluated, the most promising combinations basing on SCA results for further utilization in hybrid development in common bean were G51137A x Kijivu, G51137A x Msolini and G51495A x Msolini. These hybrids presented high estimates of specific combining ability for most of the traits, and are the most promising crosses for obtaining more productive lineages.

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