

Estimates of genetic and phenotypic variance of some traits of dry bean using a segregant population from the cross "Jalo" x "Small White"*

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ABSTRACT

The estimates of σ_A^2 , σ_D^2 , D_1 , D_2 , σ_e^2 and σ_w^2 for a cross between the dry bean cultivars "Jalo" and "Small White" were obtained from the phenotypic variance among the family means and the covariances among the progeny means of the F_3 , F_4 and F_5 generations. The D_1 estimates were always negative, showing that for this population, the frequency of favorable alleles must be lower than 0.5. Under this condition and depending on its magnitude, D_1 can minimize the genetic progress with selection; the errors associated with the estimates of the components of the genetic variance were large, indicating that when obtaining new variance estimates all attention should be directed to the processes of experimentation with the families.

INTRODUCTION

The correct choice of method for dealing with a segregant population after hybridization is important for efficient plant breeding. In this context, knowledge of the genetic variability and the predominant type of gene action controlling the trait under selection is of fundamental importance to the breeder.

Literature reports on genetic control of several traits in dry bean present results from various methodologies, including biparental crossings using the F_2 generation and backcrossings (Reis *et al.*, 1981 and Santos *et al.*, 1986), diallel crossings (Nienhuis and

Singh, 1988; Arriel *et al.*, 1990 and Vizgarra, 1991) and studies on pure lines (Scully *et al.*, 1991).

The use of a segregant population to estimate the components of genetic variance in the dry bean has been little used and the existing studies presuppose that there was no selection or sample effect, since the allelic frequency of the segregant loci is considered as 0.5. However, this is not always true and, in this situation, the additive genetic variance (σ_A^2) and dominance (σ_D^2) are not the only genetic variance components. Components such as D_1 , the covariance between the additive and dominance effects in the homozygote; D_2 , the variance of the dominance effects in the homozygote and \bar{H} , the squared inbreeding depression (Souza Jr., 1989) appear. These components affect the selection efficiency but there is no information on their magnitude or effect on selection.

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The objective of the present work was to obtain estimates of the genetic variance components, considering the allelic frequencies of the segregant loci as 0.5 and different from 0.5. By assessing segregant progenies from crosses among lines of dry beans.

MATERIAL AND METHODS

The experiments were carried out an experimental field in Lavras, state of Minas Gerais, Brazil. Progenies from the cross between cultivars "Jalo" and "Small White" were assessed. In the F₂ generation, 93 plants were selected by grain type and then inbred up to the F₅ generation by bulking within each F₂ derived family. Part of the seeds were used for generation advance and part for simultaneous assessment of the families in the F₃, F₄, and F₅ generations in the 1991 season. The F₃ families were evaluated in a 10 x 10 single lattice design which included the parents and five controls. Each plot consisted of a one meter row. The F₄ and F₅ generations were assessed in a 14 x 14 triple lattice experiment which included the parents and eight controls. Each plot consisted of a two meter row. Five plants were randomly harvested from each

plot and the number of pods and seeds, grain weight and weight of 100 seeds were determined for each plant.

The estimates of the genetic and environmental variance (σ_e^2 - environmental variance among plots and σ_w^2 - environmental variance among plants within plots) components were obtained from the among progenies mean squares in the analysis of variance of each generation and from the covariances between the family means. As the allelic frequency was different from 0.5, the genetic variance was partitioned according to the genetic covariance among relatives, using the procedure of Souza Jr. (1989). By this methodology, the covariance among relatives descendants from a common ancestor t and belonging to generations g and g' of the selfing series is:

$$\text{COV}_{g,g+i} = C_{tgg'} = (1 + I_t) \sigma_A^2 + \left[\frac{(1 - I_g)(1 - I_{g'})}{1 - I_t} \right] \sigma_D^2 + (I_g + I_{g'} + 2I_t) D_1 + \left[I_t + \frac{(I_g - I_t)(I_{g'} - I_t)}{2(1 - I_t)} \right] D_2 + \left[\frac{I_t(1 - I_g)(1 - I_{g'})}{(1 - I_t)} \right] \check{H}$$

where:

Table I - Coefficients of the phenotypic and genetic components for the respective estimates.

	σ_A^2	σ_D^{2*}	D ₁	D ₂	σ_e^2	σ_w^2
σ_w^2	0	0	0	0	0	1
$\sigma_{F_3}^2$	1.0533	0.3034	1.1067	0.165	0.5	0.1067
$\sigma_{F_4}^2$	1.0506	0.0879	1.6013	0.3129	0.3333	0.0675
$\sigma_{F_5}^2$	1.0591	0.0304	1.8683	0.4161	0.3333	0.0675
$\sigma_{d_3}^2$	0.5	0.5	1	0.375	0	1
$\sigma_{d_4}^2$	0.75	0.375	1.5	0.4688	0	1
$\sigma_{d_5}^2$	0.875	0.188	1.75	0.4922	0	1
COV _{3,4}	1	0.125	1.25	0.1875	0	0
COV _{3,5}	1	0.0625	1.375	0.2187	0	0
COV _{4,5}	1	0.312	1.625	0.3281	0	0
σ_e^2	0	0	0	0	4.932	1

$$* \sigma_D^{2*} = \sigma_D^2 + \check{H}$$

$\sigma_{F_g}^2$: Phenotypic variance among the progeny means in the gth generation; g = 3, 4 and 5.

$\sigma_{d_g}^2$: Phenotypic variance among plants within plots of the progenies of the gth generation; g = 3, 4 and 5.

COV_{g,g'}: Genetic covariance between progeny means in the gth and g'th generations; g = 3 and 4 and g' = 4 and 5.

I_t = the inbreeding coefficient of the reference generation; according to the method used

$$I_t = I_2 = 0.$$

I_g = inbreeding coefficient in the selection generation (F_g).

$I_{g'}$ = inbreeding coefficient in the F_{g+1} generation.

The coefficients of the genetic and phenotypic variance components of all estimates were obtained from this expression (Table I). From these 11 equations, estimates of six parameters were calculated using the weighted least squares method with the iterative process, following the methodology of Morais (1992) and Souza (1993). The estimates were obtained considering allele frequencies different from 0.5, using the complete model with σ_A^2 , σ_B^2 , D_1 , D_2 and, alternatively, supposing allele frequencies equal to 0.5 in the segregant loci using a model with only σ_A^2 and σ_B^2 .

The heritabilities and the expected gain from selection (10% intensity) were calculated from the estimates of the genetic variance components obtained in the complete model using a procedure similar to that of Souza Jr. (1989). As the assessment included the F_3 , F_4 and F_5 generations, the realized gain in F_4 with the selection of the 10 best offspring in F_3 and the realized gain in the F_5 with the selection of the best 10 F_3 and F_4 progenies were calculated. The realized heritabilities were also estimated (Fehr, 1987).

RESULTS AND DISCUSSION

Since the cross involved only two lines, each segregating locus had only two alleles and the squared inbreeding depression (\check{H}) is equal to σ_B^2 . The obtained σ_B^2 estimates include \check{H} .

The estimates obtained varied sharply according to the model being tested (Table II). For example, when the complete model including all the genetic variance components was fitted for grain weight per plants, σ_A^2 was greater than σ_B^2 . When the model fitted did not include D_1 and D_2 , the opposite happened, in spite of the fact that both had similar determination coefficients (R^2). It was also observed that the errors associated with the estimates of the components in the complete model were larger. For σ_A^2 , the error associated with its estimate was about 45% of its value, and for σ_B^2 , the error was larger than the estimate.

The estimates of σ_B^2 varied sharply in function of the model being tested (Table II). In the model without D_1 and D_2 , it was greater than σ_A^2 for all traits, except weight of 100 seeds. The presence of σ_B^2 in the control of these traits has also been reported on other occasions (Hamblin and Morton, 1977; Foolad and Bassiri, 1983). Most reports, however, mention that the additive effect is predominant in the control of these traits (Nienhuis and Singh, 1988; Ramalho *et al.*, 1988; Abreu, 1989; Takeda, 1990 and Vizgarra, 1991).

Table II - Estimates of the phenotypic variance components and respective standard deviations for number of pods per plant (NP), number of seeds per plant (NS), grain weight per plant (W) and weight of 100 seeds (WCS), for the two models tested.

Model	σ_A^2	σ_B^2	D_1	D_2	σ_e^2	σ_w^2	R^2	Interac- tion
$\sigma_F^2 = (\sigma_A^2, \sigma_B^2, D_1, D_2, \sigma_e^2, \sigma_w^2)$								
NP	52.74 ± 35.19	4.61 ± 23.22	-57.73 ± 38.13	129.76 ± 83.65	1.70 ± 0.16	10.71 ± 0.77	0.86	5
NS	973.86 ± 597.37	199.71 ± 389.49	-1070.08 ± 645.81	2420.30 ± 1412.09	-12.35 ± 3.91	110.39 ± 19.63	0.83	4
W	48.33 ± 21.72	9.75 ± 14.21	-56.05 ± 23.35	131.81 ± 50.70	0.94 ± 0.21	-0.19 ± 0.13	0.81	7
WCS	22.10 ± 26.72	-1.66 ± 17.34	-16.52 ± 29.71	36.49 ± 67.01	-1.04 ± 0.28	5.81 ± 1.40	0.90	1
$\sigma_F^2 = (\sigma_A^2, \sigma_B^2, \sigma_e^2, \sigma_w^2)$								
NP	0.63 ± 0.28	49.65 ± 3.95	-	-	1.08 ± 0.23	7.68 ± 1.13	0.87	2
NS	12.91 ± 5.11	888.35 ± 64.94	-	-	-10.77 ± 3.73	102.73 ± 18.08	0.83	14
W	0.08 ± 0.16	35.23 ± 2.40	-	-	-0.33 ± 0.14	3.66 ± 0.66	0.82	14
WCS	7.11 ± 0.50	7.64 ± 2.50	-	-	-1.06 ± 0.17	5.88 ± 0.84	0.89	2

* $\sigma_B^2 = \sigma_B^2 + \check{H}$

The presence of σ_D^2 has been observed to be associated with the assessment of materials made under little interplant competition. In the F₃ generation experiment a lower sowing density was used and, consequently, the intraplot competition was smaller, allowing a greater expression of the allelic interaction of dominance. The estimates of the genetic variance components must be obtained from the different families assessed under the same sowing density conditions.

The method of bulking within F₂ derived families was not adequate to obtain the estimates of the genetic variance components. In this method, the coefficient associated with σ_A^2 is always one among the families of the different generation, while the coefficient σ_D^2 is variable, and any fluctuation in the means obtained will affect the dominance variance with greater intensity (Ramalho and Vencovsky, 1978).

The estimates of D₁ and D₂ do not exist for the dry bean and are scarce for other species. For cotton (Crisóstomo, 1989) and rice (Morais, 1992), where these estimates has been obtained, D₁ is always negative, as found in our study for all the traits. As D₁ is a genetic covariance among the additive effects of the alleles and the effects of dominance of the homozygote, it can assume negative values. Simulations carried out by Crisóstomo (1989) and Fernandes (1990) showed that D₁ is negative in populations with an allelic frequency lower than 0.5 (not improved) and with directional dominance towards increasing the expression of the trait, and in populations with allelic frequency higher than 0.5 and with dominance in the direction of reduction the expression of the trait.

In a population derived from a cross between two autogamous parents, the allelic frequency of the segregant loci is 0.5 in the absence of selection. With selection, these frequencies can take on values higher or lower than 0.5 depending on selection direction. If dominance is to increase the expression of the trait, successive self pollinations will reduce the population mean, because of the reduction in frequency of the heterozygotic loci. Consequently, the mean of the F₃ generation will be greater than that of the F₄ and F₅, as occurred in this study. Since the estimates of D₁ were negative, it can be inferred that selection carried out for grain type in the F₂ generation contributed to reduce the frequency of the favorable alleles in the population for the traits assessed.

The additive variance for the weight of one hundred seeds was expressive in the two models tested. These results agree with those of Reis *et al.*, 1981; Foolad and Bassiri, 1983; Santos, 1984 and Vizgarra, 1991).

The estimates of the expected and realized heritabilities were similar for the F₄ and F₅ generations, indicating that it is possible to make inferences from the estimates of σ_A^2 , σ_D^2 , D₁ and D₂ (Table III). The two different sowing conditions did not allow reliable estimates for the F₃ generation. The estimates of h^2 varied sharply among the traits, being highest for the weight of one hundred seeds (Table III). The gains from selection for all traits, in the F_∞ generation, were also calculated using the among F₃, F₄ and F₅ family variance (Table III). The calculations were negative in some cases, due to large negative estimates for D₁. For grain weight the gain was positive only in the F₅ generation. Since the coefficient of the additive genetic variance in the bulk within F₂ method is constant along the generations, the change of sign in the calculated gain happened due to the proportionally larger increase in the coefficient of D₂ compared to that of D₁. These results underline the importance of obtaining more information about D₁ and D₂ because they affect the selection result and can guide plant breeders to the best selection strategy.

Table III - Estimates of heritability and expected and realized gains in the selection for number of pods per plant (NP), number of seeds per plant (NS), weight of grains per plant (W) and weight of 100 seeds (WCS).

Parameters	Estimates			
	NP	NS	W	WCS
$h_{3,4}^2$ (%)	25.28	27.64	22.92	70.46
$h_{r3,4}^2$ (%)	7.47	17.76	11.88	42.22
$h_{3,5}^2$ (%)	9.36	10.64	3.82	63.29
$h_{r3,5}^2$ (%)	0.4	10.47	4.44	50.79
$h_{4,5}^2$ (%)	28.98	30.58	21.67	77.68
$h_{r4,5}^2$ (%)	21.92	15.58	18.62	91.06
GSR _{3,4} (%)	4.78	14.04	9.69	14.16
GSR _{3,5} (%)	2.60	8.28	3.59	17.03
GSR _{4,5} (%)	10.49	9.82	10.54	24.95
GS ₃ (%)	-3.89	-4.41	-11.44	16.65
GS ₄ (%)	3.01	4.47	-4.82	19.70
GS ₅ (%)	13.86	19.60	20.42	21.01

$h_{g,g'}^2$: Broad sense expected heritability or realized heritability in F_{g'} with selection in F_g; g = 3 and 4, g' = 4 and 5.

GS_g and GSR_{g,g'}: Expected and realized gain, respectively, in the F_∞ and G_{g'} generation with selection in F_g.

RESUMO

A partir das variâncias fenotípicas entre médias de famílias e das covariâncias entre médias nas gerações F₃, F₄ e F₅, do cruzamento entre os cultivares de feijão Jalo e Small White foram obtidas as estimativas de σ_A^2 , σ_D^2 , D₁, D₂, σ_e^2 e σ_w^2 . Constatou-se que as estimativas de D₁ foram sempre negativas, mostrando que para essa população a frequência dos alelos favoráveis deve ser inferior a 0,5, e especialmente nessa condição, dependendo da magnitude de D₁, ele poderá minimizar o progresso genético com a seleção; o erro associado às estimativas dos componentes da variância genética foram altos indicando que na obtenção de novas estimativas da variância toda a atenção deva ser direcionada aos processos de condução das famílias.

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