

Genetic divergence for agronomic traits in common bean lines evaluated in multiple experiments

Divergência genética para caracteres agrônômicos em linhagens de feijão avaliadas em múltiplos experimentos

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ABSTRACT - The effects of genotype $\times$ environment interaction on the clustering pattern of common bean genotypes for multiple agronomic traits have been underinvestigated by breeding programs. This study aimed to evaluate whether the number of experiments influences the clustering pattern obtained using the complete linkage (Farthest Neighbor) and Ward hierarchical methods for agronomic traits in common bean genotypes, as well as to identify the most promising parents for crossing. For this purpose, plant architecture and yield-related traits important for selection were assessed in Mesoamerican common bean lines across four experiments. Analysis of variance and clustering analyses using the Farthest Neighbor and Ward methods were performed with data from individual experiments and from combinations of two, three, and four experiments. Significant differences for genotype, environment, and genotype $\times$ environment interaction were observed for several agronomic traits. The traits contributing most to genetic divergence and to the clustering pattern of genotypes varied according to the number of experiments considered. Plant height and grain yield were the descriptors that most effectively differentiated the genotypes. The Farthest Neighbor and Ward methods showed 100% agreement in grouping bean genotypes when mean data from four experiments were used. The cross between line CNFP 18552 and cultivar IPR Urutau is promising for obtaining recombinants with upright plant architecture and high grain yield.

RESUMO - Os efeitos da interação genótipo $\times$ ambiente no padrão de agrupamento de genótipos de feijão para múltiplos caracteres agrônômicos foram pouco investigados pelos programas de melhoramento. Esse estudo foi realizado com os objetivos de avaliar se o número de experimentos influencia no padrão de agrupamento obtido pelos métodos hierárquicos de ligação completa (Vizinho mais Distante) e de Ward para caracteres agrônômicos em genótipos de feijão e selecionar os parentais mais promissores a serem combinados. Para tanto, caracteres de arquitetura de planta e de produção importantes para a seleção foram determinados em linhagens de feijão Mesoamericano em quatro experimentos. As análises de variância e de agrupamento Vizinho mais Distante e Ward foram implementadas a partir de dados obtidos em experimentos individuais e em combinações de dois, três e de quatro experimentos. Diferenças significativas para genótipo, ambiente e interação genótipo $\times$ ambiente foram encontradas para vários caracteres agrônômicos. Os caracteres que mais contribuíram para a divergência genética e o padrão de agrupamento dos genótipos foram variáveis com o número de experimentos. A altura de planta e a produtividade de grãos foram os descritores que permitiram a melhor diferenciação dos genótipos. Os métodos Vizinho mais Distante e Ward são 100% concordantes na estratificação dos genótipos de feijão em grupos com o uso de dados médios de quatro experimentos. O cruzamento entre a linhagem CNFP 18552 e a cultivar IPR Urutau é promissor para a obtenção de recombinantes com arquitetura de planta ereta e alta produtividade de grãos.

Keywords: *Phaseolus vulgaris* L. Genotype $\times$ environment interaction. Complete linkage. Ward. Clustering pattern.

Palavras-chave: *Phaseolus vulgaris* L. Interação genótipo $\times$ ambiente. Ligação completa. Ward. Padrão de agrupamento.

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INTRODUCTION

Controlled crosses have been the main strategy used to generate genetic variability in common bean (*Phaseolus vulgaris* L.) breeding programs. The species is characterized as a self-pollinating plant featuring cleistogamy, that is, in which pollination and fertilization occur within the flower bud before natural flower opening. As a result, controlled crosses must be performed manually by opening the flower bud, removing the anthers from the female parent, and transferring pollen from the male parent. This is the most commonly used technique, despite its time-consuming nature and relatively low efficiency.

To optimize the selection of parents to be combined, clustering analyses have been employed, e.g., the hierarchical, optimization, principal component, and canonical variable methods (CRUZ; FERREIRA; PESSONI, 2020). Among hierarchical approaches, the Farthest Neighbor (CARGNELUTTI FILHO; STORCK; RIBEIRO, 2009; SANTOS et al., 2022) and Ward (DELFINI et al., 2017; GUPTA et al., 2021; NOGUEIRA et al., 2021; KOUAM; KAMGA-FOTSO; ANOUMAA, 2023; ASSEFA; MEKONNEN; BANTAYEHU, 2024) methods have proven effective in differentiating common bean genotypes in terms of agronomic traits. Both methods form groups with internal homogeneity (CRUZ; FERREIRA; PESSONI, 2020).

However, these previous studies were conducted in one (NOGUEIRA et al., 2021; ASSEFA; MEKONNEN; BANTAYEHU, 2024), two (GUPTA et al.,

2021; KOUAM; KAMGA-FOTSO; ANOUMAA, 2023), or four (DELFINI et al., 2017; SANTOS et al., 2022) environments (experiments) without clearly defining criteria for the number of experiments evaluated. This approach is particularly relevant when we consider that many key agronomic traits in common bean breeding exhibit significant genotype $\times$ environment interaction (DELFINI et al., 2017; ARTEAGA et al., 2019; SANTOS et al., 2022; DEMESSIE et al., 2024; RIBEIRO et al., 2025). In this case, the selection of parents with contrasting traits is expected to vary across experiments, which complicates decision-making in breeding programs.

In this context, defining the number of experiments that ensures greater repeatability in the selection of parents with superior agronomic traits may improve the efficiency of controlled crosses. The use of data from two experiments for the hierarchical Unweighted Pair Group Method with Arithmetic Mean (UPGMA) and from three experiments for the Tocher optimization method made it possible to more assertively identify common bean parents with multiple favorable plant architecture and yield traits to be combined (RIBEIRO; MAZIERO, 2022). However, increasing the accuracy of selection of common bean cultivars for agronomic traits required databases comprising six and seven experiments when the Ward and Tocher optimization methods were used, respectively (CARGNELUTTI FILHO; RIBEIRO; JOST, 2009). However, the requirement for six or more field experiments to define hybrid combinations substantially increases both the time and costs involved in developing new cultivars.

The number of experiments required for cluster analysis using the Farthest Neighbor hierarchical method has not been found in the literature. The underlying hypothesis is that defining a minimum number of experiments will enable the proper interpretation of the results generated in these cluster analyses. Therefore, this study aimed to evaluate whether the number of experiments influences the clustering pattern obtained using the Farthest Neighbor and Ward hierarchical methods for agronomic traits in common bean genotypes and to select the most promising parents for crossing.

MATERIAL AND METHODS

Plant material

Eleven Mesoamerican common bean genotypes with black seed coats, white hilum, and medium seed size (25 to 30 g) were evaluated. Of these, seven lines (BRS FP417, CNFP 18552, CNFP 17968, CNFP 17973, CNFP 17978, CNFP 17979, and CNFP 17984) were introduced from the Brazilian Agricultural Research Corporation (Embrapa), in Goiânia, Goiás, Brazil, due to their normal growth cycle (90 days). Four cultivars (BRS FP403, BRS Esteio, IPR Urutau, and IPR Uirapuru) were included as controls because of their adaptation to cultivation in Rio Grande do Sul (RS), Brazil, and their registration with the Ministry of Agriculture and Livestock (MAPA, 2025).

Field experiments

Four experiments were conducted in Santa Maria, RS,

Brazil, in an experimental field of the Federal University of Santa Maria (latitude 29°72'S, longitude 53°72'W, and altitude of 95 m). The climate of the region is humid subtropical, according to the Köppen classification, and the soil is classified as a typic alitic Argisol (Hapludalf).

The experimental design was a randomized block design with three replicates. Each plot was formed by four 4-m rows spaced 0.5 m apart. The usable area comprised the two central rows (4 m²).

The experiments were set up during four growing seasons: 2022 rainy (I), 2023 dry (II), 2023 rainy (III), and 2024 rainy (IV). Uniform crop management practices were adopted. Soil preparation involved one plowing followed by two harrowing operations. Seeds were treated with the insecticide Cruiser® 350 FS (Thiamethoxam) and the fungicide Maxim® (Fludioxonil and Metalaxyl-M). Fertilization consisted of 450 kg ha⁻¹ of the 05-20-20 (N-P₂O₅-K₂O) formulation applied at sowing and 70 kg ha⁻¹ of nitrogen (urea source) at the third fully expanded trifoliate leaf stage (V3). Weed control was done mechanically, and sprinkler irrigation was performed only at the emergence (V1) and flowering (R6) stages when water deficiency was observed.

Agronomic characterization

Lodging and general adaptation score were evaluated in the field on mature plants (R9 stage) in the usable area, using score scales. For lodging, a score of 1 corresponded to upright plants, whereas a score of 9 was assigned to prostrate plants. The general adaptation score assessed the overall plant architecture and pod production in terms of quantity and quality, with scores ranging from 1 (excellent) to 9 (very poor).

The remaining plant architecture traits (first pod insertion height, plant height, stem diameter, and number of nodes) were measured in 10 plants randomly harvested from the usable area. Mass of 100 grains and grain yield were determined in the usable area after drying the grains to standardize moisture content at 13%. Mass of 100 grains corresponded to the average weight of three 100-grain subsamples randomly collected from each replicate. Grain yield was quantified as the total weight of grains harvested and converted to kg ha⁻¹.

Data analyses

Data from the four experiments were compiled in Microsoft Excel spreadsheets, and statistical analyses were performed using the Genes (CRUZ, 2016) and R software. Heterogeneity in the number of plants harvested per plot was observed only in the 2023 rainy season experiment. To address this issue, grain yield data were corrected using the Covariance method - ideal stand, as recommended by Schmildt et al. (2001).

The assumptions of randomness, normality, and homogeneity of residual variances were verified for the data of the eight agronomic traits measured in each individual experiment (I; II; III; and IV) and in combinations of two (I and II), three (I, II, and III), and four (I, II, III, and IV) experiments. Subsequently, individual analyses of variance (ANOVA) were run for data obtained in the 2022 rainy (ANOVA I), 2023 dry (ANOVA II), 2023 rainy (ANOVA III), and 2024 rainy (ANOVA IV) seasons. Combined

analyses of variance were then conducted using data from two (ANOVA I and II), three (ANOVA I, II, and III), and four (ANOVA I, II, III, and IV) experiments, considering only environmental and error effects as random. In all seven analyses of variance, statistical significance was assessed using the F-test at the 5% probability level.

Multicollinearity diagnostics was implemented using the phenotypic correlation matrix derived from each individual and combined ANOVA. In all these cases, the condition number was the parameter used to identify the degree of multicollinearity, as proposed by Montgomery, Peck and Vining (2021).

The genetic dissimilarity matrix was obtained from the residual variance and covariance matrices of ANOVA I. Generalized Mahalanobis' distance, using standardized means, was adopted as the dissimilarity measure. This procedure was repeated using the matrices from ANOVA II, ANOVA III, ANOVA IV, and the combined analyses (ANOVA I and II; ANOVA I, II, and III; ANOVA I, II, III, and IV), resulting in seven genetic dissimilarity matrices. The traits contributing most to genetic divergence were also identified using the Generalized Mahalanobis' distance, based on data from one, two, three, and four experiments.

Cluster analyses were carried out using the Farthest Neighbor and Ward hierarchical methods, based on data from individual experiments (I; II; III; and IV) and from combinations of two (I and II), three (I, II, and III), and four (I, II, III, and IV) experiments. The Scott-Knott test was applied to differentiate the common bean genotypes allocated to the different groups. For the seven dendrograms generated in each hierarchical method, the consistency of the clustering pattern was analyzed based on the cophenetic correlation coefficient.

The concordance of cluster structures formed was evaluated individually and between methods by the adjusted Rand index (HUBERT; ARABIE, 1985). These analyses were carried out across individual experiments (I, II, III; and IV) and combinations of two, three, and four experiments, using

the 'mcclust' package of R software.

RESULTS AND DISCUSSION

Phenotypic variability in multiple experiments

In all experiments, the distribution of experimental error among plots was random, and the errors of the eight agronomic traits followed a normal distribution, confirming that both the assumptions of randomness and normality were met. However, residual variance heterogeneity was detected for first pod insertion height when data from two, three, and four experiments were considered. For this trait, it was necessary to adjust the degrees of freedom for error and genotype $\times$ environment interaction to meet the assumption of homogeneity of residual variances, as recommended by Cruz (2016). This adjustment enabled the implementation of the three combined analyses of variance for all evaluated traits.

Across the seven analyses of variance, significant differences in genotype effects were detected for a variable number of agronomic traits (Table 1). For general adaptation score, a significant genotype effect was observed only in experiments II (2023 dry season) and IV (2024 rainy season), and this trait notably exhibited the least variation among the experiments conducted. Conversely, all analyses of variance revealed a significant genotype effect on plant height, the most variable trait among the genotypes assessed in both individual and combined experiments. Recent publications have highlighted differences among common bean genotypes for several agronomic traits important for selection (GUPTA et al., 2021; NOGUEIRA et al., 2021; KOUAM; KAMGA-FOTSO; ANOUMAA, 2023; ASSEFA; MEKONNEN; BANTAYEHU, 2024; CONTRERAS-ROJAS et al., 2024). Together, previous findings and the results of the present study confirm the existence of genetic variability among common bean accessions, which can be exploited in the development of cultivars that are more productive and adapted to different growing conditions.

Table 1. Results of the F test of analysis of variance for the traits lodging (LDG), general adaptation score (GAS), first pod insertion height (FPIH, cm), plant height (PH, cm), stem diameter (SD, mm), number of nodes (NN), mass of 100 grains (M100G, g), and grain yield (GY, kg ha⁻¹) of 11 common bean genotypes evaluated in the 2022 rainy (I), 2023 dry (II), 2023 rainy (III), and 2024 rainy (IV) seasons and in the combinations of two (I and II), three (I, II, and III), and four (I, II, III, and IV) experiments.

Source of variation	Genotype							Experiment			Genotype × Experiment		
	I	II	III	IV	I and II	I, II, and III	I, II, III, and IV	I and II	I, II, and III	I, II, III, and IV	I and II	I, II, and III	I, II, III, and IV
LDG	3.40*	2.84*	0.74 ^{ns}	2.53*	3.50*	1.56 ^{ns}	0.79 ^{ns}	172.34*	39.76*	35.24*	1.35 ^{ns}	1.94*	2.53*
GAS	1.69 ^{ns}	4.00*	1.23 ^{ns}	5.06*	0.60 ^{ns}	0.59 ^{ns}	0.66 ^{ns}	339.76*	20.10*	17.00*	3.63*	2.81*	3.66*
FPIH	8.42*	1.94 ^{ns}	1.77 ^{ns}	0.55 ^{ns}	2.82 ^{ns}	4.19*	4.09*	157.64*	23.07*	21.24*	3.07*	0.81 ^{ns}	0.85 ^{ns}
PH	9.98*	4.92*	3.00*	4.32*	6.29*	3.54*	4.67*	12.41*	12.04*	11.64*	1.90 ^{ns}	2.90*	2.50*
SD	0.76 ^{ns}	2.66*	1.68 ^{ns}	2.59*	3.47*	1.08 ^{ns}	1.04 ^{ns}	53.94*	4.67 ^{ns}	53.19*	0.77 ^{ns}	1.66 ^{ns}	2.17*
NN	3.62*	0.85 ^{ns}	1.07 ^{ns}	2.71*	1.70 ^{ns}	1.76 ^{ns}	2.79*	26.71*	16.78*	16.16*	1.61 ^{ns}	1.37 ^{ns}	1.39 ^{ns}
M100G	1.71 ^{ns}	4.08*	3.40*	7.21*	3.63*	3.54*	3.04*	320.72*	26.62*	29.55*	1.10 ^{ns}	1.55 ^{ns}	2.67*
GY	9.08*	5.05*	1.93 ^{ns}	15.00*	0.43 ^{ns}	0.81 ^{ns}	1.75 ^{ns}	192.14*	21.04*	21.76*	10.14*	5.94*	8.22*

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

However, a significant environmental effect was detected for all traits in the analyses involving two, three, and four experiments, with the exception of stem diameter, which was determined using data from three experiments. Phenological, plant architecture, and yield traits in common bean genotypes have displayed variations that were associated

with environmental conditions (SANTOS et al., 2022; RIBEIRO et al., 2025). In the present study, all experiments were conducted in the same field area and received uniform management practices. It is thus inferred that the observed alterations in agronomic traits across experiments can be attributed mainly to differences in meteorological conditions,

particularly precipitation and maximum temperature, as well as to the incidence of diseases and pests in the growing seasons. In the four experiments, variations in meteorological conditions representative of common bean growing conditions in Santa Maria-RS were observed. This allows greater accuracy in the selection of parents that contrast in favorable agronomic traits by the breeding program.

The number of traits displaying significant genotype $\times$ environment interaction ranged from three to six when combined analysis of variance was executed using data from two, three, and four experiments. Significant genotype $\times$ environment interaction has been reported for morphological and yield traits in common bean (DELFINI et al., 2017; ARTEAGA et al., 2019; SANTOS et al., 2022; DEMESSIE et al., 2024; RIBEIRO et al., 2025). Consequently, when common bean genotypes are grown in different environments, key agronomic traits are modified, which represents a hindrance for breeding programs.

This occurs because, under significant genotype $\times$ environment interaction, the ranking of common bean genotypes for multiple favorable agronomic traits varies with the growing environment (RIBEIRO; MAZIERO, 2023). Accordingly, the identification of parents with promising agronomic traits to be included in crossing blocks differs among experiments. Therefore, defining the minimum number of experiments to be conducted will be crucial for ensuring accuracy in the selection of the most promising parents for

crossing.

Contribution of agronomic traits to genetic divergence

The condition number was lower than 100 in all multicollinearity diagnostic analyses, indicating weak multicollinearity according to the classification proposed by Montgomery, Peck and Vining (2021). In this case, no highly correlated variables were observed, and all evaluated traits were retained for the cluster analyses.

The agronomic traits contributing most to the genetic divergence of black common bean genotypes varied between individual and combined experiments (Figure 1). Based on data from individual experiments, the most effective descriptors for discriminating among genotypes were plant height and grain yield (2022 rainy season), stem diameter and grain yield (2023 dry season), plant height and mass of 100 grains (2023 rainy season), and grain yield and mass of 100 grains (2024 rainy season). In a previous study, when common bean accessions were cultivated over two consecutive years, plant height and seed production per plant contributed most to phenotypic diversity only in the first year (AL-BALLAT; AL-ARABY, 2019). These findings confirm that utilizing data from a single experiment may lead to errors in selecting the most effective agronomic descriptor(s) for identifying differences among common bean lines developed by the breeding program.

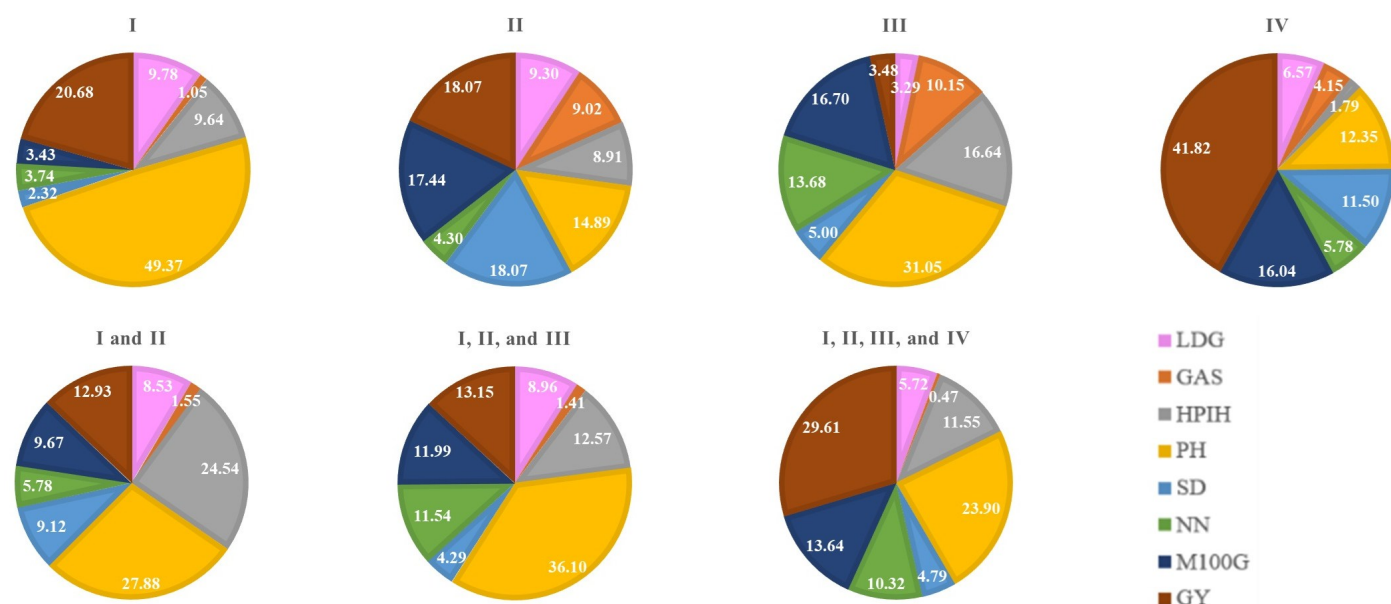


Figure 1. Relative contribution of the traits lodging (LDG), general adaptation score (GAS), first pod insertion height (FPIH, cm), plant height (PH, cm), stem diameter (SD, mm), number of nodes (NN), mass of 100 grains (M100G, g), and grain yield (GY, kg ha⁻¹), obtained from Mahalanobis' generalized distance, of 11 common bean genotypes evaluated in the 2022 rainy (I), 2023 dry (II), 2023 rainy (III), and 2024 rainy (IV) seasons and in the combinations of two (I and II), three (I, II, and III), and four (I, II, III, and IV) experiments.

For combined experiments, the greatest contributions to genotype differentiation were attributed to plant height (27.88%) and first pod insertion height (24.54%) when mean data from two experiments were used. With mean data from three experiments, plant height (36.10%) and grain yield (13.15%) were the most significant descriptors, whereas with mean data from four experiments, grain yield (29.61%) and plant height (23.90%) contributed most to genetic divergence. With the use of generalized Mahalanobis' distance, mass of 100 grains (SANTOS et al., 2022) and seed width (DELFINI et al., 2017) were identified as the most efficient descriptors based on mean data from three and four experiments, respectively. The reported discrepancies in identifying the most useful agronomic traits for assessing similarity and dissimilarity among common bean genotypes may be related to differences in the genetic diversity of the germplasm under investigation, in the number of traits assessed, and in the number of experiments conducted.

In the present study, plant height and grain yield showed the greatest relative contributions to genetic diversity in five of the seven experimental scenarios evaluated. Therefore, these appear to be the most promising descriptors for differentiating Mesoamerican, black-grained, normal-cycle common bean genotypes in breeding programs.

Cluster analysis using the Farthest Neighbor hierarchical method

The Farthest Neighbor method classified black common bean genotypes into two groups in all individual and combined experiments, except in the 2023 rainy season, in which three groups were formed using 70% dissimilarity as the grouping criterion (Figure 2). In this method, genotypes with greater similarity are those that show the smallest distance between them (CRUZ; FERREIRA; PESSONI, 2020). In the current study, the Farthest Neighbor method allowed the discrimination of common bean genotypes within the same seed class, with medium-sized seeds and a normal growth cycle.

Similarly, common bean genotypes from various seed classes were differentiated into two groups with distinct phenological, morphological, and yield traits using the Farthest Neighbor method (CARGNELUTTI FILHO; STORCK; RIBEIRO, 2009; SANTOS et al., 2022). Together, these previous results and the current findings suggest that the Farthest Neighbor method has been effective for grouping common bean genotypes with broad and narrow genetic base. This clustering method is efficient for assessing diversity among common bean genotypes based on agronomic traits relevant to selection.

In addition, the composition of genotype groups varied among analyses based on one, two, three, and four experiments (Figure 2), which complicates the identification of parents with contrasting traits for inclusion in the crossing block. The instability of the clustering patterns among individual and combined experiments was quantitatively confirmed by the adjusted Rand index (Table 2). Comparisons between the four-experiment analysis (FN7) and the

individual (FN1-FN4) experiments showed a low number of observed concordant pairs (8 to 24) and values lower than those expected by chance (9.33 to 15.22). Consequently, adjusted Rand index values ranged from -0.10 to 0.64, which can be interpreted as indicating weak to moderate agreement, according to the standards established by Hubert and Arabie (1985). Similarly, negative (-0.09) or intermediate (0.64) adjusted Rand index values were observed for comparisons between the four-experiment analysis (FN7) and the analyses based on three (FN6) and two (FN5) experiments, respectively. These results demonstrate weak to moderate agreement among clustering structures formed by the Farthest Neighbor method based on data from one, two, three, and four experiments. This may be explained by the strong influence of environmental variation on genotype discrimination and supports the need to evaluate genotypes across multiple experiments to obtain more consistent clustering patterns.

No studies have evaluated grouping patterns obtained by the Farthest Neighbor method in common bean as a function of the growing environment. However, the genotypes' clustering pattern differed when this analysis was done in the presence or absence of multicollinearity for agronomic traits (CARGNELUTTI FILHO; STORCK; RIBEIRO, 2009). In the current study, all clustering analyses were implemented under weak multicollinearity (condition number ≤ 100), allowing us to infer that the observed differences in grouping patterns may be attributed to variations in meteorological conditions and biotic factors that were not consistent across experiments.

The consistency of the clustering pattern obtained using the Farthest Neighbor method was assessed through cophenetic correlation coefficients. These values ranged from 0.42 (2023 dry season) to 0.75 (2024 rainy season) (Figure 2), representing a weaker fit between the cophenetic matrix and the dissimilarity matrix based on Mahalanobis' generalized distance (CRUZ; FERREIRA; PESSONI, 2020). This contributed to the low to moderate consistency observed in the clustering patterns of the dendrograms generated by the Farthest Neighbor method across individual and combined experiments (Table 2). Consequently, it was not possible to define the minimum number of experiments required to identify parents with favorable agronomic traits with high repeatability.

For the UPGMA hierarchical and Tocher optimization methods, two and three experiments, respectively, were reported as sufficient to select contrasting parents for several plant architecture and yield traits important for the selection of superior common bean lines (RIBEIRO; MAZIERO, 2022). In the present study, the maximum number of experiments evaluated was four, which was insufficient to draw a definitive conclusion regarding the number of experiments needed for an accurate selection of black common bean parents with favorable agronomic traits. Conducting this experiment across a larger number of environments could help determine whether the clustering pattern generated by the Farthest Neighbor method becomes repeatable when based on data from four or more experiments.

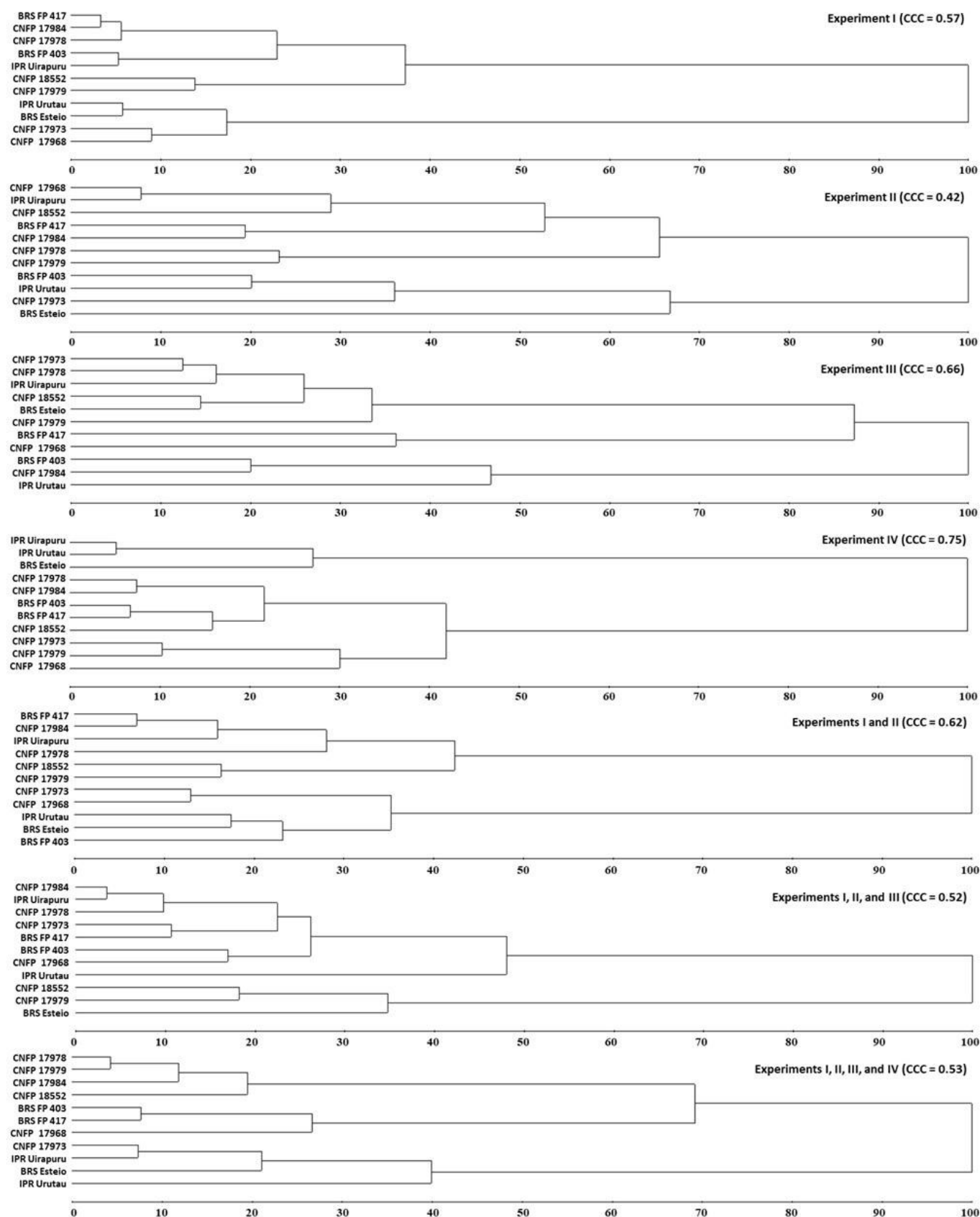


Figure 2. Dendrograms and cophenetic correlation coefficient (CCC) by the complete linkage (Farthest Neighbor) method, from Mahalanobis' generalized distance, of 11 common bean genotypes evaluated in the 2022 rainy (I), 2023 dry (II), 2023 rainy (III), and 2024 rainy (IV) seasons and in the combinations of two (I and II), three (I, II, and III), and four (I, II, III, and IV) experiments.

Table 2. Adjusted Rand index (ARI) and its components for groups formed in the Farthest Neighbor (FN) and Ward (W) methods in the (1) 2022 rainy, (2) 2023 dry, (3) 2023 rainy, and (4) 2024 rainy seasons and in the combinations of (5) two, (6) three, and (7) four experiments.

Comparison	Observed pairs	Expected by chance	Maximum	ARI
Farthest Neighbor method				
FN7 <i>versus</i> FN1	18	13.25	27.00	0.35
FN7 <i>versus</i> FN2	18	13.25	27.00	0.35
FN7 <i>versus</i> FN3	8	9.33	23.00	-0.10
FN7 <i>versus</i> FN4	24	15.22	29.00	0.64
FN7 <i>versus</i> FN5	21	12.27	26.00	0.64
FN7 <i>versus</i> FN6	14	15.22	29.00	-0.09
Ward's method				
W7 <i>versus</i> W1	18	13.25	27.00	0.35
W7 <i>versus</i> W2	12	10.31	24.00	0.12
W7 <i>versus</i> W3	8	9.33	23.00	-0.10
W7 <i>versus</i> W4	21	12.27	26.00	0.64
W7 <i>versus</i> W5	14	12.27	26.00	0.13
W7 <i>versus</i> W6	14	14.24	28.00	-0.02
Farthest Neighbor method <i>versus</i> Ward's method				
FN1 <i>versus</i> W1	27	13.25	27.00	1.00
FN2 <i>versus</i> W2	12	10.31	24.00	0.12
FN3 <i>versus</i> W3	16	6.56	19.00	0.76
FN4 <i>versus</i> W4	19	14.09	28.00	0.35
FN5 <i>versus</i> W5	16	11.36	25.00	0.34
FN6 <i>versus</i> W6	22	16.35	30.00	0.41
FN7 <i>versus</i> W7	27	13.25	27.00	1.00

Cluster analysis using Ward's hierarchical method

When Ward's method was applied to agronomic traits assessed in one, two, three, and four experiments, black common bean genotypes were grouped into two or three clusters (Figure 3), similarly to the pattern observed with the Farthest Neighbor method (Figure 2). In contrast, previous studies using Ward's method reported a greater number of genotype groups when clustering was based on morphological and agronomic traits (DELFINI et al., 2017; GUPTA et al., 2021; NOGUEIRA et al., 2021; KOUAM; KAMGA-FOTSO; ANOUMAA, 2023; ASSEFA; MEKONNEN; BANTAYEHU, 2024). In Ward's method, grouping is carried out based on the sums of squares of the deviations between genotypes (CRUZ; FERREIRA; PESSONI, 2020). The smaller range of variation recorded among the sums of squares of the deviations may have contributed to the differentiation of genotypes in two or three clusters in current study. The narrower genetic base among the evaluated black common bean genotypes likely explains the formation of fewer groups in the genetic divergence analyses.

The cophenetic correlation coefficients obtained for Ward's method were also relatively low (≤ 0.69) (Figure 3), denoting limited agreement between the original dissimilarity values and those represented in the dendrograms (CRUZ; FERREIRA; PESSONI, 2020). According to these authors, cophenetic correlation coefficients closer to 1.0 indicate lower

distortion in the clustering representation. Nonetheless, previous studies with cluster analysis applying Ward's method to common bean genotypes did not present cophenetic correlation coefficients for the dendrograms (CARGNELUTTI FILHO; RIBEIRO; JOST, 2009; DELFINI et al., 2017; GUPTA et al., 2021; NOGUEIRA et al., 2021; KOUAM; KAMGA-FOTSO; ANOUMAA, 2023; ASSEFA; MEKONNEN; BANTAYEHU, 2024), preventing direct comparison with the values observed in the present study.

As observed for the Farthest Neighbor method (Figure 2), the composition of the groups formed using Ward's method differed between individual and combined experiments (Figure 3). Therefore, the clustering pattern of common bean genotypes changed depending on the year and growing season (Figures 2 and 3). Adjusted Rand index values for clusters formed using Ward's method ranged from -0.10 to 0.64 in comparisons between the four-experiment analysis and the individual (W7 *versus* W1-W4) and combined analyses (W7 *versus* W5 and W7 *versus* W6) experiments (Table 2). In this case, weak to moderate agreement was found among the clustering structures formed by the Ward's method based on data from one, two, three, and four experiments, similar to that observed for the Farthest Neighbor method in this study. These two hierarchical methods formed compact clusters with high genetic similarity among the genotypes within each cluster.

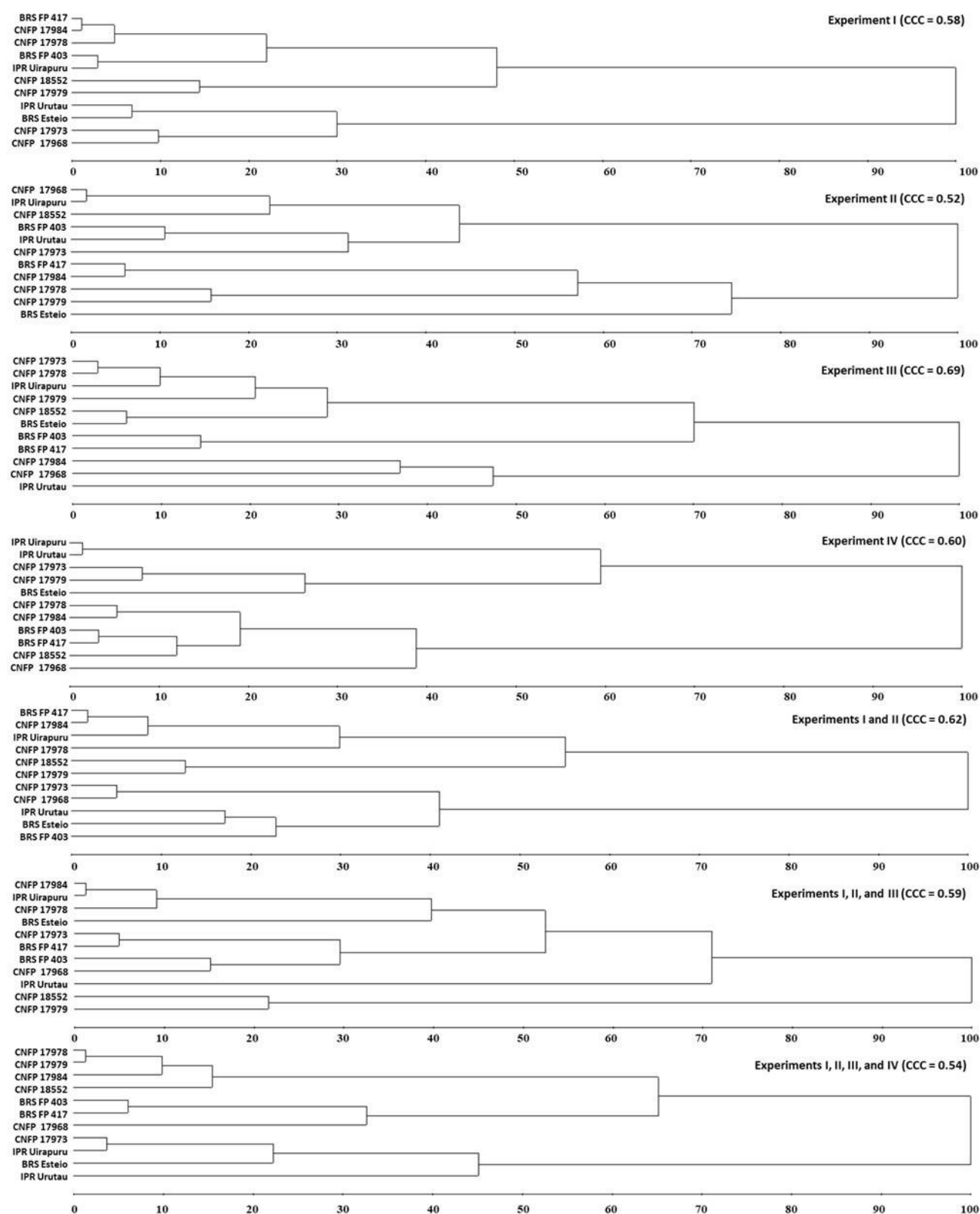


Figure 3. Dendrograms and cophenetic correlation coefficient (CCC) by Ward's method, from Mahalanobis' generalized distance, of 11 common bean genotypes evaluated in the 2022 rainy (I), 2023 dry (II), 2023 rainy (III), and 2024 rainy (IV) seasons and in the combinations of two (I and II), three (I, II, and III), and four (I, II, III, and IV) experiments.

However, when the Farthest Neighbor and Ward methods were applied to the agronomic traits determined in the 2022 rainy season, an adjusted Rand index of 1.00 was obtained, indicating perfect concordance in the clustering pattern (FN1 *versus* W1). Despite the high concordance between the clusters formed during this growing season, it is not recommended that the Farthest Neighbor and Ward methods be implemented based on data from a single experiment. This is justified by the following aspects: several agronomic traits exhibited a significant genotype $\times$ environment interaction (Table 1); the clustering pattern of genotypes varied for individual experiments (Figures 2 and 3); and weak to moderate agreement was observed among the clustering structures formed by the Farthest Neighbor and Ward methods based on data from individual experiments (Table 2).

These findings highlight the need to conduct a greater number of experiments to achieve more consistent clustering patterns and, consequently, more accurate estimates of genetic dissimilarity of the evaluated germplasm. However, the

recommendation to use data from six experiments to identify divergent common bean cultivars using Ward's method, as proposed by Cargnelutti Filho, Ribeiro and Jost (2009), limits the practical application of cluster analysis for defining parents to be included in crossing blocks aimed at expanding genetic variability in the breeding program. In the present study, the Farthest Neighbor and Ward methods differentiated common bean genotypes into two groups with identical composition when cluster analysis was undertaken using mean data from four experiments (Figures 2 and 3). One group comprised line CNFP 17973 and cultivars IPR Uirapuru, BRS Esteio, and IPR Urutau, which were highlighted for their higher grain yield (Table 3). The other group included the remaining genotypes evaluated. Line CNFP 18552 (Group 1) stood out for having the highest number of traits related to upright plant architecture. Cultivar IPR Urutau (Group 2) remarkably displayed the largest number of traits associated with high grain yield (number of nodes, mass of 100 grains, and grain yield).

Table 3. Means for the traits lodging (LDG), general adaptation score (GAS), first pod insertion height (FPIH, cm), plant height (PH, cm), stem diameter (SD, mm), number of nodes (NN), mass of 100 grains (M100G, g), and grain yield (GY, kg ha⁻¹) of each genotype allocated to the two groups formed by the Farthest Neighbor and Ward methods based on mean data from four experiments.

Genotype	LDG	GAS	FPIH	PH	SD	NN	M100G	GY
Group 1								
CNFP 17978	5.33 b*	5.17 b	22.78 a	75.31 a	7.58 b	13.88 a	23.13 c	1060.35 c
CNFP 17979	6.08 a	5.58 b	22.28 a	75.07 a	7.90 a	13.43 a	24.29 b	1089.31 c
CNFP 17984	5.25 b	4.50 b	19.15 b	73.76 a	7.66 a	13.54 a	23.02 c	1219.11 b
CNFP 18552	5.00 b	5.50 b	21.70 a	78.32 a	7.90 a	12.57 b	22.12 d	993.00 c
BRS FP403	5.42 b	5.42 b	16.76 b	64.42 c	7.26 b	13.31 a	24.38 b	937.95 c
BRS FP417	4.83 b	4.75 b	19.07 b	68.04 b	7.20 b	13.57 a	22.80 c	906.42 c
CNFP 17968	6.58 a	6.50 a	15.82 b	57.42 d	7.98 a	14.12 a	21.94 d	825.85 c
Group mean	5.50	5.35	19.65	70.33	7.64	13.49	23.10	1004.57
Group 2								
CNFP 17973	5.25 b	5.25 b	18.47 b	59.63 d	7.67 a	13.00 b	22.02 d	1354.51 b
IPR Uirapuru	5.42 b	5.17 b	17.75 b	65.30 c	7.36 b	13.66 a	23.48 c	1400.65 b
BRS Esteio	5.58 b	4.83 b	17.61 b	70.58 b	6.80 b	12.14 b	23.25 c	1573.91 a
IPR Urutau	6.17 a	4.92 b	16.97 b	57.41 d	7.28 b	13.83 a	26.26 a	1572.24 a
Group mean	5.60	5.04	17.70	63.23	7.28	13.16	23.75	1475.33

*Means followed by the same letter in the column do not differ by the Scott-Knott test at 5% probability.

Common bean genotypes were grouped with 100% agreement (adjusted Rand index = 1.00) based on agronomic traits evaluated across four experiments using the Farthest Neighbor and Ward methods (FN7 *versus* W7) (Table 2). Both clustering analyses showed 100% agreement in stratifying black common bean genotypes based on agronomic traits when mean data from the four experiments were used (Figures 2 and 3). Therefore, mean data from four experiments allow for a more accurate identification of common bean parents with multiple favorable plant architecture and yield traits to be combined in the breeding program. Under the conditions evaluated in the current study, the cross between line CNFP 18552, characterized by upright plant architecture, and cultivar IPR Urutau, which stood out

for its higher grain yield and mass of 100 grains, is promising for the breeding program.

CONCLUSIONS

The number and composition of groups formed using the Farthest Neighbor and Ward methods for agronomic traits in common bean genotypes vary according to the number of experiments considered. When mean data from four experiments are used, there is 100% agreement between the Farthest Neighbor and Ward methods in the stratification of common bean genotypes into groups. The cross between line CNFP 18552 and cultivar IPR Urutau is promising for

obtaining recombinants with upright plant architecture and high grain yield.

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