Universidade Federal Rural do Semi-Árido
Pró-Reitoria de Pesquisa e Pós-Graduação
https://periodicos.ufersa.edu.br/index.php/caatinga

ISSN 0100-316X (impresso)
ISSN 1983-2125 (online)
http://dx.doi.org/10.1590/1983-21252023v36n213rc

Simultaneous selection for architectural and yield traits in common bean lines considering environmental variability

Seleção simultânea para caracteres de arquitetura e produtividade em linhagens de feijão considerando a variabilidade ambiental

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ABSTRACT - Simultaneous selection for plant architecture and yield traits will be more efficient if a minimum number of experiments is established, but no such definition has been made for common bean. The objectives of this study were to select superior common bean lines for several plant architecture and yield traits and identify the minimum number of experiments that provide greater efficiency in simultaneous selection for agronomic traits. Twelve plant architecture and five yield traits of common bean lines were evaluated in four experiments. Analysis of variance and selection index (multiplicative) were carried out using data from individual experiments I (2016 rainy), II (2017 dry), III (2017 rainy), and IV (2018 dry-season crops), or data from two (I and II), three (I, II, and III), and four (I, II, III, and IV) experiments. Most agronomic traits showed a significant genotype × experiment interaction effect. The use of data from individual experiments resulted in variable heritability and genetic gain estimates and in the selection of different common bean genotypes for each growing environment. However, data from three or four experiments allowed 100% of coincidence in the selection of four superior common bean genotypes: LP 09-33, BRS Valente, Pérola, and Carioca. Data from at least three experiments should be used to select superior common bean lines for plant architecture and yield traits to increase the efficiency of simultaneous selection.

Keywords: *Phaseolus vulgaris*. Genotype × environment interaction. Multiplicative index.

RESUMO - A seleção simultânea para caracteres da arquitetura de planta e de produtividade será mais eficiente se um número mínimo de experimentos for estabelecido e essa definição não foi encontrada para feijão. Os objetivos deste trabalho foram selecionar linhagens de feijão superiores para vários caracteres da arquitetura de planta e da produtividade de grãos e identificar o número mínimo de experimentos que propicie maior eficiência na seleção simultânea para caracteres agronômicos. Para isso, 12 caracteres da arquitetura de planta e cinco caracteres da produtividade de linhagens de feijão foram avaliados em quatro experimentos. A análise de variância e de índice de seleção (multiplicativo) foi realizada para dados dos experimentos individuais I (safra 2016), II (safrinha 2017), III (safra 2017) e IV (safrinha 2018) e para dados de dois (I e II), três (I, II e III) e quatro (I, II, III e IV) experimentos. Interação genótipo x experimento significativa foi observada para a maioria dos caracteres agronômicos. O uso de dados de experimentos individuais resultou em estimativas de herdabilidade e de ganho genético variáveis e na seleção de diferentes genótipos de feijão para cada ambiente de cultivo. No entanto, dados de três ou de quatro experimentos possibilitaram 100% de coincidência na seleção de quatro genótipos de feijão superiores: LP 09-33, BRS Valente, Pérola e Carioca. No mínimo, dados de três experimentos devem ser usados para selecionar linhagens de feijão superiores para caracteres da arquitetura de planta e de produtividade para aumentar a eficiência da seleção simultânea.

Palavras-chave: *Phaseolus vulgaris.* Interação genótipo x ambiente. Índice multiplicativo.

Conflict of interest: The authors declare no conflict of interest related to the publication of this manuscript.

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Received for publication in: January 8, 2022.
Accepted in: January 19, 2023.

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INTRODUCTION

The development of common bean (*Phaseolus vulgaris* L.) cultivars with upright plant architecture and high grain yield contributes to the common bean agribusiness in Brazil. Therefore, common-bean breeding programs have put great effort into the evaluation of morphological traits that characterize the upright architecture, such as lodging, insertion of the first pod, plant height, internode length, stem diameter, among others (BERTOLDO et al., 2010; MOURA et al., 2013; SOLTANI et al., 2016; RIBEIRO et al., 2018a,b; NADEEM et al., 2020).

Simultaneous selection for agronomic, technological, and/or nutritional traits has shown to be efficient in the selection of superior lines of common bean (BERTOLDO et al., 2010; JOST et al., 2012; MAZIERO; RIBEIRO; STORCK, 2015; ARNS et al., 2018; RIBEIRO et al., 2018a,b, 2022; SILVA et al., 2018; DIAS et al., 2020) and snap bean (MARINHO et al., 2014; GOMES et al., 2018). To this end, several selection indices and economic weights have been employed for traits important for selection. Nevertheless, the multiplicative index proved to be more efficient for simultaneous selection in common bean, as it allowed achieving a high total genetic gain and individual genetic gains favorable to the objectives of selection of superior common bean lines when compared with other selection indices (JOST et al., 2012; MAZIERO; RIBEIRO; STORCK, 2015; RIBEIRO et al., 2022). It is also important to emphasize that the multiplicative index does not require establishing economic weights (SUBANDI; COMPTON; EMPIG, 1973), which simplifies calculations and the interpretation of results. Thus, the multiplicative index can be easily implemented in the routine of a breeding program.

However, a significant genotype × environment interaction effect has been reported for agronomic traits evaluated in common bean lines (MOURA et al., 2013; BOROS; WAVER; BORUCKA, 2014; SOLTANI et al., 2016; DELFINI et al., 2017; RIBEIRO et al., 2018a,b; NADEEM et al., 2020). For this reason, it is important to consider environmental variability in selection index analyses. Notwithstanding this, simultaneous selection for agronomic traits in common bean has been carried out based on data obtained from one (BERTOLDO et al., 2010; JOST et al., 2012), two (MAZIERO; RIBEIRO; STORCK, 2015; RIBEIRO et al., 2018b), and five (RIBEIRO et al., 2018a) experiments. None of these studies described the criterion used to define the number of experiments employed in simultaneous selection.

The number of experiments to be considered in simultaneous selection for plant architecture and yield traits using the multiplicative index has not been defined for common bean. Identifying the minimum number of experiments to be used in simultaneous selection will result in greater reliability in the selection of superior common bean lines for agronomic traits, which represents an important innovation for breeding programs. Therefore, the present study was developed to select superior common bean lines for several plant architecture and yield traits and identify the minimum number of experiments that provide greater efficiency in simultaneous selection for agronomic traits.

MATERIALS AND METHODS

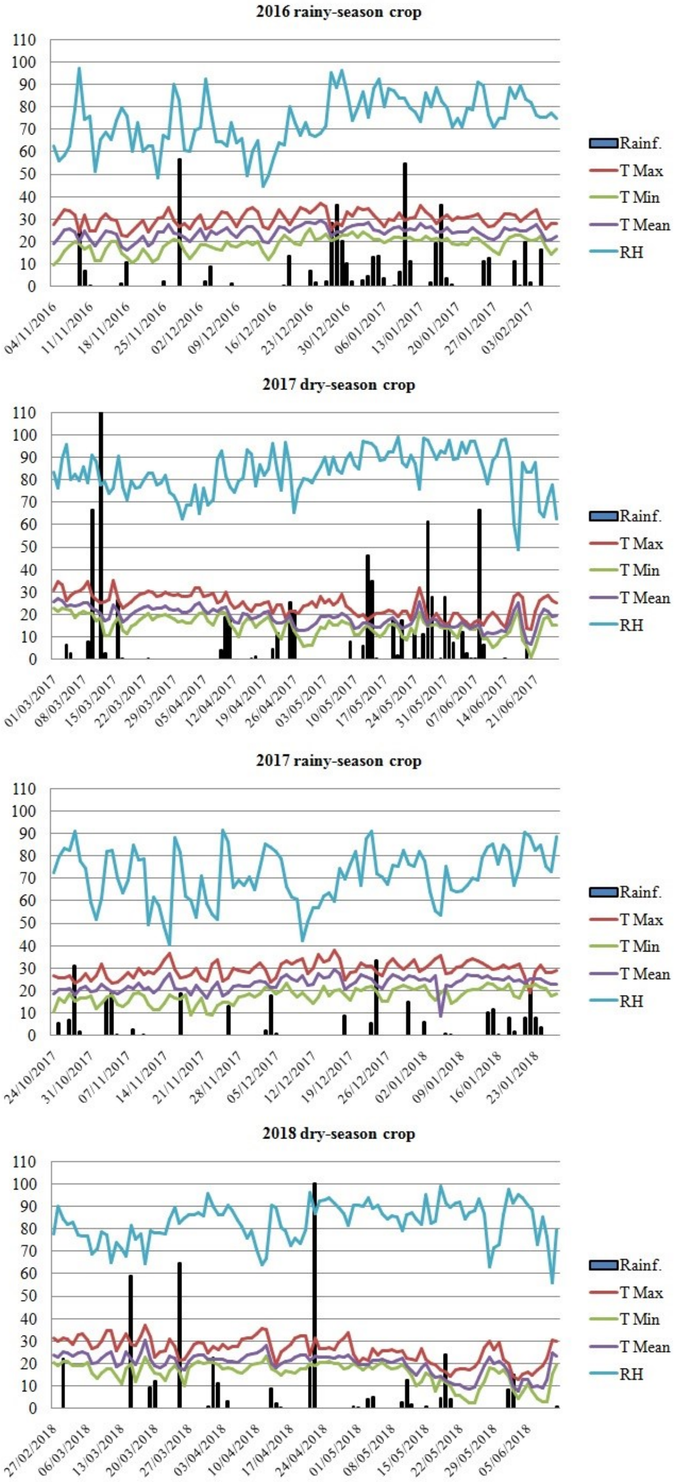
The experiments were conducted on the campus of the Federal University of Santa Maria (UFSM), in Santa Maria, Rio Grande do Sul (RS), Brazil (29º42´ S latitude, 53º49´ W longitude, and 95 m altitude). According to the Köppen classification, the climate in the region is humid subtropical (ALVARES et al., 2013), and the soil is classified as a typic alitic Argisol, Hapludalf (SANTOS et al., 2018).

A randomized-block design with three replicates was adopted in all experiments. The experimental plot consisted of four 4-m rows spaced 0.5 m apart, with only the two central rows forming the usable area of the plot (4 m^2). The analyzed treatments were 17 common bean genotypes (lines and cultivars) with the grain types most widely produced in Brazil, namely, carioca (beige seed coat with brown streaks) and black (Table 1). All genotypes evaluated belong to the Mesoamerican gene pool and represent the technological advances of public research institutions that participated in Value for Cultivation and Use (VCU) experiments of the Southern Brazilian Common-Bean Network in the 2016 and 2017 biennium. The composition of the VCU experiments is defined by the Breeding Subcommittee at the Southern Brazilian Common-Bean Meeting and will not change within the biennium.

Table 1. Common bean genotypes evaluated, origin, and commercial type of grains (Type).

Genotype	Origin	Type
1. Pérola	Brazilian Agricultural Research Corporation - Rice and Beans	Carioca
2. Carioca	Campinas Agronomic Institute	Carioca
3. SM 0312	Department of Diagnosis and Agricultural Research of the Secretariat of Agriculture, Livestock, and Rural Development of the State of Rio Grande do Sul	Carioca
4. BRS MG Uai	Brazilian Agricultural Research Corporation - Rice and Beans	Carioca
5. CNFC 15 097	Brazilian Agricultural Research Corporation - Rice and Beans	Carioca
6. LEC 02-16	State University of Maringá	Carioca
7. GEN 45-2F-293P	Campinas Agronomic Institute	Carioca
8. LP 09-33	Rural Development Institute of Paraná	Carioca
9. LEC 01-16	State University of Maringá	Carioca
10. BRS Valente	Brazilian Agricultural Research Corporation - Rice and Beans	Black
11. Guapo Brilhante	Brazilian Agricultural Research Corporation - Temperate Climate	Black
12. IAC Netuno	Campinas Agronomic Institute	Black
13. LP 11-117	Rural Development Institute of Paraná	Black
14. TB 02-19	Brazilian Agricultural Research Corporation - Temperate Climate	Black
15. CHP 04-239-52	Agricultural Research and Rural Extension Corporation of Santa Catarina	Black
16. CHP 01-182-48	Agricultural Research and Rural Extension Corporation of Santa Catarina	Black
17. TB 03-11	Brazilian Agricultural Research Corporation - Temperate Climate	Black

Two seasons are recommended for cultivation in Santa Maria-RS: rainy (September or October) and dry (January or February). The four experiments were conducted in the following combinations of growing seasons and years: 2016 rainy-season crop (I), 2017 dry-season crop (II), 2017 rainy-season crop (III), and 2018 dry-season crop (IV). Figure 1 shows the meteorological data of the four experiments. All experiments followed the minimum requirements for the determination of VCU for the registration of common bean cultivars in the National Registry of Cultivars in Brazil (BRASIL, 2006).


2016 rainy-season crop

2017 dry-season crop

2017 rainy-season crop

2018 dry-season crop

Figure 1. Meteorological data of rainfall (Rainf., mm), maximum temperature (T max, °C), minimum temperature (T min, °C), mean temperature (T mean, °C), and relative humidity (RH, %) collected by the Eighth Meteorology District at the Santa Maria Meteorology Station, located at the Federal University of Santa Maria (29°42’S, 53°49’W, and 95 m of altitude) (Rio Grande do Sul State, Brazil).

Management practices were similar in all experiments. The soil was prepared conventionally, with two plowings and one disking operation, and maintained with a black-oat crop during the winter months. The amount of fertilizer applied in each experiment was calculated based on the interpretation of the soil chemical analysis report. Insects and weeds were controlled as described in the technical recommendations for common bean growing in southern Brazil (CTSBF, 2012). Irrigation was only applied when necessary for the establishment of the initial plant population, and no shoot disease control was performed, following the VCU standards for common bean (BRASIL, 2006).

Harvesting was carried out manually at the plant maturity stage (R9). The harvested plants were identified and kept in a greenhouse until the grains could be thrashed. After thrashing, the grains were placed in paper bags and, if necessary, oven-dried until reaching 13% moisture.

Plant architecture was analyzed based on 12 traits. The traits of lodging and general adaptation score were determined in the usable area of the plots, at the R9 stage. These traits were evaluated on a scale of scores ranging from 1 to 9. On the lodging scale, the value of 1 was assigned to upright plants and the value of 9 to prostrate plants, that is, in contact with the ground. On the general adaptation score scale, the value of 1 characterized plants that did not fall and had a large number of pods, without disease symptoms, and the value of 9 represented fallen plants that exhibited few pods with many disease symptoms.

The other plant architecture traits were determined in 10 plants randomly harvested from the usable area of the plots. The traits of first- and last-pod insertion, plant height, and first-, second-, third-, fourth-, and fifth-internode lengths were measured and expressed in centimeters. Hypocotyl diameter was quantified at 1 cm below the cotyledon node, whereas epicotyl diameter was measured at 1 cm above the cotyledon node, both with a digital caliper and expressed in mm.

The following yield traits were also evaluated in 10 plants randomly harvested in the usable area of the plots: number of pods per plant, number of grains per plant, number of grains per pod, and mass of 100 grains (g). Grain yield was calculated by summing the grains harvested from the usable area and from the 10 plants and expressed in kg ha^{-1}.

The data obtained in the 2016 rainy (I), 2017 dry (II), 2017 rainy (III), and 2018 dry (IV) season experiments were subjected to individual analysis of variance, following a randomized-block model. Combined analysis of variance was performed using data from the following numbers of experiments: two (I and II), three (I, II, and III), and four (I, II, III, and IV). In all these combinations of experiments, only the genotype effect was considered fixed. Hartley's maximum F test was applied to check the homogeneity of residual variances. Residual variance was homogeneous whenever the ratio between the highest and lowest residual mean squares was less than seven.

The phenotypic correlation matrix obtained from combined analysis of variance of the four experiments was used to make multicollinearity diagnostics. Collinearity was classified as severe (condition number, CN > 1000), moderate to strong (100 < CN < 1000), or weak (CN < 100), according to the classes proposed by Montgomery, Peck, and Vining (2012). Highly correlated traits and traits with a greater weight on the latest eigenvectors, or with higher variance inflation factors, were excluded to obtain weak collinearity.

Selection index analyses were performed by the multiplicative method (SUBANDI; COMPTON; EMPIG, 1973), considering data from the four individual experiments (I, II, III, and IV) and from the combination of two (I and II), three (I, II, and III), and four (I, II, III, and IV) experiments. For each of these seven situations, broad sense heritability and genetic gain estimates were obtained and the four superior genotypes were selected for the plant architecture and yield traits. Selection intensity was set at 23.53%, aiming to achieve the lowest values for lodging and general adaptation score (inverse selection) and the highest values for the other traits (direct selection). The coincidence percentage of common bean genotypes selected by the multiplicative index was obtained for all combinations of experiments, individually (I, II, III, and IV) and combined (I and II; I, II, and III; and I, II, III, and IV). Statistical analyses were carried out using Genes (CRUZ, 2016) software.

RESULTS AND DISCUSSION

Analysis of variance and multicollinearity diagnostics

Eleven of the evaluated traits exhibited a significant genotype × experiment (environment) interaction effect (Table 2). Therefore, the common bean genotypes varied for most of the plant architecture and yield traits determined in different growing seasons and years. Previous studies have also reported a significant genotype × environment interaction effect for several agronomic traits analyzed in common bean genotypes (MOURA et al., 2013; BOROS; WAVER; BORUCKA, 2014; SOLTANI et al., 2016; DELFINI et al., 2017; RIBEIRO et al. 2018a,b; NADEEM et al., 2020). If the plant architecture and yield traits evaluated in common bean lines vary with the growing environment, the selection of superior lines cannot be based on data obtained from a single experiment. In this case, the environmental variability between seasons and years in the same growing location must be considered so that simultaneous selection for agronomic traits is efficient and representative of the genetic diversity of the germplasm.

Table 2. Mean square values of genotype (G), experiment (E), and G × E interaction in analysis of variance for the traits of lodging (LDG), general adaptation score (GAS), insertion of the first pod (IFP, cm), insertion of the last pod (ILP, cm), plant height (PH, cm), first-internode length (1stIL, cm), second-internode length (2ndIL, cm), third-internode length (3rdIL, cm), fourth-internode length (4thIL, cm), fifth-internode length (5thIL, cm), hypocotyl diameter (HD, mm), epicotyl diameter (ED, mm), number of pods per plant (NPP), number of grains per plant (NGP), number of grains per pod (NGPOD), mass of 100 grains (M100G, g), and grain yield (YIELD, kg ha^{-1}) obtained in 17 common bean genotypes evaluated in the 2016 rainy (I), 2017 dry (II), 2017 rainy (III), and 2018 dry (IV) seasons and in combined experiments I and II; I, II, and III; and I, II, III, and IV.

Experiment	LDG	GAS	IFP	ILP	PH	1stIL	2ndIL	3rdIL	4thIL
	Genotype (G)								
I	2.9^{ns}	1.0^{ns}	56.1*	127.1^{ns}	192.4^{ns}	0.7^{ns}	1.5^{ns}	1.9^{ns}	3.5^{ns}
II	1.4*	2.8*	3.0*	36.3*	58.7*	0.1^{ns}	0.5^{ns}	0.5*	0.4*
III	3.3^{ns}	0.8^{ns}	21.4*	158.2*	468.0*	0.8^{ns}	0.4*	0.6^{ns}	2.9^{ns}
IV	4.8*	1.9*	16.4*	145.9*	422.0*	0.1*	0.2*	0.3*	1.5*
I and II	1.9^{ns}	1.6^{ns}	28.5^{ns}	103.5^{ns}	180.2*	0.5^{ns}	1.4^{ns}	1.6^{ns}	2.7^{ns}
I, II, and III	1.6^{ns}	1.9^{ns}	43.3*	221.5*	499.3*	0.4^{ns}	1.4*	1.7*	3.4^{ns}
I, II, III, and IV	3.9^{ns}	2.3^{ns}	40.5*	332.3*	814.9*	0.4^{ns}	1.3*	1.5^{ns}	3.9^{ns}
	Experiment (E)								
I and II	4.3^{ns}	7.2*	2,503.3*	25,754.8*	36,972.6*	0.1^{ns}	0.1^{ns}	3.5*	57.3*
I, II, and III	2.4^{ns}	3.9^{ns}	1,416.4*	17,985.8*	29,522.7*	17.1*	41.8*	48.3*	51.0*
I, II, III, and IV	26.8*	21.6*	980.7*	12,223.9*	21,794.1*	21.4*	43.2*	48.1*	45.4*
	G x E interaction								
I and II	2.5*	2.2*	30.5*	60.0^{ns}	70.9^{ns}	0.3^{ns}	0.6^{ns}	0.7^{ns}	1.2^{ns}
I, II, and III	3.0*	1.4^{ns}	18.6*	50.1^{ns}	130.3^{ns}	0.6^{ns}	0.5^{na}	0.6^{ns}	2.1^{ns}
I, II, III, and IV	2.9*	1.4*	18.8*	45.1^{ns}	141.0*	0.5^{ns}	0.7^{ns}	0.9^{ns}	2.1^{ns}
Experiments	5thIL	HD	ED	NPP	NGP	NGPOD	M100G	YIELD	
	Genotype (G)								
I	5.8^{ns}	0.7*	0.9*	19.0^{ns}	639.7*	1.0*	26.0*	824,724.8*	
II	0.5^{ns}	0.7*	0.7*	8.1*	184.1*	0.6*	57.2*	102,321.6*	
III	5.3*	1.2^{ns}	0.8*	24.0*	321.3*	0.4*	18.5*	611,667.7*	
IV	5.7*	0.2*	0.3*	12.8*	174.6*	0.3*	20.6*	232,940.9*	
I and II	3.4^{ns}	1.0^{ns}	1.0^{ns}	17.5^{ns}	499.5^{ns}	0.9^{ns}	62.7*	554,634.6^{ns}	
I, II, and III	5.5^{ns}	1.4^{ns}	1.3*	25.0^{ns}	595.9*	1.0^{ns}	68.8*	673,028.9^{ns}	
I, II, III, and IV	8.8^{ns}	1.3^{ns}	1.3*	32.8*	637.3*	0.9*	80.9*	593,732.9^{ns}	
	Experiment (E)								
I and II	288.0*	134.6*	158.2*	391.6*	8,961.5*	2.9^{ns}	2.7^{ns}	14,277,077.7*	
I, II, and III	148.3*	76.0*	82.3*	688.4*	9,701.4*	1.8^{ns}	40.6^{ns}	15,684,271.8*	
I, II, III, and IV	102.3*	52.2*	55.5*	461.0*	6,468.8*	1.4^{ns}	570.1*	11,059,563.2*	
	G x E interaction								
I and II	2.9^{ns}	0.5*	0.6*	9.6^{ns}	324.3*	0.7*	20.4*	372,411.8*	
I, II, and III	4.2^{ns}	0.9^{ns}	0.6*	13.0*	274.6*	0.5*	16.4*	432,842.6*	
I, II, III, and IV	4.5^{ns}	0.9^{ns}	0.5*	10.4*	227.5*	0.5*	13.8*	392,640.7*	

*Significant by the F test at 0.05 probability. ^{ns}Not significant.

For the traits whose genotype × experiment interaction was not significant in any of the combinations of experiments, a significant genotype effect was observed for one or more tested situations. These results indicate that there is genetic variability for the plant architecture and yield traits, allowing simultaneous selection. However, for the traits of first-, fourth-, and fifth-internode lengths, genetic variability was detected for a very small number of experiments. Therefore, these three traits were not included in the selection index analyses.

Most combinations of experiments tested showed a significant environment effect. Therefore, differences recorded for rainfall, maximum temperature, minimum temperature, mean temperature, and relative humidity indicated that the environmental conditions varied between the four experiments (Figure 1). As a consequence, plant architecture and yield traits vary with the growing environment, highlighting the need to define the number of experiments to be employed in simultaneous selection.

Multicollinearity diagnostics revealed a CN = 3,273.23, indicating severe collinearity according to the classes established by Montgomery, Peck, and Vining (2012). To solve the problem of multicollinearity, the following traits were excluded: third-internode length, number of grains per plant, plant height, and epicotyl diameter. This resulted in weak collinearity (CN = 75.26) and prevents multicollinear variables from implicitly receiving a greater weight in the selection index analyses (CRUZ; CARNEIRO, 2006). These four traits were removed before selection index analyses were performed, which contributed to the correct interpretation of results.

Simultaneous selection for agronomic traits based on individual and combined experiments

Heritability estimates were of low (h^2 < 30%) to high (h^2 > 60%) magnitude for the plant architecture and yield traits evaluated in individual and combined experiments (Table 3), according to the classes proposed by Soltani et al. (2016). When data obtained from individual experiments were considered, heritability ranged from 0 (general adaptation score, experiment III) to 96% (mass of 100 grains, experiment II). When evaluated in different experiments, the same trait exhibited variations in heritability classes, which shows that the effects of growing seasons and years affected the magnitude of these estimates. This fact highlights the importance of considering environmental variability to obtain heritability estimates that are more representative of the genetic variability that can effectively be exploited in breeding programs.

Table 3. Heritability (h^2), genetic gain (GG), and percentage of genetic gain (GG%) for the traits of lodging (LDG), general adaptation score (GAS), insertion of the first pod (IFP), insertion of the last pod (ILP), second-internode length (2ndIL), hypocotyl diameter (HD), number of pods per plant (NPP), number of grains per pod (NGPOD), mass of 100 grains (M100G), and grain yield (YIELD) with simultaneous selection by the multiplicative index considering the four superior common bean genotypes evaluated in the 2016 rainy (I), 2017 dry (II), 2017 rainy (III), and 2018 dry (IV) seasons and in combined experiments I and II; I, II, and III; and I, II, III, and IV.

Trait	h^2 (%)	GG	GG (%)	h^2 (%)	GG	GG (%)	h^2 (%)	GG	GG (%)	h^2 (%)	GG	GG (%)
	Experiment I			Experiment II			Experiment III			Experiment IV		
LDG	37.0	0.1	1.4	65.0	-0.1	-2.0	48.5	-0.2	-3.1	70.8	-0.9	-13.6
GAS	27.6	0.0	0.3	60.7	-0.3	-6.1	0.0	0.0	0.0	70.7	-0.5	-7.5
IFP	86.8	3.9	19.4	53.4	0.3	2.6	71.1	2.0	10.8	67.5	-0.0	-0.3
ILP	35.3	1.7	3.2	67.2	0.7	3.4	71.5	5.4	10.2	83.7	-2.2	-4.9
2ndIL	30.3	0.0	0.0	39.5	0.1	1.5	51.2	-0.1	-1.6	58.0	0.1	1.8
HD	55.4	0.0	0.0	83.5	0.1	1.7	8.2	0.0	0.4	55.3	0.1	1.2
NPP	48.2	0.1	1.4	77.1	0.4	5.0	72.4	-1.0	-6.6	57.8	0.4	3.2
NGPOD	69.4	0.3	6.7	75.5	0.2	4.7	67.9	0.1	3.6	78.1	0.1	2.7
M100G	65.0	0.6	2.5	96.0	-0.9	-3.7	79.2	0.6	2.4	89.1	-1.1	-3.7
YIELD	76.1	161.3	11.0	62.3	137.3	19.2	78.0	329.7	18.3	81.3	131.5	8.5
Total gain		168.0	45.8		137.7	26.3		336.7	34.5		127.4	-12.6
Trait	Experiments I and II			Experiments I, II, and III			Experiments I, II, III, and IV					
LDG	116.5	-0.3	-5.3	0.0	0.0	0.0	26.1	-0.1	-1.0			
GAS	33.4	-0.1	-2.2	27.9	-0.1	-1.3	40.4	-0.0	-0.8			
IFP	341.1	3.7	24.6	57.1	0.9	5.4	53.7	0.5	3.3			
ILP	86.8	2.2	6.1	77.4	3.6	8.6	86.4	4.4	10.2			
2ndIL	66.0	0.1	1.0	64.9	-0.1	-2.7	68.1	-0.1	-2.5			
HD	80.8	0.1	1.0	51.5	0.0	0.3	60.1	0.0	0.2			
NPP	104.6	0.3	2.8	47.9	0.2	1.6	68.3	0.3	2.3			
NGPOD	157.4	0.3	7.2	49.1	0.0	0.8	51.3	0.0	0.7			
M100G	53.8	0.3	1.1	76.1	0.2	0.9	82.9	0.2	0.8			
YIELD	226.2	331.4	30.4	35.7	42.5	3.2	33.9	32.4	2.4			
Total gain		337.8	66.7		47.1	16.7		37.6	15.6			

When data from two experiments were used, heritability values ≥ 100% were observed, characterizing overestimates. The hypothesis is that the environmental differences observed in the 2016 rainy and 2017 dry-season crops, especially regarding precipitation and relative humidity (Figure 1), contributed to increasing the experimental error, inflating the genetic and environmental variance estimates. On the other hand, the use of data from three and four experiments resulted in more homogeneous and similar heritability values for the same trait. Heritability represents the ratio between genetic variance and total variance (genetic + environmental variances), so low heritability values are related to low genetic variance or high environmental variance. Lodging showed low heritability, whereas the other traits exhibited intermediate to high heritability. However, previous studies with common bean genotypes described high heritability for lodging (JOST et al., 2012; SOLTANI et al., 2016). The greater number of common bean genotypes analyzed in these studies contributed to the wide genetic variability detected for lodging, which explains the higher heritability values recorded. The observed low heritability for lodging in the present study indicates less genetic variability and high environmental influence, which may complicate the selection of superior common bean lines for this trait.

Grain yield showed intermediate heritability, based on data from three and four experiments. Heritability for grain yield in common bean was classified as low (GONÇALVES-VIDIGAL et al., 2008; SOLTANI et al., 2016), intermediate (CHECA; BLAIR, 2012), and high (JOST et al., 2012; RIBEIRO et al., 2018a,b). The different heritability classes described for grain yield in common bean can be related to the genetic diversity of the germplasm, the number of experiments analyzed, and the method used to obtain these estimates. In common bean, grain yield has quantitative inheritance (BLAIR et al., 2012), that is, the trait is governed by several genes and is largely influenced by environmental variation (RAMALHO et al., 2012). Therefore, for quantitative traits, such as grain yield, it is important to obtain heritability from a greater number of experiments, i.e., the environmental variability between growing seasons and years should be considered.

Carioca and black bean lines have a narrow genetic base, which makes it difficult to differentiate superior common bean lines for agronomic traits (DELFINI et al., 2017; PEREIRA et al., 2019). This is because crosses between parents of both grain types are used in the development of carioca and black bean lines, which contributes to the high genetic similarity (VELOSO et al., 2015). However, in the present study, when data from three and four experiments were considered, all traits exhibited intermediate to high heritability, except for lodging. The greater genetic variability observed in the evaluated lines for most of the plant architecture and yield traits increases the chances of success in the selection of superior carioca and black bean lines.

The highest total genetic gain values (positive and negative) were obtained when data from one or two experiments were considered. This can be attributed to the fact that most agronomic traits showed a significant genotype × experiment interaction effect (Table 2). In these cases, genetic gain overestimates or underestimates may be obtained. As a consequence, the four superior common bean genotypes for the plant architecture and yield traits identified by the multiplicative index in experiment I were different from those selected for individual (II, III, and IV) and combined (I and II) experiments (Table 4). In these experiment combinations, the coincidence percentage of common bean lines selected varied from 0 to 75% (Table 5), showing that the growing season, year, and number of experiments used changes the result of simultaneous selection. In this way, simultaneous selection for agronomic traits in common bean will have little application for breeding programs when performed based on data from individual experiments, since the selection of superior lines will be specific for each environment.

The use of data from three and four experiments resulted in total genetic gain estimates of 16.7 and 15.6%, respectively (Table 3). Data from five experiments revealed similar total genetic gain values (RIBEIRO et al., 2018a) when simultaneous selection was performed for agronomic traits of common bean genotypes by the multiplicative index. However, the use of data from one (JOST et al., 2012) and two experiments (MAZIERO; RIBEIRO; STORCK, 2015; RIBEIRO et al., 2018b) provided higher total genetic gain estimates in selection for several traits by the multiplicative index. These results reinforce the need to determine the minimum number of experiments to be considered in simultaneous selection, using the multiplicative index, which provides more reliable and highly repeatable genetic gain estimates. This will be decisive to increase the efficiency of selection of superior common bean lines for agronomic traits.

Individual genetic gain estimates favorable to the objectives of selection of high-yielding common bean lines with upright plant architecture were detected for all traits evaluated in three and four experiments, except for second-internode length, which showed a negative value. The use of selection indices has allowed simultaneous selection for several agronomic, technological, and/or nutritional traits in common bean (BERTOLDO et al., 2010; JOST et al., 2012; MAZIERO; RIBEIRO; STORCK, 2015; ARNS et al., 2018; RIBEIRO et al., 2018a,b, 2022; SILVA et al., 2018; DIAS et al., 2020) and snap bean (MARINHO et al., 2014; GOMES et al., 2018). However, the multiplicative index was considered a promising strategy for simultaneous selection in common bean, as it allowed attaining higher total and/or individual genetic gain values with a sign and magnitude favorable to the selection objectives compared with other selection indices (JOST et al., 2012; MAZIERO; RIBEIRO; STORCK, 2015; RIBEIRO et al., 2022). Nonetheless, some studies reported the difficulty in obtaining favorable individual genetic gain for all evaluated traits, but this fact did not constitute an impediment to the simultaneous selection of superior agronomic traits in common bean lines (BERTOLDO et al., 2010; RIBEIRO et al., 2018a,b, 2022).

Table 4. Common bean genotypes selected by the multiplicative index for the traits of lodging (LDG), general adaptation score (GAS), insertion of the first pod (IFP, cm), insertion of the last pod (ILP, cm), second-internode length (2^{nd}IL, cm), hypocotyl diameter (HD, mm), number of pods per plant (NPP), number of grains per pod (NGPOD), mass of 100 grains (M100G, g), and grain yield (YIELD, kg ha^{-1}) based on evaluations carried out in the 2016 rainy (I), 2017 dry (II), 2017 rainy (III), and 2018 dry (IV) seasons and in combined experiments I and II; I, II, and III; and I, II, III, and IV.

Genotypes selected	LDG	GAS	IFP	ILP	2^{nd}IL	HD	NPP	NGPOD	M100G	YIELD
					Experiment I					
BRS Valente	5.3	5.7	21.5	53.0	6.5	7.2	11.5	5.1	21.4	1,658.6
Pérola	6.3	5.0	31.3	61.0	4.7	6.6	10.3	4.0	27.5	1,749.2
IAC Netuno	6.7	6.7	25.3	56.8	5.2	6.5	12.8	4.7	25.6	2,141.1
LP 09-33	3.0	5.0	19.7	54.5	5.0	6.8	12.5	4.0	24.4	1,154.7
					Experiment II					
TB 03-11	4.7	5.0	10.6	24.8	5.6	4.4	8.1	3.8	22.2	1,006.9
LP 11-117	5.0	4.0	10.8	18.1	5.4	4.1	6.9	4.2	26.8	1,150.8
Guapo Brilhante	4.3	4.3	10.8	17.4	5.6	5.0	7.8	4.3	20.8	818.4
BRS Valente	4.3	4.7	10.2	23.1	5.7	4.8	9.4	3.5	20.5	767.6
					Experiment III					
BRS Valente	3.3	5.0	16.3	49.5	3.6	6.1	15.5	4.0	23.6	2,547.1
CHP 01-182-48	5.0	5.7	22.0	63.1	4.2	7.8	14.0	4.1	22.9	1,860.7
Carioca	5.7	5.3	19.5	62.1	3.4	6.0	15.3	4.1	27.9	2,696.8
Pérola	4.0	5.3	25.9	67.7	3.5	6.8	9.4	3.5	29.3	1,781.6
					Experiment IV					
Guapo Brilhante	4.7	5.3	14.3	37.7	4.1	5.6	12.4	3.7	28.0	1,906.6
LEC 01-16	6.7	6.7	12.8	49.5	3.7	5.8	15.0	3.8	32.7	1,961.8
TB 03-11	5.3	5.7	19.8	49.1	3.8	5.2	8.9	4.2	27.9	1,383.9
BRS MG Uai	3.7	5.7	10.5	36.1	3.8	5.8	13.1	3.7	29.2	1,568.5
					Experiments I and II					
BRS Valente	4.8	5.2	15.8	38.1	6.1	6.0	10.4	4.3	21.0	1,213.1
LP 11-117	5.0	4.7	12.9	31.8	5.5	5.4	9.8	4.5	25.6	1,668.8
Pérola	5.2	5.0	20.8	42.3	5.0	5.5	8.8	3.8	26.3	1,148.0
LP 09-33	3.8	4.8	15.0	40.8	5.1	5.8	10.0	3.7	23.7	914.8
					Experiments I, II, and III					
BRS Valente	4.3	5.1	16.0	41.9	5.3	6.0	12.1	4.2	21.8	1,657.8
Pérola	4.8	5.1	22.5	50.8	4.5	6.0	9.0	3.7	27.3	1,359.2
Carioca	4.8	5.2	15.9	45.2	4.2	5.7	13.2	4.2	24.7	1,524.9
LP 09-33	4.1	4.8	16.0	46.6	4.5	5.9	12.4	3.5	23.9	1,237.8
					Experiments I, II, III, and IV					
BRS Valente	4.6	5.3	14.8	41.9	4.9	6.0	12.3	4.1	23.3	1,600.7
Pérola	5.6	5.8	20.5	52.5	4.4	5.8	9.8	3.7	29.0	1,460.1
Carioca	5.3	5.7	15.7	47.8	4.1	5.6	13.0	4.1	26.2	1,516.9
LP 09-33	4.7	5.2	15.4	48.3	4.3	5.8	12.1	3.6	25.7	1,326.7

The use of data from three and four experiments allows the selection of line LP 09-33 and cultivars BRS Valente, Pérola, and Carioca by multiplicative index (Table 4), i.e., a coincidence percentage of 100% was obtained in the identification of superior common bean genotypes for agronomic traits (Table 5). Therefore, the inclusion of data from four experiments did not change the classification of superior common bean genotypes for plant architecture and yield traits. This shows that the use of data from three experiments was sufficient for simultaneous selection for agronomic traits in common bean lines.

Table 5. Coincidence percentage of four common bean genotypes selected by the multiplicative index for the traits of lodging, general adaptation score, insertion of the first pod, insertion of the last pod, second-internode length, hypocotyl diameter, number of pods per plant, number of grains per pod, mass of 100 grains, and grain yield based on evaluations carried out in the 2016 rainy (I), 2017 dry (II), 2017 rainy (III), and 2018 dry (IV) seasons and in combined experiments I and II; I, II, and III; and I, II, III, and IV.

Experiments	II	III	IV	I and II	I, II, and III	I, II, III, and IV
I	25	50	0	75	75	75
II		25	50	50	25	25
III			0	50	75	75
IV				0	0	0
I and II					75	75
I, II, and III						100

When data from three experiments were considered, it was possible to select three carioca bean genotypes (line LP 09-33 and cultivars Pérola, and Carioca) and one black bean cultivar (BRS Valente), which were superior to the other evaluated genotypes regarding plant architecture and yield traits (Table 4). Line LP 09-33 showed agronomic traits similar to those of control cultivars (Pérola, Carioca, and BRS Valente), as well as the lowest values of lodging and general adaptation score, that is, it stood out for its upright plant architecture. Line LP 09-33 will be selected by the breeding program; however, its genetic superiority regarding plant architecture and yield traits must be validated in experiments conducted in a greater number of environments (growing seasons, years, and locations).

The results obtained in the present study showed that most of the plant architecture and yield traits in carioca and black beans were significantly affected by the genotype × experiment interaction (Table 2). As a result, heritability and genetic gain estimates varied when data obtained from individual (I, II, III, and IV) and combined (I and II; I, II, and III; and I, II, III, and IV) experiments were considered (Table 3). The use of data from individual experiments resulted in the selection of different superior common bean genotypes for each of the growing environments (Table 4), with a low coincidence percentage in simultaneous selection (Table 5). Nevertheless, the use of data from three or four experiments allowed 100% of coincidence in the selection of four superior genotypes for agronomic traits, namely, LP 09-33, BRS Valente, Pérola and Carioca (Table 4). Therefore, the minimum number of three experiments is appropriate for simultaneous selection for plant architecture and yield traits in common bean lines. Three experiments provide repeatability and efficiency in simultaneous selection for agronomic traits in carioca and black beans.

CONCLUSIONS

Line LP 09-33 and cultivars BRS Valente, Pérola, and Carioca have several superior plant architecture and yield traits. Data from at least three experiments should be used in the selection of superior common bean lines for various plant architecture and yield traits to increase the efficiency of simultaneous selection.

ACKNOWLEDGEMENTS

To the National Council for Scientific and Technological Development (CNPq) for financial support and scholarships.

REFERENCES

ALVARES, C. A. et al. Köppen's climate classification map for Brazil. **Meteorologische Zeitschrift**, 22: 711-728, 2013.

ARNS, F. D. et al. Combined selection in carioca beans for grain size, slow darkening and fast-cooking after storage times. **Euphytica**, 214: 1-12, 2018.

BERTOLDO, J. G. et al. Genetic gain in agronomic traits of common bean in the region of Planalto Catarinense. **Euphytica**, 171: 381-388, 2010.

BLAIR, M. W. et al. Development of a Mesoamerican intra-gene pool genetic map for quantitative trait loci detection in a drought tolerant x susceptible common bean (*Phaseolus vulgaris* L.) cross. **Molecular Breeding**, 29: 71-88, 2012.

BOROS, L.; WAWER, A.; BORUCKA, K. Morphological, phonological and agronomical characterization of variability among common bean (*Phaseolus vulgaris* L.) local populations from the National Centre for Plant Genetic Resources: Polish Genebank. **Journal of Horticultural Research**, 22: 123-130, 2014.

BRASIL. **Requisitos mínimos para determinação do valor de cultivo e uso de feijão (*Phaseolus vulgaris*), para a inscrição no registro nacional de cultivares - RNC**. Anexo I. 2006. Disponível em: <http://www.agricultura.gov.br>. Acesso em: 05 out. 2021.

CHECA, O. E.; BLAIR, M. B. Inheritance of yield-related traits in climbing beans (*Phaseolus vulgaris* L.). **Crop Science**, 52: 1998-2013, 2012.

CRUZ, C. D. Genes - Software-extended and integrated with the R, Matlab and Selegen. **Acta Scientiarum. Agronomy**, 38: 547-552, 2016.

CRUZ, C. D.; CARNEIRO, P. C. S. **Modelos biométricos aplicados ao melhoramento genético**. Viçosa, MG: UFV, 2006. 585 p.

CTSBF - Comissão Técnica Sul Brasileira de Feijão. **Informações técnicas para o cultivo de feijão na Região Sul Brasileira 2012**. Florianópolis, SC: EPAGRI, 2012. 157 p.

DELFINI, J. et al. Distinctness of Brazilian common bean cultivars with carioca and black grain by means of morphoagronomic and molecular descriptors. **Plos One**, 30: 1-22, 2017.

DIAS, P. A. S. et al. Effectiveness of breeding selection for grain quality in common bean. **Crop Science**, 61: 1127-1140, 2020.

GOMES, A. B. S. et al. Genetic gain via REML/BLUP and selection indices in snap bean. **Horticultura Brasileira**, 36: 195-198, 2018.

GONÇALVES-VIDIGAL, M. C. et al. Heritability of quantitative traits in segregating common bean families using a Bayesian approach. **Euphytica**, 164: 551-560, 2008.

JOST, E. et al. Comparison among direct, indirect and index selections on agronomic traits and nutritional quality traits in common bean. **Journal of the Science of Food and Agriculture**, 93: 1097-1104, 2012.

MARINHO, C. D. et al. Indexes in the comparison of pre-commercial genotypes of common bean. **Ciência Rural**, 44: 1159-1165, 2014.

MAZIERO, S. M.; RIBEIRO, N. D.; STORCK, L. Simultaneous selection in beans for architecture, grain yield and minerals concentration. **Euphytica**, 205: 369-380, 2015.

MONTGOMERY, D. C.; PECK, E. A.; VINING, G. G. **Introduction to linear regression analysis**. 5. ed. New York, NY, USA: Wiley, 2012. 672 p.

MOURA, M. M. et al. Potencial de caracteres na avaliação da arquitetura de plantas de feijão. **Pesquisa Agropecuária Brasileira**, 48: 417-425, 2013.

NADEEM, M. A. et al. Phenotypic characterization of 183 Turkish common bean acessions for agronomic, trading, and consumer-preferred plant characteristics for breeding purposes. **Agronomy**, 272: 1-20, 2020.

PEREIRA, H. S. et al. Genetic diversity among common bean cultivars based on agronomic traits and molecular markers and application to recommendation of parent lines. **Euphytica**, 215: 1-16, 2019.

RAMALHO, M. A. P. et al. **Aplicações da genética quantitativa no melhoramento de plantas autógamas**. Lavras, MG: UFLA, 2012. 522 p.

RIBEIRO, N. D. et al. Combined selection in beans for cycle, plant architecture and grain yield. **Bioscience Journal**, 34: 108-119, 2018a.

RIBEIRO, N. D. et al. Phenological, plant architecture, and grain yield traits on common bean lines selection. **Revista Caatinga**, 31: 657-666, 2018b.

RIBEIRO, N. D. et al. Selection strategies for identifying fast cooking, mineral-biofortified bean cultivars with high agronomic performance. **Scientia Agricola**, 79: 1-11, 2022.

SANTOS, H. G. et al. **Sistema brasileiro de classificação de solos**. 5 ed. Brasília, DF: Embrapa Solos, 2018. 356 p.

SILVA, F. C. et al. Selection of parents and segregation populations of common bean with high agronomic potential and slow seed-coat darkening. **Pesquisa Agropecuária Tropical**, 48: 75-82, 2018.

SOLTANI, A. et al. Targeted analysis of dry bean growth habit: interrelations among architectural, phenological, and yield components. **Crop Science**, 56: 3005-3015, 2016.

SUBANDI, W.; COMPTON, A.; EMPIG, L. T. Comparison of the efficiencies of selection indices for three traits in two variety crosses of corn. **Crop Science**, 13: 184-186, 1973.

VELOSO, J. S. et al. Genetic divergence of common bean cultivars. **Genetics and Molecular Research**, 14: 11281-11291, 2015.