Acta Scientiarum 21(3):423-427, 1999.
ISSN 1415-6814.

Genetic control on number of days to flowering and yield components in common bean (*Phaseolus vulgaris* L.)

Marco Antonio Aparecido Barelli[1], Maria Celeste Gonçalves-Vidigal[1]*, Antonio Teixeira do Amaral Júnior[2], Pedro Soares Vidigal Filho[1] and Lucas Silvério[1]

*[1]Departamento de Agronomia, Universidade Estadual de Maringá, Av. Colombo, 5790, 87020-900, Maringá-Paraná, Brazil. [2]Universidade Estadual do Norte Fluminense, Av. Alberto Lamego, 2000, Horto, 28015-620, Campos dos Goytacazes-Rio de Janeiro, Brazil. *Author for correspondence*

ABSTRACT. Genetic control on the performance of six common bean cultivars (LPSPI 93-17, LPSPI 93-19, FT Nobre, Aporé, Rudá and Campeão-1) and their 15 diallel hybrids were carried out, based on the following traits: number of days to flowering, mean seed weight, total number of pods per plant, mean number of seeds per pod, mean seed weight and grain yield. Hayman's methodology (1954) was used for the parameter estimation. The results showed that the dominance effects were important only for the mean seed number per pod. There were high coefficients of genetic determination for number of days to flowering and mean seed weight traits and, therefore, superior lines may be obtained using simple selection methods. Aporé, Rudá and Campeão-1 cultivars should be indicated for intrapopulational breeding programs for grain yield.

Key words: *Phaseolus vulgaris* L., diallel analysis, genetic control.

RESUMO. Controle genético do número de dias para o florescimento e componentes de rendimento em feijoeiro (*Phaseolus vulgaris* L.). Inferências genéticas sobre o desempenho de seis cultivares de feijoeiro (LPSPI 93-17, LPSPI 93-19, FT Nobre, Aporé, Rudá e Campeão-1) e seus 15 híbridos dialélicos foram obtidas para as características número de dias para o florescimento, número total de vagens por planta, número médio de sementes por vagem, peso médio de sementes e produção de grãos, empregando-se a metodologia de Hayman (1954). Os resultados evidenciaram superioridade dos efeitos de dominância apenas para número médio de sementes por vagem. Elevados coeficientes de determinação genotípica ocorreram para as características número de dias para florescimento e peso médio de sementes, denotando a perspectiva de obtenção de linhagens superiores pela aplicação de métodos simples de seleção. Para produção de grãos, os cultivares Aporé, Rudá e Campeão-1 são os indicados para programas de melhoramento intrapopulacionais.

Palavras-chave: *Phaseolus vulgaris* L., análise dialélica, controle genético.

Planning and execution of a breeding program require information on the genetic systems controlling the characters of interest, so that the expected gains can be maximized with the use of the selection process (Vencovsky and Barriga, 1992; Oliveira Júnior, 1993; Viana, 1995).

Analysis of diallel crosses has been emphasized in many breeding programs for different crops because of the large amount of information they offer the breeder (Cruz and Regazzi, 1994; Viana, 1995; Amaral Júnior, 1996).

Hayman's procedure (1954), among the methodologies of diallel analysis available, is not based on previously established statistical models, but rather on the knowledge of environmental and genetic nature of statistics, such as means, variance, covariances, obtained from the diallel table (Cruz and Regazzi, 1994).

According to Santos (1981) and Cruz and Regazzi (1994), Hayman's methodology (1954) has greatly contributed to breeding. It provides an efficient study of the genetic action involved in the control of traits and identifies the presence of epistatic interactions. It also estimates the genetic component of genotype determination and the limit of selection which may be obtained in segregant generations obtained from the assessed parents.

The present study used Hayman's methodology to assess a diallel among six common bean parents for five agronomic traits, to obtain genetic information for a breeding program in the northwest of the state of Paraná.

Material and methods

The common bean cultivars LPSPI 93-17, LPSPI 93-19, FT Nobre, Aporé, Rduá and Campeão-1 were crossed in a diallel system without reciprocals.

The parents and hybrids, in a total of 21 treatments, were assessed in the greenhouse at the Nucleus for Applied Studies on Agriculture (Nupagri) of the Department of Agronomy of the State University of Maringá (PR), September through November 1997. The experimental lay-out used a randomized complete block design with ten replications, whose experimental unit consisted of one pot with two plants.

The following traits were assessed: a) number of days to flowering (FLORESC), obtained by counting the number of days from sowing to the complete opening of the first flower of each plant in each treatment; b) total number of pods per plant (NTVP), obtained by counting the total number of pods produced per plant; c) mean number of seeds per pod (NMSV) obtained from the ratio between the total number of seeds and the total number of pods produced per plant, in each treatment; d) mean seed weight (PMS), expressed in grams, obtained by weighting a sample of 50 grains from each treatment; e) grain yield (PG), expressed in g/plant, obtained from the ratio between the total grain weight of the treatments and the respective number of plants.

The computer program GENES (Cruz, 1997) was used for this.

Results and discussion

Sufficiency test of the additive-dominant model. Assuming that the genetic effects are the results of the additive and dominant action of genes, Hayman (1954) imposed a series of restrictions which required the application of tests to verify the sufficiency of the model. Table 1 shows the results of the applications of two tests for the traits assessed. The totality of the traits was not significant in either test, so the assumptions imposed were valid and indicated that the additive-dominant model was adequate to the genetic study of these traits.

Number of days to flowering. Table 2 shows the correlation between the genotypic values of the ith parents ($\hat{Y}_{ii}$) and the sum of the covariance and variance among means of the ith lines ($\hat{w}_i + \hat{v}_i$) and the expected values of the coordinates $\hat{W}_R$, $\hat{V}_R$ e $\hat{W}_D$, $\hat{V}_D$ and their sums. There was a positive correlation between $\hat{Y}_{ii}$ and $(\hat{W}_i + \hat{V}_i)$, of magnitude equal to 0.4116, showing that the alleles which act to increase the number of days to flowering are predominantly, but not exclusively, recessive. In this case, parents 1 and 3, which were closer to the recessive end of the regression of $\hat{W}_i$ over $\hat{V}_i$ (Figure 1) would be unsuitable for selection of earlier lines. Thus, the most appropriate parents are, in order, six, two and five, because they are closer to the limit where the concentration of dominant alleles predominates (Figure 1).

Figure 1 shows the possibility of obtaining even more dominant segregant material; for instance, although parent number six has the greatest concentration of dominant alleles with $\hat{W}_i + \hat{V}_i$ = 0.7084 (Table 3), its value is still lower than its potential of 0.1950 according to Table 2. The opportunity of obtaining these segregant materials becomes more evident because the high heritability value ($\hat{h}^2_R$ = 0.7523, Table 4), which ensures the success of the transmission of the desirable alleles to future generations.

Table 1. Sufficiency tests of the additive-dominant model, using Hayman's methodology (1954) for five traits assessed among six common bean parents

Traits$^{1/}$	Regression$^{2/}$	Rotation of the $\hat{W}_i$ and $\hat{V}_i$ Axle$^{3/}$
	t (H$_o$: b = 1)	F = t^2 (H$_o$: B = b – 1 = 0)
FLORESC	-0.3819^{ns}	-0.1005^{ns}
NTVP	-0.5783^{ns}	-0.9711^{ns}
NMSV	-0.2160^{ns}	-0.7441^{ns}
PMS	-0.0066^{ns}	-0.3098^{ns}
PG	-0.2760^{ns}	-0.2190^{ns}

$^{1/}$ FLORESC: number of days to flowering; NTVP: total number of pods per plant; NMSC: mean seed number per pod; PMS: mean seed weight; PG: grain yield; $^{2/}$t test, weighing the $\hat{W}_i + \hat{V}_i$, values, at 5% levels of probability; $^{3/}$F test, weighing the $\hat{W}_i$ and $\hat{V}_i$, axles by their 45° rotation, at 1% and 5% levels of probability.

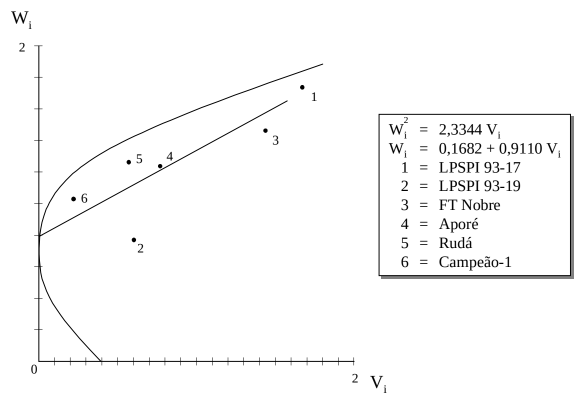

Figure 1. Regression of $\hat{W}_i$ over $\hat{V}_i$, for flowering period

Table 2. Estimates of the correlation between the genotypic value of the ith parent ($\hat{Y}_{ii}$) and the sum of the covariance with the variance among means of the ith line ($\hat{W}_i + \hat{V}_i$) and the expected values of the coordinates $\hat{W}_R$, $\hat{V}_R$ and $\hat{W}_D$, $\hat{V}_D$ and the sum of these for five traits assessed in six common bean parents, according to Hayman's methodology (1954)

Traits$^{1/}$	Estimates values						
	$r(\hat{Y}_{ii}, \hat{W}_i + \hat{V}_i)$	$\hat{W}_R$	$\hat{V}_R$	$\hat{W}_R + \hat{V}_R$	$\hat{W}_D$	$\hat{V}_D$	$\hat{W}_D + \hat{V}_D$
FLORESC	0.4116	2.3812	2.4288	4.8100	0.1810	0.0140	0.1950
NTVP	- 0.5266	9.0129	13.9678	22.9807	0.9026	0.1401	1.0427
NMSV	- 0.5830	0.1793	0.2286	0.4079	- 0.0261	0.0036	- 0.0225
PMS	- 0.2385	1.8174	1.5416	3.3590	0.3273	0.0500	0.3773
PG	- 0.9248	8.6633	11.1950	19.8583	- 1.4773	0.3255	- 1.158

$^{1/1/}$FLORESC: number of days to flowering; NTVP: total number of pods per plant; NMSC: mean seed number per pod; PMS: mean seed weight; PG: grain yield

Table 3. Values of the sum of the covariance between parent means and means of the ith line ($\hat{W}_i$) with the variance between means of the ith line ($\hat{V}_i$) and rank of the magnitude of the sum for six common bean parents, for FLORESC, according to Hayman's methodology (1954)

Parents	$\hat{W}_i + \hat{V}_i$	Classification$^{2/}$
1. LPSPI 93.17	3.4092	1º
2. LPSPI 93-19	0.8860	5º
3. FT Nobre	3.7168	2º
4. Aporé	1.6827	3º
5. Rudá	1.3877	4º
6. Campeão-1	0.7084	6º

$^{1/}$FLORESC: number of days to flowering; $^{2/}$Refers to the order of recessive allele concentration

Table 4. Estimates of the genetic components and information for the assessed traits, according to Hayman's methodology (1954)

Traits$^{1/}$	Estimates of the genetic components$^{2/}$						Estimates of genetic information$^{3/}$		
	$\tilde{\varepsilon}$	$\tilde{D}$	$\tilde{H}_1$	$\tilde{H}_2$	$\tilde{h}^2$	$\tilde{D} - \tilde{H}_1$	$\tilde{h}^2/\tilde{H}_2$	$\tilde{h}^2_R$	$\tilde{h}^2_A$
FLORESC	0.1267	2.2077	1.4154	0.8477	- 0.0790	0.7923	-----	0.7523	0.9072
NTVP	1.7802	4.0354	- 1.5162	- 0.8089	0.2072	5.5517	-----	0.3760	0.4469
NMSV	0.0346	0.1060	0.1211	0.0890	0.1509	- 0.0150	1.6959	0.2379	0.5361
PMS	0.1342	2.0082	0.4535	0.3532	0.1623	1.5547	0.4595	0.7557	0.8526
PG	3.8337	2.8704	- 1.3504	1.8890	31.5799	4.2209	16.7170	0.3258	0.3997

$^{1/}$FLORESC: number of days to flowering; NTVP: total number of pods per plant; NMSC: mean seed number per pod; PMS: mean seed weight; PG: grain yield; $^{2/}$ $\tilde{\varepsilon}$ = experimental error component; $\tilde{D}$ = additive effects component; $\tilde{H}_1$, $\tilde{H}_2$ and $\tilde{h}^2$ = dominance effects components; and $\tilde{D}$ - $\tilde{H}_1$ = component which expresses the difference between the additive and dominant effects; $^{3/}$ $\tilde{h}^2/\tilde{H}_2$ = expresses the number of genes displaying dominance; $\tilde{h}^2_R$ = narrow sense genotypic determination coefficient; and $\tilde{h}^2_A$ = broad sense genotypic determination coefficient

Table 4 shows the predominance of the additive effects ($\tilde{D}$ = 2.2077) over those related to dominance ($\tilde{H}_1$ = 1.4154; $\tilde{H}_2$ = 0.8477; $\tilde{h}^2$ = -0.0790) for the estimates of genetic components, since $\tilde{D}$ - $\tilde{H}_1$ is positive. Similar results were obtained by Foolad and Bassiri (1983) and Santos (1984) for the common bean.

Total number of pods per plant. The negative correlation value (-0.5266) between $\hat{Y}_{ii}$ and ($\hat{W}_i$ + $\hat{V}_i$) shows that the dominant alleles were responsible for the increase in the number of pods per plant, although not exclusively (Table 2).

Figure 2 shows that Cultivar 4 had the greatest concentration of dominant genes. Adopting it as direction from dominance to recessiveness, the following order emerges: 4, 6, 5, 3, 1 and 2, which is in line with the classification in Table 5. From these results, and considering that the maximum value for the parental $\hat{W}_D + \hat{V}_D$ sum is 1.0427 (Table 2), it is possible to obtain desirable pure lines, with higher numbers of pods, since parent 4 showed a value for ($\hat{W}_i$ + $\hat{V}_i$) = 2.3714 (Table 5). However, for satisfactory gains in future generations, more sophisticated breeding methods such as the pedigree are needed, because of the reduced magnitude of the genotypic determination coefficient 0.3760 (Table 4). The additive effects predominated in the estimates of the genetic components, with the positive value for $\tilde{D} - \tilde{H}_1$ (Table 4), which is in line with the results obtained by Barelli (1997) based on Griffing's diallel analysis (1956).

Mean number of seeds per pod. Similarly to the total number of pods per plant, the dominant alleles contributed mainly to an increase in the number of seeds per pod, as indicated by the correlation value for $\hat{Y}_{ii}$ and $(\hat{W}_i + \hat{V}_i)$ found for this trait (–0.5830). The order of the parents in terms of concentration of dominant genes is 5, 6, 3, 1, 2 and 4 (Table 6). Consequently, parent 5 would be indicated for interpopulational programs aiming to obtain descendents with a greater number of seeds per pod. However, bearing in mind that the additive effects were smaller than those of dominance, although only little smaller ($\tilde{D}$ - $\tilde{H}_1$= -0.0150, Table 4), the intrapopulation breeding strategy should not be discarded when it is intended to increase the number of seeds per pod. However, this search should be cautiously evaluated, because of the low value of the genotypic determination coefficient ($\tilde{h}^2_R$), equal to 0.2379 (Table 4). This indicates the low reliability of genotypes in transmitting the intended phenotype to future generations.

The additive effects predominated in the estimates of the genetic components, with the negative value for $\tilde{D} - \tilde{H}_1$ (Table 4), which is in line with the results obtained by Barelli (1997) based on Griffing's diallel analysis (1956).

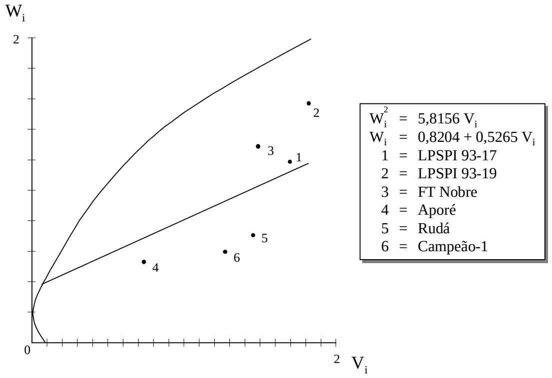

Figure 2. Regression of $\hat{W}_i$ over $\hat{V}_i$, for total number of pods per plant

The estimated number of genes displaying dominance was 1.6959 (Table 4). However, it is pointed out that the expression $\tilde{h}^2/\tilde{H}_2$ is valid when the genotypic values of the heterozygote are not nil and different in magnitude and when the difference between the parent frequency in dominant and recessive homozygosis is nil. This happens when $(\tilde{H}_1 - \tilde{H}_2)$ is approximately zero (Carvalho, 1993). In the present case, as $\tilde{H}_1 - \tilde{H}_2$ can be considered approximately equal to zero (Table 4), it is concluded that the dominant and recessive genes are equally distributed among the parents.

Table 5. Values of the sum of the covariance between parent means with the i^th^ line means ($\hat{W}_i$) and the variance between means of the i^th^ line ($\hat{V}_i$). Classification of the magnitude of the Wi+Vi sum for the six common bean parents, for NTVP[1/], according to Hayman's methodology (1954)

Parent	$\hat{W}_i + \hat{V}_i$	Classification[2/]
1. LPSPI 93-17	5.1499	2º
2. LPSPI 93-19	6.1958	1º
3. FT Nobre	4.8193	3º
4. Aporé	2.3717	6º
5. Rudá	3.8900	4º
6. Campeão-1	3.5863	5º

[1/]NTVP: Total number of pods per plant; [2/]Order of concentration of recessive alleles

Table 6. Values of the sum of the covariance between parent means with i^th^ line means ($\hat{W}_i$) and the variance between means of the i^th^ line ($\hat{V}_i$). Classification of the magnitude of the sum for six common bean parents, for NMSV[1/], according to Hayman's methodology (1954)

Parent	$\hat{W}_i + \hat{V}_i$	Classification[2/]
1. LPSPI 93-17	0.1303	3º
2. LPSPI 93-19	0.1897	2º
3. FT Nobre	0.0540	4º
4. Aporé	0.2079	1º
5. Rudá	0.0031	6º
6. Campeão-1	0.0080	5º

[1/]NMSV: mean seed number per pod; [2/]Order of recessive alleles concentration

Mean seed weight. The low and negative correlation between $\hat{W}_i$ and $\hat{V}_i$ of –0.2385 (Table 2) indicates that only part of the dominant alleles is conditioning on the increase of the trait.

Figure 3 shows that cultivar 6, which is closer to the dominant extremity of the Wi over Vi regression, has the best prospects for line selection with greater grain weight. This is ratified by the predominance of the additive effects over the dominance ($\tilde{D} - \tilde{H}_1$ = 1.5547), and also by the high value of the genotypic determination coefficient ($\tilde{h}^2_R$ = 0.7557) expressed for this trait (Table 4).

Because of the high magnitude of $\tilde{h}^2_R$, it can further be inferred that simple selection methods, such as the mass selection could reach satisfactory results in terms of plants with greater seed weight.

Grain yield. There was high negative correlation between $\hat{Y}_{ii}$ e $(\hat{W}_i + \hat{V}_i)$ of –0.9248 (Table 2) for grain yield, showing that the dominant genes, almost as a whole, act to increase in this trait.

The analysis in Figure 4 shows that the parents from which superior lines can be extracted are 4, 5 and 6, because they are closer to the dominant extreme of the $\hat{W}_i$ over $\hat{V}_i$ regression.

The positive value of $\tilde{D}-\tilde{H}_1$ (Table 4) indicates the prevalence of the additive effects, which reinforces the possibility of obtaining higher yielding lines. More sophisticated breeding strategies such as the pedigree method should be used because of the reduced size of the genotypic determination coefficient ($\tilde{h}_R^2$) found for grain yield.

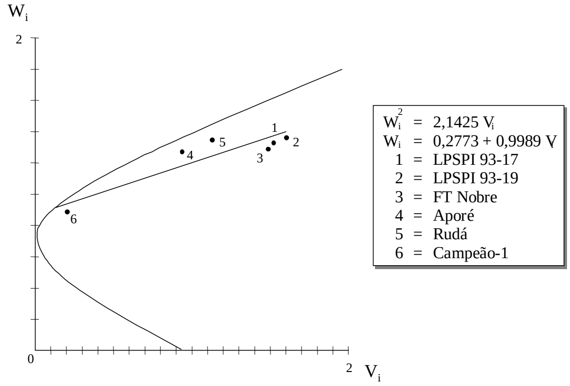

Figure 3. Regression of $\hat{W}_i$ over $\hat{V}_i$ for mean seed weight

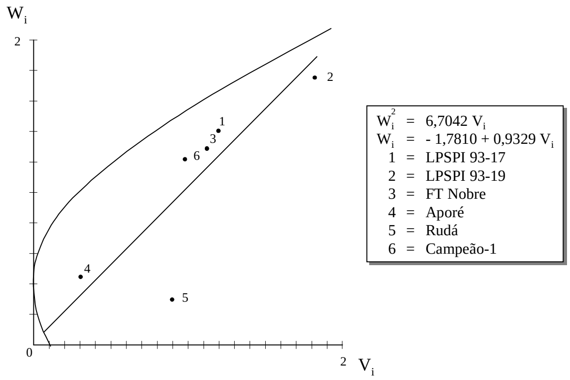

Figure 4. Regression of $\hat{W}_i$ over $\hat{V}_i$ for grain yield

References

Amaral Júnior, A.T. *Análise dialélica de betacaroteno, vitamina C, sólidos solúveis e produção e variabilidade em cultivares de tomateiro (Lycopersicon esculentum) via marcadores RAPD*. Viçosa, 1996. (Doctoral Thesis in Genetics and Breeding) - Universidade Federal de Viçosa.

Barelli, M.A.A. *Análise dialélica da capacidade combinatória de cultivares de feijão (Phaseolus vulgaris (L.) adapatadas ao nororeste Paranaense.* Maringá, 1997. (Master's Thesis in Agronomy) - Universidade Estadual de Maringá.

Carvalho, L.P. *Divergência genética e análise dialélica em Gossypium hirsutum L. var latifolium Hutch*. Viçosa, 1993. (Doctoral Thesis in Genetics and Breeding) - Universidade Federal de Viçosa.

Cruz, C.D. *Programa GENES:* aplicativo computacional em genética e estatística. Viçosa: Imprensa Universitária, 1997. 442 p.

Cruz, C.D.; Regazzi, A.J. *Modelos biométricos aplicados ao melhoramento genético*. Viçosa: Imprensa Universitária, 1994. 394 p

Foolad, M.R.; Bassiri, A. Estimates of combining ability reciprocal effects and heterosis for yield and yield components in a common bean diallel cross. *J. Agric. Sci., 100*:103-108, 1983.

Griffing, B. Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.*, *9*:462-493, 1956.

Hayman, B.I. The analysis of variance of diallel tables. *Biometrics, 10*:235-244, 1954.

Oliveira Júnior, A. *Metodologias de análise de dialelos circulante e de meia-tabela desbalanceados e correlações inter e intrapopulacionais: exemplo com a cultura do feijão (Phaseolus vulgaris L.).* Viçosa, 1993. (Master's Thesis in Genetics and Breeding) - Universidade Federal de Viçosa.

Santos, M.M. *Avaliação de quinze caracteres de seis variedades de tomate (Lycopersicon esculentum) em cruzamentos dialélicos*. Viçosa, 1981. (Master's Thesis in Genetics and Breeding) - Universidade Federal de Viçosa.

Santos, J.B.dos. *Controle genético de caracteres agronômicos e potencialidade de cultivares de feijão (Phaseolus vulgaris L.) para o melhoramento genético.* Piracicaba, 1984. (Doctoral Thesis in Agronomy) - ESALQ, Universidade de São Paulo

Vencovsky, R.; Barriga, P. *Genética biométrica no fitomelhoramento*. Ribeirão Preto: SBG, 1992. 486 p.

Viana, J.M.S. *Teoria e análise de cruzamentos dialélicos parciais, com aplicação no melhoramento genético do feijoeiro (Phaseolus vulgaris L.).* Viçosa, 1981. (Doctoral Thesis in Genetics and Breeding) - Universidade Federal de Viçosa.

Received on June 25, 1999.
Accepted on August 30, 1999.