

Environmental variability in indirect selection for grain yield in common bean lines

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ABSTRACT: An approach to the number of experiments that should be used in correlation analyses aimed at increasing efficiency in indirect selection for grain yield is unprecedented for common bean (*Phaseolus vulgaris* L.). We hypothesize that trait correlation estimates vary in response to the growing environment. This study was undertaken to investigate the correlations between plant architecture and yield traits in common bean lines and to determine the minimum number of experiments required by Pearson's linear correlation analysis to increase efficiency in indirect selection for grain yield. Seventeen common bean genotypes were evaluated for 17 agronomic traits in four experiments. Pearson's linear correlation analyses were carried out using data from individual experiments and different combinations of growing seasons and years. Ten out of the 17 agronomic traits showed a significant genotype × environment interaction effect, meaning that common bean genotypes exhibited variation for most of the traits evaluated in different growing seasons and years, which resulted in changes in the correlation estimates between these traits. Pearson's linear correlation estimates obtained between plant architecture and yield traits varied in significance, magnitude, and sign when data from individual experiments and combinations of growing seasons and years were considered. The number of grains per pod is the most promising agronomic trait used in indirect selection for grain yield in common bean lines. Data from at least three experiments should be used in Pearson's linear correlation analysis to achieve greater efficiency in indirect selection for grain yield in common bean lines.

Keywords: *Phaseolus vulgaris*, Pearson's linear correlation, genotype × environment interaction, agronomic traits

Introduction

Historical records show that bean (*Phaseolus vulgaris* L.) breeding programs in Brazil began in 1887 (Carbonell et al., 2012). After over a century of research into the development of new common bean cultivars for cultivation in different regions of the country, there is still room for genetic gains to be achieved in grain yield (Barili et al., 2016a, b; Bertoldo et al., 2014; Faria et al., 2013, 2014, 2017, 2018; Lemos et al., 2020). This can be attributed to morphological alterations making bean plants more resistant to lodging (Faria et al., 2013, 2014), which has resulted in upright plant architecture. In addition, positive genetic gains have been described for yield traits such as the number of pods per plant and mass of 100 grains (Ribeiro et al., 2008), thereby increasing the grain yield of new cultivars.

The study of correlation between plant architecture and yield traits is essential to the identification of promising secondary traits for indirect selection for grain yield (primary trait) in common bean lines. Significant correlations between agronomic traits were found in common bean genotypes evaluated in a single experiment (Pop and Ciulca, 2013). However, significant correlations between agronomic traits were seen to vary in magnitude and sign when data from two growing years (Moura et al., 2013) and locations (Barili et al., 2011) were considered. The hypothesis is that the environmental variability between growing seasons, years, and/or locations leads to changes in correlation estimates between agronomic traits analyzed in common beans.

Several studies have identified significant correlations between plant architecture and/or yield traits of common bean genotypes using average data from two (Rana et al., 2015; Ribeiro et al., 2018), three (Soltani et al., 2016) or more (Delfini et al., 2017; Nadeem et al., 2020; Ribeiro et al., 2017) experiments. However, none of these studies determined the minimum number of experiments required for Pearson's linear correlation analysis to provide high coincidence in identifying significant correlations between agronomic traits in common beans. The objectives of this study were: (1) to investigate the correlations between plant architecture and yield traits of common bean lines, considering data obtained from individual experiments and different combinations of growing seasons and years; and (2) to determine the minimum number of experiments required for Pearson's linear correlation analysis to increase efficiency in indirect selection for grain yield in common bean lines.

Materials and Methods

Plant material

Seventeen Mesoamerican common bean genotypes from the Value of Cultivation and Use (VCU) experiment in the southern Brazilian common bean network was evaluated in the 2016 and 2017 biennium. These genotypes have the following grain types: carioca (beige seed coat with brown streaks) - Pérola, Carioca, SM 0312, BRS MG Uai, CNFC 15 097, LEC 02-16, GEN 45-2F-293P, LP 09-33, LEC 01-16, and black - BRS Valente, Guapo Brilhante, IAC Netuno,

LP 11-117, TB 02-19, CHP 04-239-52, CHP 01-182-48, and TB 03-11. Cultivars Pérola, Carioca, BRS Valente, and Guapo Brillhante were considered controls since they are registered for cultivation in the state of Rio Grande do Sul, Brazil. In the VCU experiments, the number of genotypes evaluated per experiment varies from 12 to 24. Therefore, 17 common bean genotypes represent the technological advances of breeding programs in the southern region of Brazil in the 2016 and 2017 biennium.

Description of the experiments

The experiments were carried out in Santa Maria, in the state of Rio Grande do Sul (RS), Brazil, located at the following geographic coordinates: 29°42' S, 53°49' W, and at an altitude of 95 m. Seeds were sown in different growing seasons and years: 2016 rainy season, 2017 dry season, 2017 rainy season, and 2018 dry season, in agreement with the agricultural zoning of climatic risk for the common bean crop in RS.

The region has a humid subtropical climate (Alvares et al., 2013) and the soil is classified as typic alitic Argisol, Hapludalf. The traditional cultivation system, with two plowings and one disking operation, was used to execute all the experiments.

The experiments were laid out in a randomized-block design with three replicates. Each experimental unit consisted of four 4-m rows, spaced 0.5 m apart, with the two central rows forming the usable area (4 m²). These experiments were established following the minimum requirements for determining the VCU for common bean (MAPA, 2006), which are required to launch new cultivars in Brazil.

Management practices were uniform and similar for all experiments. The application of fertilizer was in accordance with the interpretation of soil analysis aimed at meet the needs of the crop. Weeds were controlled by hoeing, and insecticides were applied following the technical directions of each product. Fungicides were not used, and irrigation was implemented only when the initial plant population was being established in compliance with the VCU standards for common bean (MAPA, 2006). Grain harvesting and processing were carried out manually to prevent any mechanical damage to the grains.

Evaluation of agronomic traits

Seventeen agronomic traits were analyzed, of which 12 pertained to plant architecture and five to yield. The following plant architecture traits were evaluated in all plants in the usable area at the maturity stage (R9) by a score scale for lodging and general adaptation score. On the lodging scale, one was assigned to upright plants and nine to prostrate plants. On the scale of general adaptation score, one characterized plants that did not fall, which showed a large number of pods, and without disease symptoms, whereas nine was associated with fallen plants, few pods, and many disease symptoms.

The other plant architecture traits were measured in ten plants randomly collected from the usable area: insertion of the first pod, insertion of the last pod, plant height, and first, second, third, fourth, and fifth internode lengths (cm). Hypocotyl diameter was determined 1 cm below the cotyledonary node, whereas the epicotyl diameter was quantified 1 cm above the cotyledonary node using a digital caliper (mm).

In the ten plants randomly harvested from the usable area, the following yield traits were also evaluated: 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 as the sum of the weight of the grains in all plants harvested from the usable area and the ten plants randomly collected in the usable area, with 13 % average moisture, expressed in kg ha⁻¹.

Statistical analyses

The data obtained in the 2016 rainy (I), 2017 dry (II), 2017 rainy (III), and 2018 dry season (IV) experiments were subjected to individual analysis of variance, and the F test evaluated the significance level at 5 % probability. Hartley's maximum F test analyzed the homogeneity of residual variances.

A combined analysis of variance was carried out with the data obtained from the four experiments in which all effects were random except the genotype effect. The F test also analyzed the significance level at 5 % probability. The phenotypic correlation matrix generated in this combined analysis of variance was used for multicollinearity diagnostics. The condition number (CN) obtained related to three classes of collinearity: weak (CN < 100), moderate to strong (100 < CN < 1000), and severe (CN > 1000), according to the criteria defined by Montgomery et al. (2012).

Only the agronomic traits that showed significant genotype and/or genotype × environment interaction effects and for which multicollinearity diagnostics revealed weak collinearity were kept in the correlation analyses. Pearson's linear correlation coefficients were estimated for each of the four individual experiments (I, II, III, and IV) and for six combinations of experiments (I and II; I and III; II and IV; III and IV; I, II, and III; and I, II, III, and IV). For this, the phenotypic correlation matrix generated in each of the ten analyses of variance (I; II; III; IV; I and II; I and III; II and IV; III and IV; I, II, and III; and I, II, III, and IV) was used to obtain the different correlation analyses. Student's t test evaluated the significance of correlation coefficients at 5 % probability. The Genes software program (Cruz, 2016) was used in all analyses.

Results and Discussion

Analysis of variance and multicollinearity diagnostics

The ratio between the highest and lowest residual mean

squares of individual analysis of variance was less than seven for all traits, except for plant height, hypocotyl diameter, and first, second, third, fourth, and fifth internode lengths. For these seven traits, the degrees of freedom from error and genotype × environment interaction were corrected, as recommended by Cruz (2016), and homogeneous residual variances were obtained for all agronomic traits.

A significant genotype effect was observed for nine of the 17 traits evaluated (Table 1), evidencing the existence of genetic variability between the common bean lines and cultivars for most of the agronomic traits. Broad genetic variability for plant architecture and yield traits has been described for common bean genotypes (Arteaga et al., 2019; Boros et al., 2014; Delfini et al., 2017;

Moura et al., 2013; Nadeem et al., 2020; Ribeiro et al., 2022; Soltani et al., 2016). However, ten traits exhibited a significant genotype × environment interaction effect, which evidences that the common bean genotypes showed variation for most plant architecture and yield traits when grown in different environments, thereby confirming previously published results (Arteaga et al., 2019; Boros et al., 2014; Delfini et al., 2017; Moura et al., 2013; Nadeem et al., 2020; Ribeiro et al., 2018, 2022; Soltani et al., 2016). These results suggest that taking into consideration the environmental variability between growing seasons and years in the exact location where the experiments were conducted can increase the efficiency of indirect selection for grain yield in common bean lines.

Table 1 – Combined analysis of variance containing the degrees of freedom, mean squares, p value, mean, coefficient of experimental variation and selective accuracy for the traits of lodging, general adaptation score, insertion of the first pod, insertion of the last pod, plant height, first internode length, second internode length, third internode length, fourth internode length, fifth internode length, hypocotyl diameter, epicotyl diameter, number of pods per plant, number of grains per plant, number of grains per pod, mass of 100 grains, and grain yield obtained in 17 common bean genotypes evaluated in four experiments carried out from 2016 to 2018.

Source of variation	DF	LDG		GAS		IFP		ILP		PH		1 st IL	
		MS	p val.	MS	p val.	MS	p val.	MS	p val.	MS	p val.	MS	p val.
Block/environment	8	3.62		1.08		44.06		11.69		73.46		0.24	
Genotype (G)	16	3.87	0.206	2.32	0.084	40.54	0.020	332.26	0.000	814.87	0.000	0.42	1.000
Environment (E)	3	26.80	0.011	21.61	0.000	980.65	0.000	12223.86	0.000	21794.07	0.000	21.40	0.000
G × E	48	2.86	0.000	1.38	0.017	18.76	0.000	45.10	0.323	141.04	0.015	0.53	0.328
Residue	128	1.36		0.85		5.08		40.79		79.64		0.47	
Mean		5.24		5.61		15.65		42.57		56.88		3.01	
CEV (%)		22.27		16.47		14.40		15.00		15.69		22.85	
SA		0.51		0.64		0.73		0.93		0.91		0.00	

Source of variation	DF	2 nd IL		3 rd IL		4 th IL		5 th IL		HD		ED	
		MS	p val.	MS	p val.	MS	p val.						
Block/environment	8	0.10		0.22		1.91		2.32		0.51		0.46	
Genotype (G)	16	1.33	0.045	1.54	0.085	3.89	0.061	8.84	0.052	1.32	0.161	1.30	0.002
Environment (E)	3	43.22	0.000	48.09	0.000	45.39	0.000	102.33	0.000	52.23	0.000	55.48	0.000
G × E	48	0.66	1.000	0.87	1.000	2.07	0.339	4.46	0.125	0.87	0.428	0.45	0.000
Residue	128	0.74		0.89		1.86		3.18		0.83		0.19	
Mean		4.56		6.19		8.26		10.81		5.76		5.64	
CEV (%)		18.87		15.23		16.52		16.49		15.82		7.72	
SA		0.71		0.66		0.68		0.70		0.58		0.81	

Source of variation	DF	NPP		NGP		NGPOD		M100G		YELD	
		MS	p val.	MS	p val.	MS	p val.	MS	p val.	MS	p val.
Block/environment	8	10.03		168.96		0.36		10.83		223738.20	
Genotype (G)	16	32.77	0.001	637.28	0.003	0.94	0.028	80.76	0.000	593732.89	0.134
Environment (E)	3	461.06	0.000	6468.82	0.000	1.37	0.059	570.07	0.000	11059563.20	0.000
G × E	48	10.40	0.007	227.46	0.001	0.46	0.000	13.79	0.000	392640.71	0.000
Residue	128	5.94		112.07		0.16		4.37		103561.45	
Mean		11.41		43.72		3.81		25.80		1380.36	
CEV (%)		21.36		24.21		10.57		8.10		23.31	
SA		0.83		0.80		0.72		0.91		0.58	

DF = degrees of freedom; MS = mean squares; p val. = p value; CEV% = coefficient of experimental variation; SA = selective accuracy; LDG = lodging; GAS = general adaptation score; IFP = insertion of the first pod; ILP = insertion of the last pod; PH = plant height; 1stIL = first internode length; 2ndIL = second internode length; 3rdIL = third internode length; 4thIL = fourth internode length; 5thIL = fifth internode length; HD = hypocotyl diameter; ED = epicotyl diameter; NPP = number of pods per plant; NGP = number of grains per plant; NGPOD = number of grains per pod; M100G = mass of 100 grains; YELD = grain yield.

The genotype and genotype \times environment interaction effects were insignificant for hypocotyl diameter or first, third, fourth and fifth internode length. That is to say, these traits showed no genetic variability between common bean genotypes and were, therefore, removed from the correlation analyses. Additionally, multicollinearity diagnostics suggested severe collinearity (CN = 1,948.91), according to Montgomery et al. (2012). To obtain weak collinearity, highly correlated traits, with a greater weight in the last eigenvectors, and greater variance inflation factors were identified, i.e., number of grains per plant and insertion of the last pod. These two traits were excluded from the correlation analyses to prevent multicollinear variables from being implicitly assigned a greater weight in these analyses, as recommended by Cruz and Carneiro (2006). This methodology prevents errors in the interpretation of the correlation analysis results.

Correlation analysis using data from individual experiments

When Pearson's linear correlation coefficients were estimated considering data from individual experiments, there was variation in the magnitude and significance of the correlations obtained between pairs of traits evaluated in experiments I, II, III, and IV (Table 2). Previous studies have reported that correlations observed between agronomic traits in common bean genotypes varied by growing year (Barili et al., 2011; Moura et al., 2013) and location (Barili et al., 2011). These results show that correlation analysis performed using data from individual experiments can lead to errors in identifying promising agronomic traits for indirect selection aimed at high grain yield in common bean lines.

The significant correlations obtained differed when the four evaluated experiments were considered individually. In experiment I, four correlations were significant, whereas six correlations showed significance in experiments III and IV. However, 21 of the 45 analyzed correlations were significant in experiment II. The environmental variability observed between growing seasons and years contributed to the fact that the correlations between the plant architecture and yield traits were not constant in the four experiments. Similarly, the number of significant correlations obtained between 23 agronomic traits evaluated in common bean genotypes was not uniform in the two crop years (Moura et al., 2013). In the present study, there was a significant genotype \times environment interaction effect for most of the evaluated agronomic traits (Table 1), which resulted in variations in the number of correlations that were significant in the different experiments (Table 2).

Identifying the pairs of traits whose correlation was significant in a greater number of experiments represents greater repeatability or coincidence in defining the most effective traits to be used in indirect selection.

The following correlations were significant in two experiments: insertion of the first pod and plant height; plant height and second internode length; lodging and mass of 100 grains; general adaptation score and mass of 100 grains; and number of grains per pod and grain yield. On the other hand, the correlations between lodging and general adaptation score and between epicotyl diameter and number of pods per plant were significant in three experiments. No significant correlation was observed for the four concurrent experiments. Therefore, when data from individual experiments were considered there was low coincidence in the significant correlations between different agronomic traits evaluated in common bean lines.

The use of agronomic traits highly correlated with yield increases the efficiency of indirect selection for grain yield in common bean lines. However, when this was applied using data from individual experiments, as in the present study and previous works (Barili et al., 2011; Moura et al., 2013), many significant correlations observed in one environment were different from those determined in another, which compromises the efficiency of indirect selection. This is because the identification of promising agronomic traits for indirect selection for grain yield in common bean lines will differ for each experiment. No study was found in the literature that defined the minimum number of environments to be considered in Pearson's linear correlation analysis that provides high coincidence in identifying agronomic traits for use in indirect selection for grain yield in common bean lines.

Correlation analysis using data from two experiments

An alternative to be evaluated in correlation analysis is to use data from two experiments, considering combinations of growing seasons and years, to identify agronomic traits that are efficient in indirect selection for grain yield in common bean lines. When the correlations were estimated using data from experiments conducted in the same growing season and in different years (I and III: 2016 and 2017 rainy seasons; II and IV: 2017 and 2018 dry seasons), three significant correlations coincided: lodging and general adaptation score; epicotyl diameter and number of pods per plant and number of grains per pod and grain yield (Table 3). However, correlation estimates obtained using data from experiments conducted in different growing seasons and years (I and II: 2016 rainy and 2017 dry seasons; III and IV: 2017 rainy and 2018 dry seasons) resulted in five significant coincident correlations: lodging and general adaptation score; plant height and second internode length; epicotyl diameter and number of pods per plant; general adaptation score and mass of 100 grains, and number of grains per pod and mass of 100 grains. Similarly, many significant correlations between agronomic traits evaluated in common bean genotypes

Table 2 – Pearson's correlation coefficients obtained between the traits of lodging, general adaptation score, insertion of the first pod, plant height, second internode length, epicotyl diameter, number of pods per plant, number of grains per pod, mass of 100 grains, and grain yield obtained in 17 common bean genotypes evaluated in experiments I (2016 rainy season), II (2017 dry season), III (2017 rainy season) and IV (2018 dry season).

TRAITS	GAS	IFP	PH	2 nd IL	ED	NPP	NGPOD	M100G	YIELD
Experiment I									
LDG	0.58*	0.45 ^{ns}	0.25 ^{ns}	0.10 ^{ns}	0.05 ^{ns}	-0.30 ^{ns}	-0.02 ^{ns}	-0.12 ^{ns}	0.06 ^{ns}
GAS		0.18 ^{ns}	0.38 ^{ns}	-0.12 ^{ns}	0.25 ^{ns}	-0.10 ^{ns}	-0.05 ^{ns}	-0.22 ^{ns}	-0.25 ^{ns}
IFP			0.59*	-0.32 ^{ns}	-0.29 ^{ns}	-0.37 ^{ns}	0.06 ^{ns}	0.22 ^{ns}	0.14 ^{ns}
PH				-0.53*	0.18 ^{ns}	0.03 ^{ns}	-0.16 ^{ns}	-0.10 ^{ns}	-0.26 ^{ns}
2 nd IL					-0.07 ^{ns}	-0.02 ^{ns}	0.21 ^{ns}	0.04 ^{ns}	0.21 ^{ns}
ED						0.20 ^{ns}	-0.21 ^{ns}	-0.45 ^{ns}	-0.73*
NPP							0.41 ^{ns}	-0.34 ^{ns}	-0.12 ^{ns}
NGPOD								-0.20 ^{ns}	0.42 ^{ns}
M100G									0.34 ^{ns}
Experiment II									
LDG	0.56*	0.12 ^{ns}	-0.36 ^{ns}	0.41 ^{ns}	-0.71*	-0.71*	-0.59*	0.79*	-0.29 ^{ns}
GAS		0.16 ^{ns}	-0.50*	0.42 ^{ns}	-0.60*	-0.62*	-0.59*	0.75*	-0.54*
IFP			-0.09 ^{ns}	0.61*	-0.33 ^{ns}	-0.32 ^{ns}	-0.10 ^{ns}	0.24 ^{ns}	0.19 ^{ns}
PH				-0.16 ^{ns}	0.30 ^{ns}	0.44 ^{ns}	0.01 ^{ns}	-0.48*	0.22 ^{ns}
2 nd IL					-0.22 ^{ns}	-0.41 ^{ns}	-0.33 ^{ns}	0.57*	-0.25 ^{ns}
ED						0.67*	0.48*	-0.60*	0.03 ^{ns}
NPP							0.69*	-0.83*	0.33 ^{ns}
NGPOD								-0.57*	0.55*
M100G									-0.38 ^{ns}
Experiment III									
LDG	0.47 ^{ns}	0.16 ^{ns}	0.25 ^{ns}	0.02 ^{ns}	-0.04 ^{ns}	0.09 ^{ns}	0.37 ^{ns}	0.31 ^{ns}	0.23 ^{ns}
GAS		0.19 ^{ns}	0.06 ^{ns}	0.24 ^{ns}	0.09 ^{ns}	-0.14 ^{ns}	0.20 ^{ns}	0.43 ^{ns}	0.02 ^{ns}
IFP			0.50*	0.01 ^{ns}	-0.36 ^{ns}	-0.60*	0.14 ^{ns}	0.47 ^{ns}	0.21 ^{ns}
PH				-0.52*	0.40 ^{ns}	0.18 ^{ns}	-0.07 ^{ns}	0.19 ^{ns}	0.45 ^{ns}
2 nd IL					-0.28 ^{ns}	-0.57*	0.14 ^{ns}	0.02 ^{ns}	-0.42 ^{ns}
ED						0.67*	-0.22 ^{ns}	-0.11 ^{ns}	-0.06 ^{ns}
NPP							-0.22 ^{ns}	-0.31 ^{ns}	-0.07 ^{ns}
NGPOD								-0.16 ^{ns}	0.51*
M100G									0.09 ^{ns}
Experiment IV									
LDG	0.84*	0.44 ^{ns}	0.20 ^{ns}	0.06 ^{ns}	-0.42 ^{ns}	-0.07 ^{ns}	-0.36 ^{ns}	0.52*	-0.28 ^{ns}
GAS		0.11 ^{ns}	0.01 ^{ns}	-0.09 ^{ns}	-0.34 ^{ns}	-0.09 ^{ns}	-0.31 ^{ns}	0.79*	-0.41 ^{ns}
IFP			0.19 ^{ns}	0.23 ^{ns}	-0.68*	-0.50*	-0.01 ^{ns}	-0.10 ^{ns}	-0.30 ^{ns}
PH				-0.33 ^{ns}	-0.02 ^{ns}	0.32 ^{ns}	0.17 ^{ns}	-0.08 ^{ns}	0.38 ^{ns}
2 nd IL					-0.11 ^{ns}	-0.08 ^{ns}	-0.39 ^{ns}	-0.04 ^{ns}	-0.13 ^{ns}
ED						0.47*	0.02 ^{ns}	0.00 ^{ns}	0.46 ^{ns}
NPP							-0.27 ^{ns}	-0.25 ^{ns}	0.48 ^{ns}
NGPOD								-0.27 ^{ns}	0.23 ^{ns}
M100G									-0.27 ^{ns}

*Significant by *t* test at 0.05 probability; ^{ns}Non-significant; LDG = lodging; GAS = general adaptation score; IFP = insertion of the first pod; PH = plant height; 2ndIL = second internode length; ED = epicotyl diameter; NPP = number of pods per plant; NGPOD = number of grains per pod; M100G = mass of 100 grains; YIELD = grain yield.

were not coincident when data from two years (Moura et al., 2013) and two locations (Barili et al., 2011) were considered. In path analysis, the direct and indirect effects varied in magnitude and sign for different agronomic traits determined in common bean genotypes in experiments conducted in different locations (Zilio et al., 2013). These results validate the hypothesis that environmental variability between growing seasons,

years, and/or locations results in changes in the observed correlation estimates between agronomic traits analyzed in common bean genotypes.

When data from two experiments were used, two correlations showed significance in all combinations of growing seasons and years tested: lodging and general adaptation score ($r \geq 0.66$); and epicotyl diameter and number of pods per plant ($r \geq 0.55$). For common beans,

Table 3 – Pearson's correlation coefficients obtained between the traits of lodging, general adaptation score, insertion of the first pod, plant height, second internode length, epicotyl diameter, number of pods per plant, number of grains per pod, mass of 100 grains, and grain yield obtained in 17 common bean genotypes evaluated in the experiments I and II (2016 rainy and 2017 dry seasons), I and III (2016 rainy and 2017 rainy seasons), II and IV (2017 dry and 2018 dry seasons) and III and IV (2017 rainy and 2018 dry seasons).

TRAITS	GAS	IFP	PH	2 nd IL	ED	NPP	NGPOD	M100G	YIELD
Experiments I and II									
LDG	0.71*	0.17 ^{ns}	-0.20 ^{ns}	0.23 ^{ns}	-0.26 ^{ns}	-0.52*	-0.18 ^{ns}	0.42 ^{ns}	-0.16 ^{ns}
GAS		0.07 ^{ns}	-0.34 ^{ns}	0.25 ^{ns}	-0.30 ^{ns}	-0.61*	-0.37 ^{ns}	0.53*	-0.24 ^{ns}
IFP			0.52*	-0.22 ^{ns}	-0.27 ^{ns}	-0.24 ^{ns}	-0.01 ^{ns}	0.00 ^{ns}	0.05 ^{ns}
PH				-0.54*	0.39 ^{ns}	0.38 ^{ns}	0.14 ^{ns}	-0.42 ^{ns}	-0.21 ^{ns}
2 nd IL					-0.03 ^{ns}	-0.20 ^{ns}	-0.08 ^{ns}	0.35 ^{ns}	-0.03 ^{ns}
ED						0.55*	0.10 ^{ns}	-0.52*	-0.58*
NPP							0.64*	-0.72*	-0.06 ^{ns}
NGPOD								-0.62*	0.39 ^{ns}
M100G									-0.04 ^{ns}
Experiments I and III									
LDG	0.69*	0.42 ^{ns}	0.23 ^{ns}	-0.32 ^{ns}	-0.01 ^{ns}	-0.17 ^{ns}	0.03 ^{ns}	0.07 ^{ns}	0.20 ^{ns}
GAS		0.20 ^{ns}	0.27 ^{ns}	-0.08 ^{ns}	0.34 ^{ns}	-0.09 ^{ns}	-0.01 ^{ns}	0.11 ^{ns}	0.00 ^{ns}
IFP			0.55*	-0.39 ^{ns}	-0.30 ^{ns}	-0.44 ^{ns}	0.05 ^{ns}	0.33 ^{ns}	0.19 ^{ns}
PH				-0.71*	0.37 ^{ns}	0.20 ^{ns}	-0.17 ^{ns}	0.02 ^{ns}	-0.10 ^{ns}
2 nd IL					-0.12 ^{ns}	-0.33*	0.12 ^{ns}	-0.07 ^{ns}	-0.08 ^{ns}
ED						0.56*	-0.42 ^{ns}	-0.30 ^{ns}	-0.67*
NPP							0.13 ^{ns}	-0.41 ^{ns}	-0.13 ^{ns}
NGPOD								-0.28 ^{ns}	0.63*
M100G									0.19 ^{ns}
Experiments II and IV									
LDG	0.66*	0.47 ^{ns}	0.00 ^{ns}	0.05 ^{ns}	-0.69*	-0.44 ^{ns}	-0.51*	0.60*	-0.46 ^{ns}
GAS		0.27 ^{ns}	-0.33 ^{ns}	0.17 ^{ns}	-0.57*	-0.61*	-0.57*	0.81*	-0.74*
IFP			0.05 ^{ns}	0.37 ^{ns}	-0.82*	-0.60*	-0.09 ^{ns}	0.25 ^{ns}	-0.12 ^{ns}
PH				-0.46 ^{ns}	0.24 ^{ns}	0.50*	0.23 ^{ns}	-0.45 ^{ns}	0.33 ^{ns}
2 nd IL					-0.25 ^{ns}	-0.41 ^{ns}	-0.22 ^{ns}	0.34 ^{ns}	-0.29 ^{ns}
ED						0.67*	0.36 ^{ns}	-0.45 ^{ns}	0.37 ^{ns}
NPP							0.40 ^{ns}	-0.81	0.42 ^{ns}
NGPOD								-0.47 ^{ns}	0.67*
M100G									-0.53*
Experiments III and IV									
LDG	0.75*	0.56*	0.42 ^{ns}	0.04 ^{ns}	-0.22 ^{ns}	-0.11 ^{ns}	-0.15 ^{ns}	0.56*	0.14 ^{ns}
GAS		0.50*	0.12 ^{ns}	0.12 ^{ns}	-0.18 ^{ns}	-0.29 ^{ns}	-0.30 ^{ns}	0.76*	-0.26 ^{ns}
IFP			0.40 ^{ns}	0.20 ^{ns}	-0.59*	-0.55*	0.21 ^{ns}	0.28 ^{ns}	0.13 ^{ns}
PH				-0.53*	0.19 ^{ns}	0.28 ^{ns}	0.07 ^{ns}	0.05 ^{ns}	0.56*
2 nd IL					-0.26 ^{ns}	-0.54*	0.14 ^{ns}	0.11 ^{ns}	-0.59*
ED						0.73*	-0.39 ^{ns}	-0.10 ^{ns}	-0.08 ^{ns}
NPP							-0.27 ^{ns}	-0.32 ^{ns}	0.20 ^{ns}
NGPOD								-0.50*	0.36 ^{ns}
M100G									-0.27 ^{ns}

* Significant by t test at 0.05 probability. ^{ns}Non-significant; LDG = lodging; GAS = general adaptation score; IFP = insertion of the first pod; PH = plant height; 2ndIL = second internode length; ED = epicotyl diameter; NPP = number of pods per plant; NGPOD = number of grains per pod; M100G = mass of 100 grains; YIELD = grain yield.

no studies were found in the literature that analyzed the effect of combinations of growing seasons and years on correlation estimates between important agronomic traits for the selection of superior common bean lines. However, when correlation analyses were performed based on average data from two growing seasons, most of the correlations between agronomic traits and grain yield in common bean genotypes were of low magnitude (Ribeiro et al., 2018).

In the present study, the magnitude and sign of the significant correlations were similar when data from two experiments conducted in the same growing season and in different years (I and III; II and IV) were considered. This was repeated when data from experiments carried out in different growing seasons and years (I and II; III and IV) were analyzed. Nevertheless, only two significant correlations were 100 % coincident in the four combinations of experiments tested: lodging and

general adaptation score; and epicotyl diameter and number of pods per plant. Therefore, using data from two experiments, involving combinations of growing seasons and years in Pearson's linear correlation analysis, resulted in low coincidence for most pairs of correlated agronomic traits. Consequently, similar to what was observed with data from individual experiments, using data from two experiments can lead to errors in interpreting results of correlation analyses. This is because the identification of pairs of correlated agronomic traits varies with the experiment (Table 2) and the combinations of growing seasons and years when data from two experiments are used (Table 3). In this case, to increase the efficiency of indirect selection for grain yield in common bean lines, it is necessary to determine the minimum number of experiments for Pearson's linear correlation analysis.

Correlation analysis using data from three and four experiments

When data from three and four experiments were used, ten significant correlations were obtained, eight coincident in magnitude and sign (Table 4). Therefore,

the inclusion of data from four experiments showed that 80 % of the significant correlations observed for agronomic traits were similar to those obtained using data from three experiments. Thus, using data from at least three experiments enables identifying pairs of correlated agronomic traits with high coincidence, which, in turn, allows for correctly interpreting the results of Pearson's linear correlation analysis.

In the present study, 15 correlations between pairs of plant architecture traits were tested, but only three correlations were significant: lodging and general adaptation score ($r = 0.66$); insertion of the first pod and plant height ($r = 0.50$); and plant height and second internode length ($r = -0.68$). Previous studies also showed a significant correlation between certain plant architecture traits analyzed in common bean genotypes (Moura et al., 2013; Nadeem et al., 2020; Ribeiro et al., 2018; Soltani et al., 2016). A non-significant correlation between two traits indicates that there are no linked genes or pleiotropic effects. In this case, the genetic values of the traits are independent, which facilitates the selection of superior genotypes (Balestre et al., 2013). However, selecting one trait will change the other, if the correlation is significant.

Table 4 – Pearson's correlation coefficients obtained between the traits of lodging, general adaptation score, insertion of the first pod, plant height, second internode length, epicotyl diameter, number of pods per plant, number of grains per pod, mass of 100 grains, and grain yield obtained in 17 common bean genotypes evaluated in the experiments I, II and III (2016 rainy, 2017 dry and 2017 rainy seasons) and I, II, III and IV (2016 rainy, 2017 dry, 2017 rainy and 2018 dry seasons).

TRAITS	GAS	IFP	PH	2 nd IL	ED	NPP	NGPOD	M100G	YIELD
Experiments I, II and III									
LDG	0.66*	0.25 ^{ns}	0.05 ^{ns}	-0.18 ^{ns}	-0.25 ^{ns}	-0.37 ^{ns}	-0.13 ^{ns}	0.26 ^{ns}	0.04 ^{ns}
GAS		0.13 ^{ns}	-0.16 ^{ns}	0.18 ^{ns}	-0.21 ^{ns}	-0.48*	-0.31 ^{ns}	0.52*	-0.12 ^{ns}
IFP			0.50*	-0.27 ^{ns}	-0.32 ^{ns}	-0.36 ^{ns}	0.02 ^{ns}	0.15 ^{ns}	0.07 ^{ns}
PH				-0.68*	0.42 ^{ns}	0.35 ^{ns}	-0.02 ^{ns}	-0.24 ^{ns}	-0.07 ^{ns}
2 nd IL					-0.16 ^{ns}	-0.40 ^{ns}	-0.07 ^{ns}	0.26 ^{ns}	-0.24 ^{ns}
ED						0.68*	-0.16 ^{ns}	-0.46 ^{ns}	-0.56*
NPP							0.38 ^{ns}	-0.71*	-0.01 ^{ns}
NGPOD								-0.66*	0.56*
M100G									-0.14 ^{ns}
Experiments I, II, III and IV									
LDG	0.73*	0.57*	0.19 ^{ns}	-0.24 ^{ns}	-0.42 ^{ns}	-0.39 ^{ns}	-0.32 ^{ns}	0.45 ^{ns}	-0.02 ^{ns}
GAS		0.41 ^{ns}	-0.09 ^{ns}	0.03 ^{ns}	-0.36 ^{ns}	-0.55*	-0.50*	0.68*	-0.32 ^{ns}
IFP			0.43 ^{ns}	-0.16 ^{ns}	-0.45 ^{ns}	-0.34 ^{ns}	0.03 ^{ns}	0.20 ^{ns}	0.07 ^{ns}
PH				-0.71*	0.33 ^{ns}	0.42 ^{ns}	0.06 ^{ns}	-0.25 ^{ns}	0.08 ^{ns}
2 nd IL					-0.16 ^{ns}	-0.46 ^{ns}	-0.03 ^{ns}	0.20 ^{ns}	-0.35 ^{ns}
ED						0.67*	-0.15 ^{ns}	-0.41 ^{ns}	-0.41 ^{ns}
NPP							0.28 ^{ns}	-0.69*	0.13 ^{ns}
NGPOD								-0.73*	0.52*
M100G									-0.32 ^{ns}

* Significant by *t* test at 0.05 probability; ^{ns}Non-significant. LDG = lodging; GAS = general adaptation score; IFP = insertion of the first pod; PH = plant height; 2ndIL = second internode length; ED = epicotyl diameter; NPP = number of pods per plant; NGPOD = number of grains per pod; M100G = mass of 100 grains; YIELD = grain yield.

Correlated traits provide similar information for selection, allowing the breeder to choose only one of these traits for use in the routine of the breeding program. In this respect, it is recommended to use lodging and plant height to select common bean lines with upright plant architecture, as these two traits are easy to evaluate and are rapidly determined. Using a smaller number of traits to be evaluated reduces the time and resources employed in selecting common bean lines with upright plant architecture, thereby contributing to increasing the efficiency of the breeding program.

Correlations with different signs were obtained between plant architecture and yield traits. The following correlations were positive: general adaptation score and mass of 100 grains ($r = 0.52$) and epicotyl diameter and number of pods per plant ($r = 0.68$), showing that higher values of general adaptation score and epicotyl diameter resulted in increases in the mass of 100 grains and the number of pods per plant, respectively. However, two negative correlations were also observed between general adaptation score and number of pods per plant ($r = -0.48$) and epicotyl diameter and grain yield ($r = -0.56$), which means a reduction in one of these traits would increase the other. Similarly, positive and negative correlations between plant architecture traits and grain yield were found in segregating progenies of common bean (Silva et al., 2013). Thus, it is possible to select common bean lines with upright plant architecture and superior yield traits. Nonetheless, previous studies did not identify a correlation between plant architecture traits and grain yield in common bean genotypes (Moura et al., 2013; Ribeiro et al., 2018). This suggests that, in addition to genetic variability between common bean genotypes, environmental variability between growing seasons and years can change the significance, magnitude, and sign of Pearson's linear correlation estimates.

The correlations obtained between the yield traits showed that increasing the mass of 100 grains resulted in a reduction in the number of pods per plant ($r = -0.71$) and the number of grains per pod ($r = -0.66$). However, in previous studies, no correlation had been observed between the mass of 100 grains and the other primary yield components evaluated in common bean genotypes (Ribeiro et al., 2017, 2018). On the other hand, the number of grains per pod and grain yield correlated positively ($r = 0.56$), which coincides with reports in other studies on common beans (Barili et al., 2011; Delfini et al., 2017; Ribeiro et al., 2017). Therefore, the number of grains per pod is the most promising agronomic trait to be used in indirect selection for grain yield in common bean lines.

The present results allow us to infer that data from at least three experiments should be used in Pearson's linear correlation analysis. This strategy makes it possible to identify correlations between plant architecture and yield traits with high coincidence,

thereby increasing the efficiency of indirect selection for grain yield in common bean lines.

The definition of ideal bean plant architecture has changed over the years. After a half-century of a common bean program in Brazil, Lemos et al. (2020) proposed a plant ideotype. Currently, bean plants should still be as upright as possible and should have many highly upright branches, primarily until flowering, forming many tendrils to facilitate the collection of cut plants by the harvester reel and decrease harvest losses. This plant ideotype was found in the genotypes evaluated in the present study that showed indeterminate growth habit with either short (type II) or long guides (type III).

The changes observed in common bean plant architecture and reproductive allocation could be understood as plastic (Beebe et al., 2013) or genetic adaptive (Beebe et al., 2008; Cortés and López-Hernández, 2021) strategies that result in adaptation to abiotic stress, especially heat and drought tolerance. The heat and drought tolerance showed polygenic inheritance (Burbano-Erazo et al., 2021) and pleiotropic effects with abiotic responses (Cortés et al., 2013; Cortés and Blair, 2018) in common bean, indicating difficulties in the selection of superior genotypes.

In a climate change scenario, developing new common bean cultivars with more significant heat and drought tolerance represents crucial technological innovation for breeding programs. To achieve this objective, the Mesoamerican common bean Brazilian genotypes could be crossed with wild bean parents with heat and drought tolerance. Improved abiotic tolerance in interracial crosses combining Durango and Mesoamerican races has been reported in common beans (Beebe et al., 2008). *Phaseolus acutifolius* (Terapy bean) is a significant genetic resource for improving heat and drought tolerance in Mesoamerican common bean elite lines (Buitrago-Bitar et al., 2021; Burbano-Erazo et al., 2021). Common bean genotypes obtained by interspecific congruity backcrosses showed adaptation to heat and drought conditions (Burbano-Erazo et al., 2021).

However, transferring variation from wild exotic donors into common bean elite lines may induce undesired linked trait variation such as flowering delay and reduced crop yields (Cortés and López-Hernández, 2021). Genes related to biological and physiological mechanisms that were correlated with plant tolerance to high temperature were identified, such as time to flowering, germination and seedling development, cell wall stability, and the signaling of the pathway of abiotic stress via abscisic acid and auxin (López-Hernández and Cortés, 2019). A vast amount of knowledge about biological and physiological mechanisms related to heat and drought tolerance is required to bring about changes in plant architecture capable of producing an increase in grain yield in the new common bean cultivar for cultivation in Brazil.

Conclusions

Pearson's linear correlation estimates between plant architecture and yield traits in common bean lines vary in significance, magnitude, and sign in analyses performed using data from individual experiments and different combinations of growing seasons and years. Data from at least three experiments should be used in Pearson's linear correlation analysis to increase efficiency in indirect selection for grain yield in common bean lines.

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Authors' Contributions

Conceptualization: Ribeiro, N.D. **Data curation:** Ribeiro, N.D. **Formal analysis:** Maziero, S.M. **Funding acquisition:** Ribeiro, N.D. **Investigation:** Ribeiro, N.D.; Maziero, S.M. **Methodology:** Ribeiro, N.D.; Maziero, S.M. **Project administration:** Ribeiro, N.D. **Resources:** Ribeiro, N.D. **Supervision:** Ribeiro, N.D. **Validation:** Ribeiro, N.D.; Maziero, S.M. **Visualization:** Ribeiro, N.D.; Maziero, S.M. **Writing – original draft:** Ribeiro, N.D. **Writing – review & editing:** Ribeiro, N.D.

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