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Combining ability of black common bean developed under a biological nitrogen fixation system

Abstract – The objective of this work was to select parents and segregating populations of black common bean developed under a biological nitrogen fixation system. Twenty-eight segregating populations were obtained from complete diallel crosses among eight parents with black grains, a high yield, and a high potential for biological fixation. The segregating populations were evaluated for grain yield and 100-grain weight in four environments, where the main source of nitrogen was rhizobial inoculation. The diallel analysis indicated a predominance of additive effects for 100-grain weight and of nonadditive effects for grain yield. Parents 'BRS FP403', CNFP 15188, and 'BRS Esteio' showed the highest general combining ability estimates for 100-grain weight, whereas parents 'BRS Esplendor' and CNFP 15310 were the most suitable for forming populations with a higher yield in biological fixation systems. The 'BRS FP403'/'BRS Esplendor' and 'BRS FP403'/CNFP 15310 populations combined good mean estimates and specific combining ability for both evaluated traits, which makes them promising for the extraction of superior lines for cultivation in production systems without chemical nitrogen fertilization and with nitrogen supply predominantly through biological fixation.

Index terms: *Phaseolus vulgaris*, *Rhizobium*, rhizobia, segregating populations, symbiotic nitrogen fixation.

Capacidade de combinação de feijão-comum preto desenvolvido em sistema de fixação biológica de nitrogênio

Resumo – O objetivo deste trabalho foi selecionar genitores e populações segregantes de feijão-comum preto desenvolvidos sob sistema de fixação biológica de nitrogênio. Foram obtidas 28 populações segregantes a partir de cruzamentos, em esquema dialélico completo, entre oito genitores com grãos pretos, alta produtividade e elevado potencial para fixação biológica. As populações segregantes foram avaliadas quanto à produtividade e à massa de 100 grãos em quatro ambientes, cuja principal fonte de nitrogênio foi a inoculação com rizóbio. A análise dialélica indicou predominância de efeitos aditivos para massa de 100 grãos e de efeitos não aditivos para produtividade de grãos. Os genitores 'BRS FP403', CNFP 15188 e 'BRS Esteio' apresentaram as maiores estimativas de capacidade geral de combinação para massa de 100 grãos, enquanto os genitores 'BRS Esplendor' e CNFP 15310 foram os mais indicados para formar populações com maior produtividade, em sistemas de fixação biológica. As populações 'BRS FP403'/'BRS Esplendor' e 'BRS FP403'/CNFP 15310 aliaram boas estimativas de médias e capacidade específica de combinação para os dois caracteres avaliados, sendo promissoras para extração de linhagens superiores para cultivo em sistemas de produção sem adubação química com nitrogênio e com fornecimento de nitrogênio predominantemente por fixação biológica.

Termos para indexação: *Phaseolus vulgaris*, *Rhizobium*, rizóbio, populações segregantes, fixação simbiótica de nitrogênio.

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Introduction

Common bean (*Phaseolus vulgaris* L.) is one of the most important legumes in human nutrition, covering large growing areas in the tropics of Latin America and in Eastern and Southern Africa (Barbosa et al., 2018). In Brazil, however, this crop's grain yield is only 1,571 kg ha^{-1} (Embrapa Arroz e Feijão, 2024), contrasting with the production potential of improved cultivars of more than 5,000 kg ha^{-1} (Souza et al., 2019).

A major limiting factor for the grain yield of common bean is nitrogen deficiency, which leads large producers to apply high rates of up to 180 kg ha^{-1} nitrogen fertilizers (Soratto et al., 2017). However, less than 50% of the applied nitrogen is effectively used by the plants, with the majority being lost through leaching, volatilization, and denitrification, resulting in significant economic losses and environmental impacts for producers (Farid et al., 2017).

From both environmental and economic perspectives, an attractive strategy for replacing mineral nitrogen fertilizers partially or completely is the use of biological nitrogen fixation (BNF). In this process, plants form a symbiotic association (BNF system) with soil bacteria of the genus *Rhizobium*, known as rhizobia, which convert atmospheric nitrogen into ammonia, a form that plants can assimilate (Kamfwa et al., 2019). However, the efficiency of this symbiosis varies, and common bean is often characterized as a poor nitrogen fixer (Kamfwa et al., 2019; Reinprecht et al., 2020). Part of these results is attributed to the insufficient efforts of some breeding programs to increase the BNF of this crop (Kamfwa et al., 2019).

Over the course of different programs, the symbiotic fixation ability of legume species is reduced due to line selection in soils with high levels of mineral nitrogen (Reinprecht et al., 2020; Sousa et al., 2022). McKenzie et al. (2001) explained that this reduction occurs because BNF is a process that requires energy from plants, and less energy expenditure is necessary to absorb mineral nitrogen.

In the literature, cultivars and elite lines of common bean have been phenotyped in contrasting environments to test their performance under conditions of mineral nitrogen fertilization and BNF (Pereira et al., 2015; Dias et al., 2020, 2024; Reinprecht et al., 2020). The identification of lines responsive to BNF would allow their direct use by farmers and facilitate the incorporation of this trait through crossing, particularly since these genotypes present favorable alleles for agronomic traits of interest (Pereira et al., 2015). However, up to this moment, the grain yield averages of these genotypes have been lower in BNF systems than in those with mineral nitrogen fertilization (Pereira et al., 2015; Dias et al., 2020, 2024; Reinprecht et al., 2020). This occurs because, in natural selection, lines with higher yields are obtained under the conditions in which they were developed; in this case, under mineral N fertilization (Pereira et al., 2015).

An alternative to favor the expression of BNF is developing and conducting populations from the first segregating generations onwards under BNF conditions, i.e., without nitrogen fertilization (Pereira et al., 2015; Dias et al., 2024). For the efficient selection of segregating populations, diallel crosses are particularly useful as they allow of favorable alleles from different parents to recombine, increasing the likelihood of the occurrence of superior genotypes (Ferreira et al., 2018). However, recent studies aimed at the selection of segregating parents and populations in BNF-dependent systems are still not available in the literature, especially under field conditions and considering environmental effects. This is important since the development and selection of genotypes in BNF systems can increase the likelihood of obtaining more productive lines under these conditions.

The objective of this work was to select parents and segregating populations of black common bean developed under a BNF system.

Materials and Methods

The following eight black common bean genotypes were chosen as parents for full diallel crosses due to their high grain yields under BNF systems, disease resistance, and high number and dry mass of nodules: elite lines CNFP 10807, CNFP 15171, CNFP 15188, CNFP 15295, and CNFP 15310; and cultivars BRS Esteio, BRS Esplendor, and BRS FP403. These parents were previously selected by Dias et al. (2020) in experiments performed in multiple environments under BNF systems. In the present study, the crosses between the eight parents were carried out in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil (-16°30'S, 49°16'W), where 28 populations were obtained, being advanced until generation F_2 in a greenhouse.

The obtained populations were evaluated in four experiments: three in Santo Antônio de Goiás (experiments I to III) and one (experiment IV) in Brasília, in the Federal District, Brazil (-15°54'S, -48°02'W). Experiments I, II, and III were conducted using generations F_2, F_3, and F_4, sown in the winter crop season in May 2015, 2016, and 2017, respectively; and experiment IV was carried out with generation F_4 during the rainy crop season in December 2017. The climate of the study regions is classified as Aw, corresponding to a tropical savanna, according to Köppen’s classification. The predominant soil type is a Typic Haplustox, with a clayey texture and a flat relief (Santos et al., 2018).

The experimental areas are exclusively used for research and are characterized by an intensive soil use and by a low-to-medium organic matter content (Table 1). All soil management was done according to soil analyses. The study areas were only fertilized with P_2O_5 and K_2O during planting and did not receive any mineral nitrogen. The naturally low nitrogen levels in the soil, the absence of mineral nitrogen fertilization, and the inoculation with rhizobia are factors that should ensure that BNF is the main source of the nutrient to the plants, although potential contributions from residual soil sources cannot be excluded.

The seeds from generations F_3 and F_4 were obtained by sampling generations F_2 and F_3, respectively, harvested in bulk from experiments I and II. Four controls were included in all four experiments, i.e., cultivars BRS Esplendor, BRS Esteio, BRS FP403, and IPR Uirapuru. All treatments, in all experiments, were evaluated in a randomized complete block design with four replicates, in plots containing two 4.0 m rows, spaced at 0.5 m from each other.

Seed inoculation was performed at the Soil Biology Laboratory of Embrapa Arroz e Feijão using a peat-based inoculant, consisting of a 1:1:1 mixture of strains SEMIA 4077 and SEMIA 4088 of *Rhizobium tropici* and SEMIA 4080 of *Rhizobium freirei*, registered at Ministério da Agricultura e Pecuária (MAPA) for common bean (Dias et al., 2020). The inoculant had a density of 10^9 cells per gram of peat and was applied at a proportion of 500 g product per 50 kg seeds. A solution of 10% saccharose was poured over the seeds to improve the adhesion of the peat inoculant, followed by stirring for a proper homogenization. Afterwards, the peat inoculant was applied to the seeds, which were stirred again for the product to be spread evenly over their surface. Finally, the seeds were dried in the shade and were sown in up to 24 hours for the bacteria not to lose their viability (Dias et al., 2020, 2024).

The genotypes were evaluated for two traits: yield and 100-grain mass. Yield-related traits are useful indicators of BNF capacity when plants are grown in environments with minimal or no nitrogen (Bliss, 1993). According to the same authors, since nitrogen is the macronutrient required in larger quantities by common bean, the more productive plants in soils with low natural levels of the nutrient, absence of mineral nitrogen fertilization, and with rhizobial inoculation will be those that better associate with bacteria. Grain yield, adjusted for 13% moisture, was measured in grams per plot by weighing the grains harvested from all plants in the two rows, being later converted into kg ha^{-1}. The 100-grain mass trait was obtained by collecting 100 random grains from each plot, which were later weighed to determine their mass in grams.

Individual and joint analyses of variance were carried out for each trait, considering the effects of the

Table 1. Chemical properties of the soil samples collected at a depth of 0–20 cm from the different study environments.

Chemical property(1)	Environment(2)			
	I	II	III	IV
pH (H_2O)	6.1	5.3	6.0	6.3
Ca (cmol$_c$ dm^{-3})	17.8	10.1	8.9	7.1
Mg (cmol$_c$ dm^{-3})	12.5	6.6	8.8	6.7
Al (cmol$_c$ dm^{-3})	0.0	1.0	0.0	0.0
H+Al (cmol$_c$ dm^{-3})	19.0	32.0	26.0	27.0
P (mg dm^{-3})	5.3	17.1	9.7	7.5
K (mg dm^{-3})	128.0	109.0	148.0	97.0
Cu (mg dm^{-3})	1.5	1.9	2.9	1.0
Zn (mg dm^{-3})	4.9	4.4	3.7	5.0
Fe (mg dm^{-3})	19.5	22.7	17.3	10.6
Mn (mg dm^{-3})	29.4	32.1	41.4	17.1
Organic matter (g kg^{-1})	23.6	24.7	23.0	25.1
SB (cmol$_c$ dm^{-3})	33.5	19.5	12.7	9.6
CEC (cmol$_c$ dm^{-3})	52.5	51.5	38.7	36.6
CECe (cmol$_c$ dm^{-3})	33.5	20.5	21.5	16.3
Aluminium saturation (%)	0.0	4.9	0.0	0.0
Base saturation (%)	63.8	37.8	32.8	26.3

(1)SB, sum of bases; CEC, cation exchange capacity; and CECe, effective cation exchange capacity. (2)I, F_2 generation in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil, during the 2015 winter crop season; II, F_3 generation in Santo Antônio de Goiás during the 2016 winter crop season; III, F_4 generation in Santo Antônio de Goiás during the 2017 winter crop season; and IV, F_4 generation in Brasília, in the Federal District, Brazil, during the 2017 rainfall crop season.

genotypes and environments as fixed. The joint analyses were performed after verifying the homogeneity of residual variances by Hartley's test (Cruz et al., 2012). Experimental precision was estimated based on the coefficient of experimental variation and on selective accuracy (Resende & Duarte, 2007). Means were compared by the Scott-Knott clustering analysis test ($p \leq 0.05$).

Individual and joint diallel analyses were conducted according to method IV of Griffing (1956). The general combining ability (GCA); and specific combining ability (SCA) and the sum of squares for the analysis of variance were estimated based on the least squares method. The quadratic components associated with the GCA and the SCA were estimated using the method of moments based on mean square expectations. All statistical analyses were performed with the GENES software (Cruz, 2013).

Results and Discussion

The estimates obtained for the coefficient of variation ranged from 3.6 to 8.4% for 100-grain mass and from 15.7 to 24.9% for grain yield in the individual analyses, indicating an adequate experimental precision for the evaluated traits. This satisfactory precision was confirmed by the selective accuracy estimates, which were high (0.70 < selective accuracy < 0.90) or very high (selective accuracy ≥ 0.90), showing the good informativity of the experiments for the selection of superior genotypes (Resende & Duarte, 2007).

The joint analysis revealed significant differences between populations regarding the two evaluated traits (Table 2), indicating that the selection of parents with favorable alleles for agronomic traits and BNF generated genetic variability among the studied populations. However, the contrast of the controls versus populations was not significant for both traits, which shows that the experimental populations achieved the agronomic standards required for commercial use, highlighting the good performance of these genotypes developed for BNF systems.

The joint diallel analysis revealed statistical differences between populations for the GCA and SCA of the two analyzed traits (Table 2). These results are

Table 2. Mean squares of joint diallel analyses for 100-seed weight (100SW) and grain yield of 28 populations and four checks of black common bean (*Phaseolus vulgaris*) evaluated in environments where the main nitrogen source was biological fixation.

Source of variation(1)	DF	100SW (g)		Grain yield (kg ha^{-1})	
		Mean squares	R^2 (%)(3)	Mean squares	R^2 (%)
Genotypes (G)	31	26.8**	20.8	446,362**	3.6
Checks (C)	3	89.8**	6.8	137,520	0.1
Populations (P)	27	20.7**	14.0	494,592**	3.5
General combining ability (GCA)	7	65.9**	11.6	770,748**	1.4
Specific combining ability (SCA)	20	4.9**	2.5	397,937**	2.1
C x P	1	0.1	0.0	70,672	0.0
Environments (E)	3	401.1**	30.2	88,314,943**	69.5
Genotypes x E	93	2.1**	4.9	281,358**	6.9
Checks x E	9	3.4*	0.8	290,254*	0.7
Populations x E	81	2.0*	4.1	285,632**	6.1
GCA x E	21	3.1**	1.6	441,054**	2.4
SCA x E	60	1.7	2.5	231,234*	3.6
(C x P) x E	3	0.9	0.1	139,254	0.1
Residue	372	1.4	-	151,089	-
$\hat{\varphi}$GCA (1)	-	0.6	-	1,733	-
$\hat{\varphi}$SCA (2)	-	0.1	-	12,901	-
Mean of the populations	-	22.7	-	2,203	-
Mean of the checks	-	22.6	-	2,239	-
Coefficient of variation (%)		5.3	-	17.6	-
Selective accuracy		0.97	-	0.81	-

(1)Quadratic component associated with the GCA. (2)Quadratic component associated with the SCA. The evaluated populations resulted from crosses between eight parents that were advanced until generation F_2. Checks were cultivars BRS Esteio, BRS Esplendor, and BRS FP403. **and *Significant at 5 and 1% probability, respectively, by the F-test.

an indicative that there are differences in the frequency of favorable alleles between parents and populations, as well as that nonadditive genetic effects may have altered the expression of traits in the genotypes evaluated in environments where the main nitrogen source was BNF.

For grain yield, the estimate of the quadratic component associated with the effects of the SCA ($\hat{\varphi}\mathrm{SCA}$) was higher than that of the quadratic component associated with the effects of the GCA ($\hat{\varphi}\mathrm{GCA}$) (Table 2). The predominance of nonadditive effects in the genetic control of grain yield suggests that the resulting hybrids can surpass the yield of the parent, indicating that line selection should start in advanced endogamic generations. It should be noted that the lower proportion of additive effects for yield, however, is not common for common bean, as observed in studies with nitrogen mineral fertilization (Moura et al., 2018; Torres et al., 2021). Cruz et al. (2012) added that, since the parents used are cultivars or lines previously selected for high yield, there is less variability among them, which may have contributed to the lower proportion of additive effects.

For 100-grain mass, the $\hat{\varphi}\mathrm{GCA}$ was higher than the one associated with the $\hat{\varphi}\mathrm{SCA}$, indicating that, although nonadditive genetic effects act in the expression of this trait, there was a predominance of additive genetic effects (Table 2). Similar results were reported for the grain mass of common bean by Torres et al. (2021). This predominance of additive effects suggests the possibility of selecting promising progenies with larger grain sizes in the first segregating generations, i.e., in F_2, F_3, and F_4 (Cruz et al., 2012).

The effect of the environments was also significant for both studied traits, with a percentage of contribution to total variation amounting to 69.5% for grain yield and to 30.2% for 100-grain mass (Table 2). BNF can be a contributing factor for variations between environmental means since nodulated plants are more sensitive to abiotic stresses (Shamseldin & Velázquez, 2020). In tropical regions, seasonal climatic fluctuation, high temperatures, low moisture, and soil acidity are the main triggers of nodulation flaws, affecting symbiotic relationship, plant development, and rhizobia survival in the soil (Hungria & Vargas, 2000).

In the joint analyses, the effects of generations, years, crop seasons, and locations were confounded in the source of variation environments and may have affected trait expression. For common bean, this confounding is common in combined diallel analyses, mainly because the experiments are conducted with different segregating generations in several locations and in up to three crops per year (Ferreira et al., 2018; Moura et al., 2018; Torres et al., 2021).

The effects of the interactions between genotypes and environments were significant for both traits (Table 2), i.e., the yield of the populations and controls varied depending on the environment where they were grown. Other authors reported a differential behavior of genotypes grown in different environments when using rhizobial inoculation (Pereira et al., 2015; Farid et al., 2017; Dias et al., 2020, 2024). This differential response highlights the importance of understanding the interactions between genotypes and environments to improve rhizobial inoculation strategies and enhance crop performance.

Regarding combining abilities, for grain yield, the interactions with the environments were significant for the GCA and SCA (Table 2), suggesting the need to explore parents and populations specific to each environment considering their particular behavior under specific environmental variations. For 100-grain mass, the only significant effect was due to the GCA x environments interaction. The absence of interaction of the SCA estimates with the environments suggests that nonadditive effects were more stable than the additive ones in the studied environments (Moura et al., 2018).

The 'BRS Esplendor' parent obtained significant and positive GCA estimates in most environments and in the joint analysis for grain yield, showing significantly superior results to those of parent CNFP 15310, which also stood out in this analysis (Table 3). These findings indicate that both of these lines contain alleles that contribute to increase grain yield in environments with BNF in the crosses they participate in. For 100-grain mass, parents 'BRS FP403', CNFP 15188, and 'BRS Esteio' showed positive GCA estimates in the four environments and in the joint analysis, with 'BRS FP403' being superior to the others. Torres et al. (2021), in a study evaluating mineral nitrogen, found similar results for the latter cultivar, concluding that it has a high frequency of favorable alleles for increasing 100-grain mass.

The means for 100-grain mass ranged from 20.8 to 24.8 g for the populations and from 20.1 to 25.7 g for the controls (Table 4), which are values similar to those reported by Dias et al. (2020) for black common bean evaluated under rhizobial inoculation. Among the studied genotypes, the highest mean was observed for parent 'BRS FP403' and the lowest one for 'BRS Esplendor'. The increase in 100-grain mass is essential for increasing the market value of common bean due to the requirements of the Brazilian market for larger grains, especially weighing more than 22 g in the case of black common bean (Faria et al., 2013).

The grain yield means ranged from 1,900 kg ha^{-1} for population CNFP 10807/CNFP 15295 to 2,581 kg ha^{-1} for population 'BRS Esplendor'/CNFP 15188 (Table 4). Two groups of means were formed: one with 11 populations and the 'BRS FP403', 'BRS Esplendor', and 'IPR Uirapuru' controls; and the other with 17 populations and the 'BRS Esteio' control. These means were similar to those reported by other authors when evaluating common bean under rhizobial inoculation (Pereira et al., 2015; Dias et al., 2020, 2024) and nitrogen fertilization (Torres et al., 2021; Carloni et al., 2022). The obtained results show the potential of populations developed exclusively in BNF systems.

In studies carried out to test the performance of elite common bean genotypes under different nitrogen sources, no lines with a higher grain yield were identified under BNF when compared with mineral fertilization (Farid & Navabi, 2015; Pereira et al., 2015; Dias et al., 2020, 2024; Reinprecht et al., 2020). In those studies, the genotypes inoculated with rhizobia showed an inferior performance to those fertilized with mineral nitrogen. This could be partially explained by the fact that, in breeding programs, these genotypes were selected in soils fertilized with high contents of nitrogen fertilizers (Pereira et al., 2015). In the literature, a negative correlation between BNF and the nitrogen content available in the soil has been consistently reported (Tamagno et al., 2018; Reinprecht et al., 2020; Sousa et al., 2022).

An alternative to develop highly-productive cultivars under biological fixation may be developing populations based on parents with favorable alleles for agronomic traits related to BNF and conducting them in soils whose main nitrogen source corresponds to BNF. In early stages of the breeding program, due to the high volume of genotypes to be evaluated, the focus should be on yield-related traits since BNF can be significantly associated with grain yield in legume crops (Farid & Navabi, 2015; Heilig et al., 2017; Barbosa et al., 2018). In later stages, traits directly related to BNF should be evaluated, including nodule number and activity (Dias et al., 2020), atmospheric nitrogen content, and plant dry mass (Jiang et al., 2020).

Specific combining ability (SCA) was estimated for the F_2 generation, with 50% of the loci in heterozygosis. In autogamous plants, such as common bean, manual

Table 3. Estimates of the general combining ability effects ($\hat{g}_i$) of eight black common bean (*Phaseolus vulgaris*) parents evaluated in four experiments (I, II, III, and IV) in environments where the main nitrogen source was biological fixation, as well as the joint analysis for 100-seed weight (100SW) and grain yield.

Parent	100SW (g)					Grain yield (kg ha^{-1})				
	I(1)	II(2)	III(3)	IV(4)	Joint	I(1)	II(2)	III(3)	IV(4)	Joint
CNFP 10807	0.15	-0.31	0.08	0.17	0.02	163.89*	-118.04*	70.69	-103.53*	3.25
'BRS Esteio'	0.44*	0.15	0.96*	0.56*	0.53*	14.34	-90.79*	-127.31*	-20.66	-56.10*
'BRS FP403'	1.28*	1.78*	1.49*	1.05*	1.40*	-24.95	24.71	24.98	-277.66*	-63.23*
'BRS Esplendor'	-1.19*	-0.53*	-1.64*	-0.74*	-1.03*	58.93	194.88*	165.23*	357.05*	194.02*
CNFP 15171	-0.90*	-1.11*	-0.73*	-0.42*	-0.79*	-283.87*	116.92*	-122.19*	238.26*	-12.72
CNFP 15188	0.88*	0.93*	0.22*	0.69*	0.68*	6.59	-87.83*	-138.56*	-94.28	-78.52*
CNFP 15310	-0.56*	-0.61*	-0.14	-1.20*	-0.63*	99.18*	-40.38	113.15*	54.34	56.57*
CNFP 15295	-0.10	-0.31	-0.25*	-0.12	-0.19*	-34.12	0.54	14.02	-153.53*	-43.27*
$\hat{\sigma}_{\hat{g}i}$ (5)	0.22	0.32	0.16	0.18	0.11	60.83	56.20	79.25	94.31	37.11
$\hat{\sigma}_{(\hat{g}_i-\hat{g}_{i'})}$ (6)	0.33	0.49	0.25	0.26	0.17	91.97	84.96	119.81	142.59	56.08

(1) F_2 generation in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil, during the 2015 winter crop season. (2) F_3 generation in Santo Antônio de Goiás during the 2016 winter crop season. (3) F_4 generation in Santo Antônio de Goiás during the 2017 winter crop season. (4) F_4 generation in Brasília, in the Federal District, Brazil, during the 2017 rainfall crop season. (5) Standard deviation associated with the GCA effect of the parent ($\hat{g}_i$). (6) Standard deviation associated with the contrast between the parents.

pollination limits F_1 seed production, explaining why diallel analyses using the F_2 generation are common (Moura et al., 2018). Of the studied populations, six showed positive and significant estimates of SCA for productivity (Table 4). For the breeder, it is important to ally significant and high-magnitude SCA estimates ($\hat{s}_{ii'}$) to high means, involving at least one parent with favorable GCA estimates (Cruz et al., 2012). Populations 'BRS Esplendor'/CNFP 15188, 'BRS FP403'/CNFP 15310, and 'BRS Esteio'/'BRS Esplendor' managed to combine good $\hat{s}_{ii'}$ estimates, high means in most environments and in the joint analysis, and at

Table 4. Estimates of the mean and specific combining ability ($\hat{s}_{ii'}$) for 100-seed weight (100SW) and grain yield of 28 populations and four checks of black common bean (*Phaseolus vulgaris*) evaluated in environments where the main nitrogen source was biological fixation(1).

Genotype	100SW (g)		Grain yield (kg ha^{-1})	
	Mean	$\hat{s}_{ii'}$ (2)	Mean	$\hat{s}_{ii'}$ (2)
'BRS Esplendor'/CNFP 15188	22.3d	0.73*	2,581a	384.88*
'BRS FP403'/'BRS Esplendor'	23.6c	1.15*	2,468a	50.67
'BRS Esplendor'/CNFP 15295	21.5e	-0.22	2,406a	-53.91
CNFP 10807/CNFP 15310	22.1d	0.14	2,397a	60.09
'BRS Esplendor'/CNFP 15171	20.8e	-0.42	2,369a	26.84
CNFP 15171/CNFP 15295	21.7d	0.24	2,367a	43.13
'BRS FP403'/CNFP 15310	24.3b	1.27*	2,366a	305.17*
CNFP 15171/CNFP 15310	21.4e	-0.31	2,348a	-31.41
'BRS Esteio'/'BRS Esplendor'	21.4e	-0.51*	2,344a	137.63*
'BRS FP403'	25.7a	-	2,321a	-
CNFP 10807/CNFP15171	21.8d	-0.01	2,315a	-245.91*
'BRS Esplendor'	20.1f	-	2,270a	-
'IPR Uirapuru'	21.7d	-	2,258a	-
CNFP 10807/'BRS Esteio'	22.9c	-0.61*	2,252a	-110.58
CNFP 10807/'BRS Esplendor'	21.8d	-0.22	2,211b	-245.91*
'BRS Esplendor'/CNFP 15310	21.1e	-0.51*	2,209b	-300.20*
CNFP 15310/CNFP 15295	21.7d	-0.36	2,189b	290.34*
CNFP 10807/'BRS FP403'	24.5b	0.06	2,186b	50.46
'BRS Esteio'/CNFP 15310	22.0d	-0.15	2,186b	-133.37
CNFP 10807/CNFP 15188	23.7c	1.21*	2,181b	102.17
'BRS Esteio'/CNFP 15188	23.9c	-0.84*	2,153b	148.46*
'BRS Esteio'/CNFP 15295	24.2b	0.89*	2,150b	-161.33*
'BRS FP403'/CNFP 15295	23.4c	0.06	2,120b	-20.29
'BRS Esteio'	23.0c	-	2,106b	-
CNFP 15188/CNFP 15310	22.4d	-0.09	2,068b	-190.62*
CNFP 15188/CNFP 15295	23.1c	0.24	2,032b	75.42
'BRS Esteio'/'BRS FP403'	24.9b	0.02	2,001b	-179.24*
'BRS Esteio'/CNFP 15171	22.6d	1.20*	2,000b	298.42*
CNFP 15171/CNFP 15188	23.3c	0.44	1,992b	-483.83*
'BRS FP403'/CNFP 15171	22.3d	-1.14*	1,957b	-170.29*
'BRS FP403'/CNFP 15188	24.2b	-1.42*	1,946b	-36.49
CNFP 10807/CNFP 15295	22.0d	-0.57*	1,900b	-173.37*
$\hat{\sigma}(\hat{s}_{ii'})$ (3)	-	0.48	-	134.63
$\hat{\sigma}(\hat{s}_{ii'} - \hat{s}_{ik})$ (4)	-	0.74	-	205.65
$\hat{\sigma}(\hat{s}_{ii'} - \hat{s}_{kl})$ (5)	-	0.66	-	183.94

(1)Mean values followed by equal letters do not differ statistically from each other by the Scott-Knott test, at 5% probability. Mean estimates were obtained from the joint analysis. (2)Estimates obtained for the F_2 generation. (3)Standard deviation associated with the effect of $\hat{s}_{ii'}$ of the segregating population. (4 and 5)Standard deviation associated with the contrast between segregating populations.

least one parent with a favorable estimate for the GCA effects ($\hat{g}_i$).

The 'BRS Esteio'/CNFP 15295, 'BRS FP403'/CNFP 15310, 'BRS FP403'/'BRS Esplendor', and CNFP 10807/CNFP 15188 populations stood out for presenting positive and significant $\hat{s}_{ii'}$ estimates for 100-grain mass. In addition to favorable $\hat{s}_{ii'}$, the cited genotypes also showed good means and at least one parent with positive and significant estimates for $\hat{g}_i$.

The best populations were selected by giving a greater weight to the $\hat{g}_i$ estimates and means, as the estimates for $\hat{s}_{ii'}$ were obtained based on evaluations in only one environment. Populations 'BRS Esplendor'/CNFP 15188, 'BRS FP403'/'BRS Esplendor', CNFP 10807/CNFP 15310, and 'BRS FP403'/CNFP 15310 showed good averages for both traits, with at least one of the parents with good $\hat{g}_i$ estimates for both or just one of the traits. Therefore, the genotypes originating from these populations are promising for the improvement of superior lines in terms of yield and grain mass in BNF environments.

Conclusions

1. In black common bean (*Phaseolus vulgaris*) cultivation systems with biological nitrogen fixation and without nitrogen fertilization, parents 'BRS FP403', CNFP 15188, and 'BRS Esteio' are indicated to form populations with a greater 100-grain mass, whereas parents 'BRS Esplendor' and CNFP 15310 are indicated to form populations with a higher grain yield.

2. Populations 'BRS Esplendor'/CNFP 15188, 'BRS FP403'/'BRS Esplendor', CNFP 10807/CNFP 15310, and 'BRS FP403'/CNFP 15310 are the most promising for the extraction of black common bean lines that combine a high mass and grain yield in environments with biological nitrogen fixation.

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