



High precision experimental statistics for the selection of common bean lines that have superior agronomic performance

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ABSTRACT. The identification of a single statistic that allows selection of superior genotypes for several agronomic traits with high experimental precision would be useful for bean breeding programs. We examined correlations between 12 statistics for agronomic traits to determine which would be useful for the selection of common bean lines that have superior agronomic performance. For this purpose, 21 experiments were carried out between 1998 and 2015, evaluating 156 common bean genotypes and seven agronomic traits. Error mean square presented a positive correlation estimate from intermediate to high magnitude with the coefficient of experimental variation and a significant minimum difference. Thus, these statistics are not adequate to evaluate the experimental precision of traits that confer high agronomic performance in common beans. Genotype mean square showed a positive correlation with the statistics: F-test value for genotype, coefficient of genetic variation, heritability, coefficient of relative variation and selective accuracy; these statistics were correlated with each other for most of the traits. Correlated statistics gave information similar as to the experimental precision of a trait, so they should not be used together. Selective accuracy (SA) is recommended as a classification measure of experimental precision in the selection of common bean lines that have superior agronomic

performance in Value of Cultivation and Use experiments. The SA makes the correct ranking of the common bean genotypes for agronomic performance traits possible, based on genetic superiority; consequently, SA should be implemented in the routine of common bean breeding programs.

Key words: *Phaseolus vulgaris*; Primary yield components; Earliness; Upright plant architecture

INTRODUCTION

Brazil is one of the world's largest bean (*Phaseolus vulgaris* L.) producers, with an estimated annual production of 3,418 thousand tons (Conab, 2017). Beans of varied colors and sizes are produced in the different regions. However, the cultivation of carioca (beige seed coat with brown streaks) and black beans predominate; they have a medium grain size (mass of 100 grains from 20 to 25 g) and are both from the Mesoamerican gene pool.

Most of the common bean cultivars registered in the National Register of Cultivars, of the Ministry of Agriculture, Livestock and Supply (RNC-MAPA) are composed of carioca and black beans, as these are also the bean grain types most consumed in the Brazil. This is a result of the efforts of several breeding programs that have recorded annual genetic gains from 0.72 to 1.10% in the grain yield of carioca and black beans (Ribeiro et al., 2008; Faria et al., 2013, 2014).

Bean cultivars that present high agronomic performance provide technological advantages for producers. In addition to grain yield, it is important to evaluate the primary yield components (number of pods per plant, number of grains per pod, and mass of 100 grains), earliness (flowering and cycle), upright plant architecture (lodging and insertion of the first pod), among other traits.

In order for the breeding program to select common bean lines with superior agronomic performance, it is necessary to use high experimental precision statistics that allow correct ranking of the genotypes evaluated, taking into account genetic variability (genetic variance). In order to launch a new common bean cultivar in Brazil, it is necessary to conduct experiments of Value of Cultivation and Use (VCU), following the predicted guidelines and presenting information concerning the descriptors demanded by Brazil (2006). In these experiments, experimental precision is evaluated exclusively for grain yield, considering two statistics: coefficient of experimental variation (CEV) $\leq 25\%$ and the F-test value for genotype (F_c) must be significant at 5% probability. Evaluating the quality of competition experiments of genotypes based on the CEV is inadequate according to Resende and Duarte (2007), because this statistic does not consider the level of genotypic variation expressed in the trait. In addition, a significant effect of genotype does not qualify an experiment as precise (Benin et al., 2013).

The statistics F_c , heritability (h^2) and selective accuracy (SA) have been shown to be adequate to evaluate the experimental precision of grain yield in competition experiments with common bean (Cargnelutti Filho et al., 2009; Ribeiro et al., 2017), soybean (Cargnelutti Filho et al., 2009), and wheat (Benin et al., 2013) genotypes. Recently, it was demonstrated that these statistics enable the selection of common bean genotypes with high experimental precision for primary yield components (Ribeiro et al., 2017) and for earliness and upright

plant architecture traits (Ribeiro ND, Steckling SDM, Maziero SM and Kläsener GR, unpublished results). However, in the routine of a breeding program, it is not feasible to use various experimental precision statistics to select common bean genotypes that have superior agronomic performance. Consequently, it would be useful to examine correlations between experimental precision statistics in order to identify those correlated with genotype mean square (GMS).

In competition experiments involving common bean genotypes, a positive correlation estimate was observed between F_c and h^2 , F_c and coefficient of relative variation (CRV), F_c and SA, h^2 and CRV, h^2 and SA, and CRV and SA for grain yield (Ribeiro et al., 2017). This means that these statistics should not be used together, because they involve redundant information.

For other traits that confer agronomic performance in the common bean, primary yield components, earliness and upright plant architecture, no previous studies of correlations between experimental precision statistics have been published. The identification of a single statistic that allows the selection of superior genotypes for several agronomic traits with high experimental precision has not been achieved for common bean and other autogamous plant species. We evaluated correlations between 12 statistics for agronomic traits to determine which would be useful for the selection of common bean lines that have superior agronomic performance.

MATERIAL AND METHODS

The 21 VCU experiments were carried out in Santa Maria, Rio Grande do Sul, Brazil, located in the following geographic coordinates: latitude 29°42'S, longitude 53°43'W, and 95 m altitude. The region's climate is characterized as humid subtropical, with hot summers and a not clearly defined dry season. The soil of the field area is classified as typical alitic Argisol, Hapludalf, belonging to the Santa Maria mapping unit, and was prepared in a conventional manner.

The experimental design consisted of randomized blocks, with three to four repetitions, depending on the quantity of seeds available for each growing season. The experimental unit consisted of four 4-m-long rows, spaced at 0.50 m. The useful area comprised the two central rows of each experimental unit, totaling 4 m². In each experiment, from 13 to 26 common bean genotypes were evaluated, including inbred lines obtained by various research institutions and cultivars (controls). A total of 156 common bean genotypes were evaluated between 1998 and 2015, representing the most widely consumed types of beans in Brazil: carioca (beige seed coat with brown streaks), black, cranberry (cream seed coat with red streaks), mouro (gray seed coat with brown streaks), red, yellow and pink. Approximately 85% of the bean production in Brazil is of carioca and black beans, therefore most of the genotypes evaluated were of these types of beans. The cranberry, mouro, red, yellow and pink beans are cultivated on a smaller scale and predominantly in family farming.

Between 1998 and 2015, 16 experiments were conducted during a normal rainy season and five experiments in the dry season. In the normal rainy season, sowing was carried out in October, which corresponds to the traditional bean growing season in the region. In the dry season, sowing was carried out in February in 2009, 2011, 2013, 2014 and 2015. Normally, in this second growing season, higher precipitation intensities are observed during the period from pod filling to maturity, and this contributes to a reduction in grain yield and the loss of a large number of experiments. Consequently, data obtained in only five experiments

of cultivation during the dry season are presented in this study. All experiments were performed following the RNC-MAPA guidelines for the registration of new common bean cultivars in Brazil (Brazil, 2006).

Management practices were uniform and consisted of: (1) fertilizer application, providing the necessary quantities identified by the interpretation of the soil chemical analysis report for each year of cultivation; (2) seed treatment with Maxim XL fungicide (fludioxonil and metalaxyl-M) and Cruiser insecticide (thiamethoxam), both at a dose of 200 mL/100 kg of seeds; (3) mechanical control of weed plants; and (4) application of Engeo Pleno insecticide (thiamethoxam and lambda-cyhalothrin) at a dose of 125 mL/ha, whenever insect infestation reached approximately 5% damage. No fungicide was applied during the development of the bean plants. Irrigation was only used when a lack of moisture in the soil could compromise seedling emergence.

The primary yield components (number of pods per plant, number of grains per pod, and mass of 100 grains) were determined in 10 plants at maturity (R9), randomly collected from the useful area. Earliness was evaluated based on flowering and plant cycle. The number of days from emergence (V1) to the opening of the first flower (R6) characterized flowering, and the number of days from emergence (V1) until maturity (R9) constituted the cycle. Both traits were defined considering an analysis of 51% of the plants in the useful area.

The upright architecture of the plants was analyzed by lodging and insertion of the first pod traits, both in plants at the R9 stage. A score scale varying from 1 to 9 was used to determine lodging, where score 1 characterized upright plants (100% upright plants) and score 9 referred to lodging plants (all fallen plants touching the soil). Lodging was evaluated by visual observation of the plants of the useful area, before harvest. The insertion of the first pod was measured with a ruler. For that, the distance from cotyledon node to insertion point of the first pod was measured in 10 plants randomly collected from the useful area.

Analysis of variance was performed for each of the 21 experiments, considering the seven traits. Twelve statistics were analyzed in this study: block mean square (BMS), genotype mean square (GMS), error mean square (EMS), overall mean of the experiment (M), amplitude of the means (A), F-test value for genotype (Fc), coefficient of experimental variation (CEV), coefficient of genetic variation (CGV), significant minimum difference (SMD) among genotypes means estimated by the Tukey's test at 5% probability, heritability (h^2), coefficient of relative variation (CRV) and selective accuracy (SA). The statistics A, Fc, CEV, CGV, SMD, h^2 , CRV and SA were obtained as described by Ribeiro et al. (2017).

Pearson's linear correlation analysis was performed among the 12 statistics, for each of the seven traits evaluated, considering the mean values obtained for the 21 experiments and using the phenotypic matrix. The Student *t*-test was used to verify the significance of the coefficients, at 5% probability. Statistical analyzes were performed using Microsoft Office Excel and Genes software (Cruz, 2013).

RESULTS AND DISCUSSION

Statistics for the selection of superior common bean lines for primary yield components

When the number of pods per plant was analyzed, BMS presented a positive correlation estimate with EMS ($r = 0.722$), M ($r = 0.687$), A ($r = 0.606$), and SMD ($r = 0.728$) (Table 1). Benin et al. (2013), similarly, observed that BMS was correlated with other experimental precision statistics when evaluating grain yield in 572 competition experiments of wheat genotypes and significance was attributed to the large number of degrees of freedom (570).

Table 1. Pearson's correlation coefficients among the statistics: block mean square (BMS), genotype mean square (GMS), error mean square (EMS), mean (M), amplitude (A), F-test value for genotype (Fc), coefficient of experimental variation (CEV), coefficient of genetic variation (CGV), significant minimum difference by the Tukey's test at 5% probability (SMD), heritability (h²), coefficient of relative variation (CRV), and selective accuracy (SA) estimated for number of pods per plant, number of grains per pod and mass of 100 grains obtained in 21 common bean experiments carried out between 1998 and 2015.

Number of pods per plant											
	GMS	EMS	M	A	Fc	CEV	CGV	SMD	h ²	CRV	SA
BMS	0.265 ^{ns}	0.722*	0.687*	0.606*	-0.303 ^{ns}	0.278 ^{ns}	-0.243 ^{ns}	0.728*	-0.239 ^{ns}	-0.307 ^{ns}	-0.182 ^{ns}
GMS		0.488*	0.438*	0.795*	0.293 ^{ns}	0.122 ^{ns}	0.539*	0.439*	0.507*	0.378 ^{ns}	0.513*
EMS			0.741*	0.801*	-0.408 ^{ns}	0.542*	-0.230 ^{ns}	0.924*	-0.268 ^{ns}	-0.417 ^{ns}	-0.196 ^{ns}
M				0.680*	-0.296 ^{ns}	-0.070 ^{ns}	-0.408 ^{ns}	0.707*	-0.165 ^{ns}	-0.303 ^{ns}	-0.103 ^{ns}
A					-0.105 ^{ns}	0.371 ^{ns}	0.165 ^{ns}	0.839*	0.114 ^{ns}	-0.041 ^{ns}	0.153 ^{ns}
Fc						-0.555*	0.629*	-0.521*	0.603*	0.960*	0.531*
CEV							0.028 ^{ns}	0.596*	-0.306 ^{ns}	-0.510*	-0.265 ^{ns}
CGV								-0.218 ^{ns}	0.838*	0.781*	0.793*
SMD									-0.291 ^{ns}	-0.483*	-0.224 ^{ns}
h ²										0.784*	0.991*
CRV											0.719*
Number of grains per pod											
	GMS	EMS	M	A	Fc	CEV	CGV	SMD	h ²	CRV	SA
BMS	0.155 ^{ns}	0.343 ^{ns}	-0.355 ^{ns}	0.073 ^{ns}	-0.182 ^{ns}	0.443*	0.212 ^{ns}	0.321 ^{ns}	-0.192 ^{ns}	-0.269 ^{ns}	-0.181 ^{ns}
GMS		0.184 ^{ns}	-0.335 ^{ns}	0.464*	0.720*	0.261 ^{ns}	0.894*	0.101 ^{ns}	0.819*	0.737*	0.806*
EMS			-0.552*	0.342 ^{ns}	-0.469*	0.899*	0.297 ^{ns}	0.874*	-0.180 ^{ns}	-0.366 ^{ns}	-0.148 ^{ns}
M				-0.124 ^{ns}	-0.019 ^{ns}	-0.843*	-0.719*	-0.480*	-0.262 ^{ns}	-0.190 ^{ns}	-0.270 ^{ns}
A					0.127 ^{ns}	0.269 ^{ns}	0.317 ^{ns}	0.163 ^{ns}	0.230 ^{ns}	0.074 ^{ns}	0.260 ^{ns}
Fc						-0.311 ^{ns}	0.590*	-0.514*	0.853*	0.956*	0.811*
CEV							0.535*	0.797*	-0.200 ^{ns}	-0.173 ^{ns}	0.006 ^{ns}
CGV								0.239 ^{ns}	0.787*	0.714*	0.783*
SMD									-0.285 ^{ns}	-0.389 ^{ns}	-0.260 ^{ns}
h ²										0.935*	0.995*
CRV											0.903*
Mass of 100 grains											
	GMS	EMS	M	A	Fc	CEV	CGV	SMD	h ²	CRV	SA
BMS	0.042 ^{ns}	0.102 ^{ns}	-0.205 ^{ns}	0.047 ^{ns}	-0.116 ^{ns}	0.238 ^{ns}	-0.001 ^{ns}	0.165 ^{ns}	-0.143 ^{ns}	-0.199 ^{ns}	-0.131 ^{ns}
GMS		-0.196 ^{ns}	0.192 ^{ns}	0.884*	0.781*	-0.246 ^{ns}	0.900*	-0.164 ^{ns}	0.598*	0.794*	0.583*
EMS			-0.018 ^{ns}	0.159 ^{ns}	-0.500*	0.896*	-0.037 ^{ns}	0.906*	-0.594*	-0.518*	-0.586*
M				0.199 ^{ns}	0.207 ^{ns}	-0.425 ^{ns}	-0.125 ^{ns}	-0.124 ^{ns}	0.385 ^{ns}	0.250 ^{ns}	0.382 ^{ns}
A					0.612*	0.065 ^{ns}	0.832*	0.192 ^{ns}	0.406 ^{ns}	0.658*	0.391 ^{ns}
Fc						-0.585*	0.706*	-0.580*	0.703*	0.975*	0.675*
CEV							0.004 ^{ns}	0.904*	-0.696*	-0.579*	-0.688*
CGV								-0.015 ^{ns}	0.577*	0.775*	0.568*
SMD									-0.641*	-0.523*	-0.627*
h ²										0.804*	0.998*
CRV											0.783*

* Significant by t test at 0.05 probability. ns Not significant

However, for the number of grains per pod and for the mass of 100 grains, BMS showed no correlation with the other statistics, or it was of low magnitude ($r \leq 0.490$). Cargnelutti Filho et al. (2009) and Ribeiro et al. (2017) also found an absence of correlation or low correlation between BMS and other statistics evaluated for grain yield in competition experiments of common bean genotypes, which agrees with the results obtained in our study for the number of grains per pod and mass of 100 grains.

For the number of pods per plant, the largest BMS resulted in larger EMS, M, A, and SMD. This can be attributed to the large variation observed among common bean genotypes for the number of pods per plant between experimental plots in the same experiment, and between different experiments. In turn, the number of grains per pod and the mass of 100 grains varied little among the common bean genotypes evaluated within and between different experiments. This is because all common bean lines and cultivars evaluated are of the *Phaseolus vulgaris* species, which is characterized by presenting from 4 to 10 grains per pod (Zimmermann and Teixeira, 1996). Most of the common bean genotypes evaluated in our study were carioca and black beans, and these present from small (25 g /100 grains) to medium (25 to 30 g /100 g grains) size grains, according to the classification proposed by Blair et al. (2010). Therefore, for the number of grains per pod and for the mass of 100 grains, the classification of the experimental precision by the statistics evaluated was independent of the BMS.

GMS was not significantly correlated with CEV and SMD for the number of pods per plant, number of grains per pod, and mass of 100 grains. A similar result was observed for grain yield in competition experiments of common bean genotypes (Cargnelutti Filho et al., 2009; Ribeiro et al., 2017). CEV and SMD did not consider the genetic variability (GMS) among the genotypes evaluated; thus they were not adequate statistics to evaluate the experimental precision of grain yield in competition experiments of common bean (Ribeiro et al., 2017), soybean (Cargnelutti Filho et al., 2009), and wheat (Benin et al., 2013) genotypes. In our study, CEV showed a positive correlation with the SMD for the number of pods per plant ($r = 0.596$), number of grains per pod ($r = 0.797$), and the mass of 100 grains ($r = 0.904$), indicating that the combined use of these statistics must be avoided, because they give redundant information regarding the classification of experimental precision. In addition, CEV and SMD were independent of the GMS; therefore the use these statistics for the selection of superior common bean genotypes for the primary yield components is not recommended.

However, positive correlation estimates from intermediate ($0.500 \leq r < 0.690$) to high ($r \geq 0.700$) magnitude were obtained between the GMS and the statistics F_c , CGV, h^2 , CRV, and SA for all primary yield components; except for the number of pods per plant in which the correlations between the GMS and F_c , and GMS and CRV were not significant. Positive correlation and of low magnitude was found between the GMS and F_c , GMS and h^2 , and GMS and SA for yield in competition experiments of common bean (Cargnelutti Filho et al., 2009) and wheat (Benin et al., 2013) genotypes. In our study, the statistics F_c , CGV, h^2 , CRV and SA considered the genetic variability (GMS) in the ranking of genotype for the number of pods per plant, number of grains per pod, and mass of 100 grains. Therefore, they are statistics recommended for use in common bean experiments.

EMS was positively correlated with CEV and SMD for the number of pods per plant, number of grains per pod, and mass of 100 grains. Benin et al. (2013) also observed a positive correlation between the EMS and the statistics CEV and SMD for grain yield in competition

experiments of wheat genotypes. CEV and SMD depended on the residual variance (EMS) and were independent on the genetic variance (GMS) for number of pods per plant, number of grains per pod, and mass of 100 grains. Therefore, they are not statistics that allow the selection of common bean genotypes with genetic superiority for primary yield components.

For the number of pods per plant and number of grains per pod, EMS showed no correlation or was of low magnitude with the statistics Fc, CGV, h², CRV and SA. Conversely, for the mass of 100 grains, negative correlation estimates of intermediate magnitude were observed between EMS and the statistics Fc (r = -0.500), h² (r = -0.594), CRV (r = -0.518), and SA (r = -0.586). In this case, for the lower values of EMS, higher scores were obtained for the statistics Fc, h², CRV and SA, which is in agreement with previous results observed for yield in competition experiments of common bean (Ribeiro et al., 2017) and wheat (Benin et al., 2013) genotypes.

In the routine of a breeding program, selection is usually performed for several traits simultaneously. If for each of these traits, several experimental precision statistics were analyzed to make inferences about genotype means, this would result in a longer and more complex process of selection of superior genotypes. Therefore, it is important to evaluate correlations between experimental precision statistics in order to identify those correlated to the GMS and to avoid the use of redundant statistics. For the number of pods per plant, number of grains per pod, and mass of 100 grains, positive correlations from intermediate to high magnitude were observed between the statistics: Fc and h², Fc and CRV, Fc and SA, CGV and h², CGV and CRV, CGV and SA, h² and CRV, h² and SA, and CRV and SA. For grain yield in competition experiments of common bean genotypes, Ribeiro et al. (2017) obtained a positive correlation between Fc and h², Fc and CRV, Fc and SA, h² and CVR, h² and SA, and CRV and SA.

Correlated statistics show similar information for the experimental precision of a trait, so they must not be presented together. In our study, all the statistics that presented a positive correlation with the GMS (Fc, CGV, h², CRV, and SA) were also correlated with each other. All these statistics enabled the selection of superior common bean lines for the primary yield components with high experimental precision. Therefore, any of these statistics could be used in the routine of a common bean breeding program.

However, the use of SA for the classification of experimental precision in competition experiments of common bean genotypes is more promising for the selection of genetically superior lines. This is because SA refers to the correlation between the true genotypic value of the genetic treatment and that is estimated or predicted from the information of the experiments (Resende and Duarte, 2007). Therefore, it allows the correct ranking of the genotypes evaluated in one or more experiments. The use of SA was adequate to evaluate the experimental precision of grain yield in competition experiments of common bean and soybean (Cargnelutti Filho et al., 2009) and wheat (Benin et al., 2013) genotypes. In addition, SA was the most appropriate statistic to select genetically superior common bean lines for grain yield, and with smaller number of experiments discarded by breeders due to the low experimental precision (Ribeiro et al., 2017). In our study, the SA was the most appropriate statistic to select common bean lines that have superior number of pods per plant, number of grains per pod, and mass of 100 grains. No previous studies defining a single statistic that allows selection of superior genotypes for several agronomic traits with high experimental precision were found in literature for common bean. Therefore, we recommend the use of SA

for the selection of genetically superior common bean lines for the number of pods per plant, number of grains per pod, and mass of 100 grains.

Statistics for the selection of superior common bean lines for earliness

For flowering, no significant correlation was obtained between BMS and the other statistics (Table 2). However, in the analysis of cycle, it was observed that BMS was positively correlated with the statistics EMS ($r = 0.735$), M ($r = 0.600$), A ($r = 0.734$), CEV ($r = 0.798$), and SMD ($r = 0.764$). In this case, the greater heterogeneity in the blocks resulted in higher values of EMS, M, A, CEV and SMD for the cycle. The cycle, similar to that observed for the number of pods per plant, showed wide variation within and among the evaluation experiments of common bean genotypes.

GMS was not significantly correlated with the CEV and SMD for flowering. Conversely, GMS presented a positive correlation with the statistics A, Fc, CGV, h^2 , CRV, and SA. For the cycle, positive correlation estimates of intermediate magnitude were obtained between GMS and the statistics CEV ($r = 0.516$) and SMD ($r = 0.539$), and there was no correlation between GMS and the statistics Fc, h^2 , CRV and SA, which was not expected. This can be justified by the fact that in the evaluation of cycle heterogeneity among the plants of the same experimental plot in relation the maturation of the plants is often observed. Therefore, the harvest should be delayed until the majority of the plants in the useful area are at R9 stage (maturity) and when soil moisture conditions make it possible to harvest. This contributed to the occurrence of a greater experimental error in the evaluation of the cycle in the common bean genotypes, making selection more difficult, especially in rainy years.

Positive correlation of high magnitude was found between EMS and CEV, EMS and SMD, and CEV and SMD for flowering and cycle. A similar response was obtained in our study for the number of pods per plant, number of grains per pod, and mass of 100 grains (Table 1). Regarding grain yield, Benin et al. (2013), also obtained positive correlation estimates between these statistics in competition experiments of wheat genotypes. These results allow us to infer that the statistics CEV and SMD are not adequate for the selection of superior common bean genotypes for the primary yield components and for traits related to earliness, since they are very dependent on the residual variance (EMS).

For flowering and cycle the following positive correlations between the statistics: Fc and CRV, h^2 and CRV, h^2 and SA, and CRV and SA were coincident (Table 2). Similar correlation estimates on magnitude and sign for these pairs of statistics were obtained for the number of pods per plant, number of grains per pod, and mass of 100 grains (Table 1). The study of correlations between experimental precision statistics for flowering and cycle is unprecedented in competition experiments of common bean genotypes. For other species of autogamous plants, no previous studies of correlations evaluation between these statistics were found.

Correlation estimates obtained for the statistics evaluated for flowering and cycle (Table 2) confirmed the findings observed for the number of pods per plant, number of grains per pod, and mass of 100 grains (Table 1). Therefore, the use of SA is recommended for the selection of genetically superior common bean lines for flowering and cycle. The smaller the absolute deviations between the parametric genetic values and the estimated or predicted genetic values, the higher the SA (Resende and Duarte, 2007). According to these authors, if the analysis presents $Fc \geq 2$ and $SA \geq 0.70$, it will be of high experimental precision, regardless of the trait and species evaluated.

Table 2. Pearson's correlation coefficients among the statistics: block mean square (BMS), genotype mean square (GMS), error mean square (EMS), mean (M), amplitude (A), F-test value for genotype (Fc), coefficient of experimental variation (CEV), coefficient of genetic variation (CGV), significant minimum difference by the Tukey's test at 5% probability (SMD), heritability (h^2), coefficient of relative variation (CRV), and selective accuracy (SA) estimated for flowering and cycle obtained in 21 common bean experiments carried out between 1998 and 2015.

	Flowering										
	GMS	EMS	M	A	Fc	CEV	CGV	SMD	h^2	CRV	SA
BMS	0.021 ^{ns}	0.194 ^{ns}	0.057 ^{ns}	0.256 ^{ns}	-0.184 ^{ns}	0.285 ^{ns}	0.065 ^{ns}	0.302 ^{ns}	0.017 ^{ns}	-0.161 ^{ns}	0.037 ^{ns}
GMS		-0.049 ^{ns}	-0.062 ^{ns}	0.539 [*]	0.893 [*]	-0.079 ^{ns}	0.916 [*]	-0.080 ^{ns}	0.625 [*]	0.953 [*]	0.574 [*]
EMS			-0.149 ^{ns}	0.550 [*]	-0.171 ^{ns}	0.960 [*]	0.124 ^{ns}	0.955 [*]	0.062 ^{ns}	-0.306 ^{ns}	0.100 ^{ns}
M				-0.049 ^{ns}	-0.030 ^{ns}	-0.281 ^{ns}	-0.211 ^{ns}	-0.064 ^{ns}	-0.173 ^{ns}	-0.085 ^{ns}	-0.127 ^{ns}
A					0.207 ^{ns}	0.570 [*]	0.773 [*]	0.601 [*]	0.627 [*]	0.460 [*]	0.609 [*]
Fc						-0.257 ^{ns}	0.683 [*]	-0.278 ^{ns}	0.387 ^{ns}	0.955 [*]	0.341 ^{ns}
CEV							0.132 ^{ns}	0.962 [*]	0.053 ^{ns}	-0.330 ^{ns}	0.076 ^{ns}
CGV								0.098 ^{ns}	0.817 [*]	0.839 [*]	0.769 [*]
SMD									0.211 ^{ns}	-0.341 ^{ns}	0.054 ^{ns}
h^2										0.603 [*]	0.993 [*]
CRV											0.551 [*]
	Cycle										
BMS	0.413 ^{ns}	0.735 [*]	0.600 [*]	0.734 [*]	-0.410 ^{ns}	0.798 [*]	0.238 ^{ns}	0.764 [*]	-0.299 ^{ns}	-0.299 ^{ns}	-0.283 ^{ns}
GMS		0.420 ^{ns}	0.738 [*]	0.743 [*]	0.206 ^{ns}	0.516 [*]	0.915 [*]	0.539 [*]	0.336 ^{ns}	0.341 ^{ns}	0.317 ^{ns}
EMS			0.739 [*]	0.837 [*]	-0.347 ^{ns}	0.947 [*]	0.692 [*]	0.969 [*]	-0.158 ^{ns}	-0.204 ^{ns}	-0.165 ^{ns}
M				0.762 [*]	-0.115 ^{ns}	0.693 [*]	0.567 [*]	0.758 [*]	0.243 ^{ns}	0.239 ^{ns}	0.228 ^{ns}
A					-0.100 ^{ns}	0.895 [*]	0.869 [*]	0.901 [*]	0.151 ^{ns}	0.226 ^{ns}	0.138 ^{ns}
Fc						-0.434 [*]	0.440 ^{ns}	-0.387 ^{ns}	0.783 [*]	0.967 [*]	0.764 [*]
CEV							0.613 [*]	0.985 [*]	-0.336 ^{ns}	-0.371 ^{ns}	-0.340 ^{ns}
CGV								0.703 [*]	0.427 ^{ns}	0.450 ^{ns}	0.409 ^{ns}
SMD									-0.228 ^{ns}	-0.236 ^{ns}	-0.237 ^{ns}
h^2										0.865 [*]	0.998 [*]
CRV											0.849 [*]

* Significant by t test at 0.05 probability. ns Not significant

Statistics for selection of superior common bean lines for upright plant architecture

For lodging we found that BMS showed no significant correlation with any of the statistics evaluated, except for SMD ($r = 0.472$) (Table 3). Positive correlation estimates from intermediate to high magnitude were obtained between GMS and the statistics: A ($r = 0.616$), Fc ($r = 0.714$), CGV ($r = 0.855$), h^2 ($r = 0.623$), CRV ($r = 0.742$), and SA ($r = 0.548$), similar to what we found for the number of grains per pod, mass of 100 grains and flowering. No previous studies of correlation analysis were found between the experimental precision statistics for lodging in competition experiments of common bean genotypes or of other autogamous plant species.

Table 3. Pearson's correlation coefficients among the statistics: block mean square (BMS), genotype mean square (GMS), error mean square (EMS), mean (M), amplitude (A), F-test value for genotype (Fc), coefficient of experimental variation (CEV), coefficient of genetic variation (CGV), significant minimum difference by the Tukey's test at 5% probability (SMD), heritability (h^2), coefficient of relative variation (CRV), and selective accuracy (SA) estimated for lodging and insertion of the first pod obtained in 21 common bean experiments carried out between 1998 and 2015.

Lodging											
	GMS	EMS	M	A	Fc	CEV	CGV	SMD	h^2	CRV	SA
BMS	0.032 ^{ns}	0.436*	0.067 ^{ns}	0.220 ^{ns}	-0.267 ^{ns}	-0.249 ^{ns}	-0.071 ^{ns}	0.472*	-0.178 ^{ns}	-0.223 ^{ns}	-0.164 ^{ns}
GMS		0.139 ^{ns}	-0.367 ^{ns}	0.616*	0.714*	0.242 ^{ns}	0.855*	0.142 ^{ns}	0.623*	0.742*	0.548*
EMS			-0.141 ^{ns}	0.542*	-0.426 ^{ns}	0.781*	-0.078 ^{ns}	0.931*	-0.494*	-0.482*	-0.479*
M				-0.204 ^{ns}	-0.242 ^{ns}	-0.699*	-0.632*	-0.105 ^{ns}	-0.171 ^{ns}	-0.206 ^{ns}	-0.116 ^{ns}
A					0.154 ^{ns}	0.486*	0.471*	0.640*	0.075 ^{ns}	0.164 ^{ns}	0.030 ^{ns}
Fc						-0.233 ^{ns}	0.676*	-0.434*	0.672*	0.925*	0.580*
CEV							0.306 ^{ns}	0.724*	-0.258 ^{ns}	-0.267 ^{ns}	-0.275 ^{ns}
CGV								-0.032 ^{ns}	0.765*	0.787*	0.707*
SMD									-0.467*	-0.442*	-0.467*
h^2										0.876*	0.977*
CRV											0.799*
Insertion of the first pod											
BMS	0.518*	0.604*	0.654*	0.556*	-0.026 ^{ns}	0.052 ^{ns}	-0.022 ^{ns}	-0.581*	-0.162 ^{ns}	-0.708 ^{ns}	-0.136 ^{ns}
GMS		0.854*	0.643*	0.907*	0.126 ^{ns}	0.494*	0.558*	0.841*	0.144 ^{ns}	0.172 ^{ns}	0.159 ^{ns}
EMS			0.773*	0.926*	-0.285 ^{ns}	0.630*	0.297 ^{ns}	0.979*	-0.204 ^{ns}	-0.184 ^{ns}	-0.152 ^{ns}
M				0.698*	-0.207 ^{ns}	0.105 ^{ns}	-0.071 ^{ns}	0.731*	-0.189 ^{ns}	-0.182 ^{ns}	-0.160 ^{ns}
A					-0.035 ^{ns}	0.643*	0.537*	0.935*	0.044 ^{ns}	0.057 ^{ns}	0.084 ^{ns}
Fc						-0.364 ^{ns}	0.536*	-0.272 ^{ns}	0.853*	0.957*	0.759*
CEV							0.535*	0.703*	-0.202 ^{ns}	-0.218 ^{ns}	-0.145 ^{ns}
CGV								0.377 ^{ns}	0.669*	0.690*	0.666*
SMD									-0.186 ^{ns}	-0.154 ^{ns}	-0.134 ^{ns}
h^2										0.929*	0.982*
CRV											0.868*

* Significant by t test at 0.05 probability. ns Not significant

The statistics Fc, CGV, h^2 , CRV and SA considered the genetic variability (GMS) in ranking of the common bean genotypes. Therefore, they were more adequate statistics for the selection of common bean genotypes with genetic superiority for lodging than CEV and SMD. This is because CEV and SMD showed a high correlation with EMS: $r = 0.781$ and $r = 0.931$, respectively. Therefore, when considering CEV and SMD in the selection of superior common bean genotypes for lodging, high experimental precision was obtained in experiments in which the GMS was not significant ((Ribeiro ND, Steckling SDM, Maziero SM and Kläsener GR, unpublished results). In this case, the selection of superior genotypes could be performed in experiments that do not present genetic variability, which is an error.

For the insertion of the first pod, correlation estimates of intermediate magnitude were observed between BMS and the statistics GMS, EMS, M, A, and SMD. For this trait, GMS presented positive correlation estimates with CEV ($r = 0.494$) and SMD ($r = 0.841$), and the correlations between GMS and the statistics Fc, h^2 , CRV, and SA were not significant, which was not expected. As we observed, in relation to the number of pods per plant and

cycle, the insertion of the first pod had a wide variation within and among evaluation experiments of common bean genotypes. It contributed to a greater experimental error in the evaluation of these traits, justifying the absence of correlation between GMS and the statistics F_c , h^2 , CRV , and SA . The insertion of the first pod was evaluated after harvesting in 10 plants at the $R9$ stage, randomly collected in the useful area. In rainy agricultural years, there is a greater heterogeneity among the plants of the same experimental plot for the insertion of the first pod. Therefore, researchers could increase the sample size used in competition experiments of common bean genotypes to reduce the experimental error in the evaluation of insertion of the first pod.

EMS showed a positive correlation with CEV and SMD for the insertion of the first pod, similar to that observed for the other traits: number of pods per plant, number of grains per pod, mass of 100 grains, flowering, cycle, and lodging. CEV and SMD were also dependent on the residual variation (EMS) for grain yield in competition experiments of common bean genotypes (Ribeiro et al., 2017). Therefore, evaluating the quality of competition experiments of genotypes based on the CEV or the SMD is not adequate, since the level of genotypic variation expressed in the trait is not considered (Resende and Duarte, 2007). The use of these statistics for the classification of experimental precision should be avoided by common bean breeders in the selection of genotypes with superior agronomic performance.

However, the use of statistics F_c , h^2 and SA has been recommended to evaluate the experimental precision of traits that confer high agronomic performance to the common bean (Cargnelutti Filho et al., 2009; Ribeiro et al., 2017; Ribeiro ND, Steckling SDM, Maziero SM and Kläsener GR, unpublished results). Ribeiro et al. (2017) also recommended the use of the CRV for the evaluation of the experimental precision of primary yield components in competition experiments of common bean genotypes. In our study, all these statistics were correlated when evaluating the lodging, insertion of the first pod and other traits. This confirms that the combined use of these statistics should be avoided, as they are redundant.

SA was the most appropriate statistic to select common bean lines with genetic superiority for yield (Ribeiro et al., 2017). In the experiments in which $F_c \geq 2$ and $SA \geq 0.70$ were obtained, the selection of superior genotypes can be performed with high experimental precision, independent of the trait and species evaluated (Resende and Duarte, 2007). The use of SA allowed selection of common bean genotypes with high experimental precision for grain yield, number of pods per plant, number of grains per pod, and mass of 100 grains (Ribeiro et al., 2017), flowering, cycle, lodging, insertion of the first pod, and insertion of the last pod (Ribeiro ND, Steckling SDM, Maziero SM and Kläsener GR, unpublished results). SA showed a high positive correlation with GMS and the statistics F_c , CGV , CRV and h^2 for most of the traits evaluated in our study. Therefore, the use of SA is recommended as a measure of classification of experimental precision in the selection of common bean lines that have superior agronomic performance in the Value of Cultivation and Use experiments. The SA makes the correct ranking of the common bean genotypes for agronomic performance traits possible, based on genetic superiority; so SA should be implemented in the routine of common bean breeding programs.

CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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