Genetics/ Original Article

Combining ability for resistance to Fusarium wilt and yield in black bean

Abstract – The objective of this work was to investigate the genetic control of black bean (*Phaseolus vulgaris*) and to select parents and segregating populations with high resistance to Fusarium wilt, high yield, and greater 100-seed weight (100SW), using a partial diallel cross. Twenty-five populations were obtained from two groups of parents – the first with five parents resistant to and the second with five parents susceptible to Fusarium wilt. The segregating populations were evaluated in experiments in three years/generations for reaction to Fusarium wilt, yield, and 100SW in an area naturally infested with the pathogen. The diallel analysis showed additive and nonadditive effects in control of the three studied traits, with predominance of additive effects. CNFP 15194, CNFP 15207, and 'BRS Esplendor' are the genotypes with high and negative general combining ability estimates ($\hat{g}_i$ = -0.59, -0.76, and -0.13, respectively), being recommended for use as parents for resistance to Fusarium wilt. Among them, CNFP 15194 also forms populations with a greater 100SW ($\hat{g}_i$ = 0.69). The BRS FP403 cultivar is recommended as a parent to increase yield ($\hat{g}_i$ = 218) and 100SW ($\hat{g}_i$ = 1.46). Six populations were selected to obtain black bean lines that combine resistance to Fusarium wilt, high yield, and high 100SW.

Index terms: *Fusarium oxysporum* f. sp. *phaseoli*, *Phaseolus vulgaris*, diallel crosses, genetic control, plant breeding.

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Capacidade combinatória para resistência à murcha-de-fusário e produtividade em feijão-preto

Resumo – O objetivo deste trabalho foi investigar o controle genético de feijão-preto (*Phaseolus vulgaris*) e selecionar genitores e populações segregantes com alta resistência à murcha-de-fusário, alta produtividade e maior massa de 100 grãos (M100), com uso de um dialelo parcial. Foram obtidas 25 populações de dois grupos de genitores – o primeiro com cinco genitores resistentes e o segundo com cinco genitores suscetíveis à murcha-de-fusário. As populações segregantes foram avaliadas em experimentos, em três anos/gerações, quanto a reação à murcha-de-fusário, produtividade e M100, em uma área naturalmente infestada com o patógeno. A análise dialélica mostrou efeitos aditivos e não aditivos no controle das três características estudadas, com predominância dos efeitos aditivos. CNFP 15194, CNFP 15207 e 'BRS Esplendor' são os genótipos com estimativas de capacidade geral de combinação alta e negativa ($\hat{g}_i$ = -0,59, -0,76 e -0,13, respectivamente), sendo recomendados para uso como genitores para resistência à murcha-de-fusário. Entre eles, CNFP 15194 também forma populações com maior M100 ($\hat{g}_i$ = 0,69). Já a cultivar BRS FP403 é recomendada como genitor para aumentar a produtividade ($\hat{g}_i$ = 218) e a M100 ($\hat{g}_i$ = 1,46). Seis populações foram selecionadas para obter linhagens de feijão-preto que combinam resistência à murcha-de-fusário, alta produtividade e maior M100.

Termos para indexação: *Fusarium oxysporum* f. sp. *phaseoli*, *Phaseolus vulgaris*, cruzamento dialélico, controle genético, melhoramento vegetal.

Introduction

Black bean (*Phaseolus vulgaris* L.) is the second most produced commercial bean class in Brazil, representing 20% of the country's common bean production, which, in 2020, was approximately 2.5 million metric tons of grain (Acompanhamento…, 2021). Unlike the carioca class, which is the most widely grown in Brazil but has a low demand in the international market (Carbonell et al., 2019), black bean is not only consumed within the country but also has export potential, since it is valued by international cuisine. However, Brazil does not yet produce a sufficient amount of black bean to supply the domestic market, importing approximately 120 thousand tons in 2020 (Acompanhamento…, 2021).

Among the factors that lead to a low domestic production of black bean is the occurrence of diseases in the main black bean-production regions, located in the South and Southeast of Brazil. These diseases are intensified by planting the same crop in succession and by milder temperatures (Pereira et al., 2018). One of these diseases is Fusarium wilt, caused by the soil fungus *Fusarium oxysporum* f. sp. *phaseoli*, which may result in losses of up to 100% when susceptible cultivars are used and when environmental conditions are favorable to the occurrence of the disease (Toledo-Souza et al., 2012; Pereira et al., 2019a; Sasseron et al., 2020).

The use of cultivars with genetic resistance in integrated management systems has proven to be the most effective and economical way to control Fusarium wilt, with the lowest negative impact on humans and the environment (Pereira et al., 2019a). However, although wide genetic variability has been reported in the literature (Pereira et al., 2009; Batista et al., 2016, 2017; Negreiros et al., 2020; Pereira et al., 2020), there are still few resistant black bean cultivars currently on the market (Pereira et al., 2016, 2018).

A way of obtaining segregating populations and selecting the best ones for obtaining lines in the future is the use of diallel crosses. Partial diallel crosses allow: estimating the effects of the general combining ability (GCA) of the parents, which reflect the additive genetic effects and the frequency of favorable alleles; estimating the effects of the specific combining ability (SCA) of the populations, which provide information regarding nonadditive effects and the genetic divergence between the parents; and joining

of favorable phenotypes that are found in different groups of parents (Vale et al., 2015; Moura et al., 2018).

However, only a few studies have used diallel crosses to investigate reactions to Fusarium wilt. Pereira et al. (2009) and Batista et al. (2016) evaluated the result of the artificial inoculation of the pathogen under controlled conditions in a partial diallel cross, whereas Pereira et al. (2019a) assessed a complete diallel under conditions of natural infestation of the pathogen in the field. The authors concluded that the additive and dominant genetic effects are important in the reaction to Fusarium wilt. Evaluations under natural infestation conditions and in various environments allow estimating the effect of the interaction between genotypes and environments, as well as selecting parents and populations that are genetically superior, in a more consistent way.

Besides having disease resistance, a new cultivar must also meet the needs of the market; currently, the main requirements are related to a high yield and a greater 100-seed weight (Pereira et al., 2019a).

The objective of this work was to investigate the genetic control of black bean and to select parents and segregating populations with high resistance to Fusarium wilt, high yield, and high 100-seed weight, using a partial diallel cross.

Materials and Methods

All experiments were conducted in the experimental field of Embrapa Arroz e Feijão, located in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil (16º30'17"S, 49º16'53"W, at 819 m altitude). The area where the experiments were set up has a high natural infestation of the pathogen and has been used in other studies for the evaluation of the reaction to Fusarium wilt (Pereira et al., 2016, 2018, 2019a, 2020). In all experiments, water was supplied by a center pivot irrigation system.

To obtain the F_1 seeds, ten cultivars/elite lines of black bean were crossed in a partial diallel arrangement in 2015. The parents were stratified into two groups according to reaction to Fusarium wilt (Pereira et al., 2016, 2019b). Group I consisted of five cultivars/ elite lines that have different levels of resistance to Fusarium wilt and different origins: BRS Campeiro, originated from a mutation of cultivar Corrente; BRS Esplendor, originated from the CB911863/AN9123293

cross; BRS FP403, originated from the POT51///ICA PIJAO/XAN170//BAC16/XAN91 cross; CNFP 15207, originated of the TB94-01/FPGCF058 cross; and CNFP 15194, originated from the TB94-01/98203893 cross. Group II was formed by five cultivars/elite lines that do not have resistance to Fusarium wilt but that have other desirable phenotypes: BRS Esteio, BRS Supremo, VP 22, CNFP 11976, and CNFP 11995.

The F_1 seeds were sown in pots in a greenhouse in 2015. In 2016, in the winter crop season (sowing in May), in the area naturally infested by the pathogen, the 25 F_2 populations obtained and three check cultivars (BRS FP403, BRS Esteio, and BRS Supremo) were evaluated. A randomized complete block experimental design was used, with four replicates and plots of two 4 m rows, with 12 plants sown per meter. In 2017, also in the winter crop season, the experiment was repeated in a similar manner with the F_3 populations; the used seeds were those harvested in the F_2 generation. This procedure was repeated in 2018, when the F_4 generation was evaluated.

Three traits were assessed: reaction to Fusarium wilt, yield, and 100-seed weight. The reaction to Fusarium wilt was evaluated using a scoring scale, ranging from 1 to 9, adapted from Pastor-Corrales & Abawi (1987), in which: 1 represents 0% of susceptible plants; 2, 0.1 to 5%; 3, 5.1 to 10%; 4, 10.1 to 20%; 5, 20.1 to 40%; 6, 40.1 to 60%; 7, 60.1 to 80%; 8, 80.1 to 90%; and 9, 90.1 to 100%. Yield was obtained from harvesting the whole plot and converting the results to kg ha^{-1}. Finally, 100-seed weight (g) was determined by weighing a random sample of 100 seeds from each plot.

Individual analyses of variance were performed on the data for each trait in each year/generation. After checking the homogeneity of the residual variances by the Hartley test (Ramalho et al., 2012), joint analyses involving the three years/generations were carried out considering the effects of genotypes and years/generations as fixed (Cruz, 2013). The mean values were clustered by the Scott-Knott procedure, at 10% probability. The experimental coefficient of variation (CV) and selective accuracy were also estimated.

Diallel analyses for each year/generation, as well as joint analyses, were performed using the IV model of Griffing. This model uses only the populations in which the effects of the GCA of the parents ($\hat{g}_i$ and $\hat{g}_j$) and the SCA of the populations ($\hat{s}_{ij}$) are estimated, as described by Cruz et al. (2012). The standard deviations of the estimates of $\hat{g}_i$ and $\hat{g}_j$ and $\hat{s}_{ij}$ were obtained by the square root of variances (Cruz et al., 2012). The coefficient of determination (R^2) was also estimated using the relative contribution of the sum of squares of the SCA and GCA in relation to the sum of squares of the populations. All statistical analyses were performed with the assistance of the GENES computer software (Cruz, 2013).

Results and Discussion

The estimates of the CV ranged from 20.8 to 29.0% (data not shown) for reaction to Fusarium wilt, considered acceptable due to the natural occurrence of the disease, the heterogeneous distribution of the fungus in the soil, and the low mean of the trait (Pereira et al., 2019a, 2020). The estimates of selective accuracy were considered very high, i.e., higher than 0.90 (data not shown), indicating good informativeness of the experiments for the selection of superior genotypes. The estimates of the CV ranged from 15.6 to 16.9% for grain yield and from 4.6 to 5.1% for 100-seed weight, also indicating a good experimental accuracy, confirmed by the estimates of selective accuracy, considered high (from 0.70 to 0.90) for grain yield and very high (greater than 0.90) for 100-seed weight (data not shown).

Significant differences were detected among the populations for all traits in all evaluated years/generations, as well as in the joint analyses, confirming the existence of variability among the populations and the possibility of the selection of the best ones. There was an effect of years/generations for the three studied traits (Table 1), indicating that, although the experiments were set up in the same location and crop season, the factors related to years and/or generations – such as mean temperature that has a direct effect on the development of the pathogen (Pastor-Corrales & Abawi, 1987) or natural selection that causes effects within the populations – were sufficient to detect differences among the years/generations. The mean values of the three studied traits showed a wide variation among the years/generations: 1,401 kg ha^{-1} to 3,245 kg ha^{-1} for yield, 21.4 to 25.6 g for 100-seed weight, and 3.0 to 4.4 for reaction to Fusarium wilt, confirming that the traits were affected by the years/generations, corroborating the results obtained by Fernandes et al. (2015).

The effect of the interaction among populations and years/generations was significant for the three

evaluated traits (Table 1), showing that there was a differential response of the populations among years/generations. In the case of reaction to Fusarium wilt, this interaction may be the consequence of the presence of more than one race in the infested area and/or of the prevalence of different races in different years. However, the estimates, two by two, of the genetic correlations between years/generations were significant and considered high, ranging from 0.80 to 0.88, indicating that the interaction is predominantly simple, which suggests the existence or predominance of one or a few races in the experimental area. A similar result was observed by Pereira et al. (2019a) in the same area. Up to date, at least seven races of this pathogen have been described (Henrique et al., 2015). However, there is a variation in the race definition systems, including different forms of evaluation and different sets of differentiating cultivars (Henrique et al., 2015), which makes it difficult to understand the pathogenic variability of Fusarium wilt (Cruz et al., 2018). Consequently, there are few studies on the prevalence of races in the main producing regions in Brazil, which hinders the development of new cultivars with a broad resistance.

GCA and SCA were significant for all traits (Table 1), which indicates the existence of additive and nonadditive gene action in the control of the reaction to Fusarium wilt (Batista et al., 2016, 2017) and also of yield and 100-seed weight (Vale et al., 2015; Moura et al., 2018; Pereira et al., 2019a). However, the relative contributions (R^2) of the GCA of Group I and the GCA of Group II were greater than those of the SCA, indicating that, although there are nonadditive genetic effects in the expression, there was a predominance of the additive genetic effects for the three analyzed traits. This result differed from those reported in the studies of Batista et al. (2016), with the inoculation of the pathogen under controlled conditions, and of Pereira et al. (2019a), without inoculation under field conditions, who found similar contributions of additive and nonadditive genetic effects for reaction to Fusarium wilt.

Table 1. Summary of joint analyses of variance for the evaluation of 25 black bean (*Phaseolus vulgaris*) populations for reaction to Fusarium wilt, yield, and 100-seed weight.

Source of variation	DF[1]	Fusarium wilt (1–9 score)[2]		Yield (kg ha-1)		100-seed weight (g)	
		Mean square	R² (%)[3]	Mean square	R² (%)[3]	Mean square	R² (%)[3]
Block / Year	9	1.8	-	335454	-	0.90	-
Treatment	27	21.9**	-	646888**	-	30.84**	-
Check cultivar (C)	2	49.8**	-	2402536**	-	118.16**	-
Population (P)	24	16.9**	-	488758**	-	24.85**	-
GCA I[4]	4	42.6**	42	1088615**	49	87.43**	62
GCA II[5]	4	50.5**	50	907581**	41	49.91**	36
SCA[6]	16	2.1**	8	234088*	10	2.94**	2
C vs P	1	86.4**	-	930690**	-	0.01	-
Year / Generation (YG)	2	52.1**	-	103919699**	-	491.85**	-
Treatment × YG	57	2.5**	-	340966**	-	2.59**	-
Check cultivar × YG	4	2.3	-	926701**	-	1.53	-
Population × YG	48	2.5**	-	300997**	-	2.18**	-
GCA I × YG	8	5.2**	-	474353**	-	2.12	-
GCA II × YG	8	1.9	-	444336**	-	3.13*	-
SCA × YG	32	2.0**	-	221823**	-	1.95*	-
(C vs P) × YG	2	2.8	-	128755	-	14.68**	-
Residue	243	1.0	-	133571	-	1.32	-
Mean of the populations	-	3.8		2146		23.21	
CV (%)[7]	-	25.7		17		4.95	

[1]Degrees of freedom. [2]Fusarium wilt scores according to Pastor-Corrales & Abawi (1987). [3]Relative contribution. [4]General combining ability of Group I. [5]General combining ability of Group II. [6]Specific combining ability. [7]Coefficient of variation. * and **Significant at 5 and 1% probability, respectively.

High additive genetic effects indicate predicted genetic gains of a greater magnitude (Cruz et al., 2012; Ramalho et al., 2012). In addition, the additive effects of the genes are accumulated over the generations and are the main sources of genetic variation to be exploited within breeding programs of autogamous species, since their selection furthers the fixation of characteristics of interest (Ramalho et al., 2012). Therefore, the selection of populations for high yield, greater 100-seed weight, and reaction to Fusarium wilt can be carried out in the initial generations.

The estimates of $\hat{g}_i$ and $\hat{s}_{ij}$ allow the individual effect of the GCA of the parents of each group and of the SCA of the populations, respectively, to be known, making the identification of superior parents and segregating populations possible (Cruz et al., 2012). For reaction to Fusarium wilt, the desirable genotypes are those with low mean values that reflect a greater resistance and with negative and significant estimates of $\hat{g}_i$. The CNFP 15207 line was the only one from Group I that had negative (-0.76) and significant estimates of $\hat{g}_i$ in the joint analysis and in all years/generations (Table 2). The CNFP 15194 line and the BRS Esplendor cultivar also had negative and significant $\hat{g}_i$ estimates of -0.59 and -0.13, respectively, in the joint analysis. These genotypes have a concentration of alleles that contributes to an increase in resistance to Fusarium wilt when in crosses. When there is interest in decreasing the mean of the trait in the population, at least one of the parents must have negative and significant estimates of $\hat{g}_i$ (Cruz et al., 2012). Among the genotypes, CNFP 15207 and CNFP 15194 had estimates of $\hat{g}_i$ statistically superior to that of 'BRS Esplendor', indicating that they generate superior populations. Those two lines had a parent in common (TB94-01), which is a resistance source already described in the literature (Antunes et al., 2007; Torres, 2020). Moreover, 'BRS Esplendor' is one of the genotypes with the highest level of per se resistance to the disease (Pereira et al., 2016, 2019b). However, Pereira et al. (2019a) reported that this cultivar did not stand out in the generation of superior populations in evaluations of a complete diallel in the field. Among the lines susceptible to Fusarium wilt in Group II, CNFP 11976 and CNFP 11995 proved to be less sensitive to the pathogen ($\hat{g}_i$ = -1.13* and -0.84*, respectively), both in the joint analysis and in the individual analyses (Table 2).

For the breeder, it is interesting to determine if there are negative and significant estimates of $\hat{s}_{ij}$ for reaction to Fusarium wilt, associated with lower mean values, involving, at least, one of the parents with more favorable estimates of $\hat{g}_i$. The estimates of $\hat{s}_{ij}$ are deviations in the response of the population from what is expected in relation to the GCA of the parents, being an important indication of dominance and epistatic genetic effects (Cruz et al., 2012) and

Table 2. Estimates of the effects of the general combining ability of Group I ($\hat{g}_i$) and of Group II ($\hat{g}_j$) of the parents of black bean (*Phaseolus vulgaris*) for reaction to Fusarium wilt, yield, and 100-seed weight, assessed in different years/generations.

Parent	Reaction to Fusarium wilt (1–9 score)[1]				Grain yield (kg ha⁻¹)				100-seed weight (g)			
	F_2/2016	F_3/2017	F_4/2018	Joint	F_2/2016	F_3/2017	F_4/2018	Joint	F_2/2016	F_3/2017	F_4/2018	Joint
'BRS Esplendor'[2]	-0.24*	0.06	-0.20*	-0.13*	12	-31	-59	-26	-1.87*	-1.78*	-1.65*	-1.77*
'BRS FP403'[2]	0.41*	0.21	-0.30*	0.11	-6	160*	500*	218*	1.34*	1.95*	1.09*	1.46*
CNFP 15207[2]	-0.94*	-0.69*	-0.65*	-0.76*	72*	26	-47	17	-0.16	-0.79*	-0.05	-0.33*
CNFP 15194[2]	-0.14	-1.49*	-0.15	-0.59*	-76*	-46	-95	-72*	0.79*	0.48*	0.78*	0.69*
'BRS Campeiro'[2]	0.91*	1.91*	1.30*	1.37*	-2	-110*	-300*	-137*	-0.11	0.15	-0.17	-0.04
'BRS Esteio'[3]	0.66*	0.81*	1.20*	0.89*	113*	79*	90	94*	-0.36*	-0.18	-0.05	-0.19*
'BRS Supremo'[3]	0.36*	0.61*	0.85*	0.61*	-158*	23	-392*	-176*	-1.52*	-1.36*	-1.47*	-1.45*
VP 22[3]	0.71*	0.36*	0.35*	0.47*	-135*	25	-62	-57*	0.29*	0.92*	0.71*	0.64*
CNFP 11995[3]	-0.44*	-0.99*	-1.10*	-0.84*	86*	55*	255*	132*	1.44*	0.19	0.99*	0.87*
CNFP 11976[3]	-1.30*	-0.79*	-1.30*	-1.13*	95*	-183*	110*	7	0.14	0.42*	-0.18*	0.13
$\sigma(\hat{g}_i) = (\hat{g}_j)$[4]	0.18	0.24	0.19	0.12	52.5	47.0	100.1	41.0	0.24	0.23	0.20	0.13
$\sigma(\hat{g}_i - \hat{g}_j)$[5]	0.29	0.38	0.30	0.19	83.0	74.0	159.6	65.0	0.39	0.37	0.31	0.20

[1]Fusarium wilt scores according to Pastor-Corrales & Abawi (1987). [2]Parents of Group I. [3]Parents of Group II. [4]Standard deviation of $\hat{g}_i$ and $\hat{g}_j$. [5]Error associated with the difference in the $\hat{g}_i$ of parent i with parent j.

of the selection of genetically superior populations. For reaction to Fusarium wilt, the mean values of the populations based on the joint analysis ranged from 1.9 to 6.8 (Table 3), forming four groups by the Scott-Knott test. The first group gathered seven populations and the BRS FP403 resistant check cultivar, showing that these populations have a greater resistance. In addition, 13 populations formed the second group, with acceptable mean values from 3.2 to 4.3, which were better than those of the BRS Supremo and BRS Esteio check cultivars. In relation to the estimates of

$\hat{s}_{ij}$, only the 'BRS FP403'/CNFP 11995 population had a negative and significant estimate of -0.71, associated with a low mean value of 2.33 (Table 3) in the joint analysis and in the three years/generations, indicating a more stable response.

In addition to resistance to Fusarium wilt, a higher yield and greater 100-seed weight are also important in the process of obtaining new lines with the aim of obtaining new cultivars. For grain yield, the BRS FP403 cultivar was the only parent of Group I that contributed with favorable alleles for an increase in

Table 3. Estimates of the specific combining ability ($\hat{s}_{ij}$) and mean values for reaction to Fusarium wilt, yield, and 100-seed weight of segregating populations of black bean (*Phaseolus vulgaris*) based on joint analyses[1].

Population	Fusarium wilt (1–9 score)[2]		Yield (kg ha^{-1})		100-seed weight (g)	
	Mean	$\hat{s}_{ij}$	Mean	$\hat{s}_{ij}$	Mean	$\hat{s}_{ij}$
CNFP 15194/CNFP 11976	1.9a	-0.14	2,134b	53	24.2c	0.18
CNFP 15207/CNFP 11976	2.2a	0.36*	2,221b	50	23.0e	-0.02
'BRS FP403'/CNFP 11995	2.3a	-0.71*	2,553a	56	25.7b	0.17
CNFP 15194/CNFP 11995	2.3a	-0.01	2,222b	16	25.0c	0.21
'BRS Esplendor'/CNFP 11976	2.4a	-0.11	2,251b	123*	21.6g	0.06
CNFP 15207 CNFP 11995	2.4a	0.24	2,246b	-50	23.1e	-0.62
'BRS FP403'/CNFP11976	2.8a	0.08	2,143b	-229*	24.4c	-0.41
'BRS FP403'	3.1a	-	2,458a	-	26.8a	-
CNFP 15207/'BRS Supremo'	3.2b	-0.37*	2,013c	26	21.8f	0.36
CNFP 15207/'BRS Esteio'	3.6b	-0.32*	2,120b	-138*	22.4f	-0.31
CNFP 15207/VP 22	3.6b	0.09	2,218b	112*	24.1c	0.59
CNFP 15194/'BRS Supremo'	3.6b	-0.21	1,884c	-15	22.2f	-0.25
'BRS Esplendor'/CNFP 11995	3.7b	0.86*	2,185b	-68	22.0f	-0.30
'BRS Esplendor'/VP 22	3.8b	-0.29*	2,026c	-37	22.0f	-0.12
'BRS Campeiro'/CNFP 11976	3.8b	-0.19	2,020c	4	23.5d	0.19
CNFP15194/VP 22	3.9b	0.26*	1,869c	-148*	24.5c	0.01
'BRS Campeiro'/CNFP 11995	3.9b	-0.39*	2,186b	45	24.6c	0.54
BRS Esplendor/'BRS Supremo'	4.0b	-0.26*	2,087b	143**	20.2h	0.21
'BRS FP403'/VP 22	4.1b	-0.27*	2,532a	225**	25.8b	0.52
CNFP 15194/ 'BRS Esteio'	4.2b	0.09	2,261b	93**	23.5d	-0.14
'BRS Esplendor'/'BRS Esteio'	4.3b	-0.21	2,054c	-160**	21.4g	0.15
'BRS FP403'/'BRS Supremo'	5.0c	0.51*	2,105b	-84**	23.3d	0.11
'BRS FP403'/'BRS Esteio'	5.2c	0.39*	2,490a	32	24.1c	-0.39
'BRS Campeiro'/VP 22	5.8d	0.21	1,800d	-151	22.8e	-1.00
'BRS Campeiro'/'BRS Esteio'	6.1d	0.04	2,276b	173**	23.7d	0.70
'BRS Campeiro'/'BRS Supremo'	6.1d	0.33*	1,763d	-70	21.2g	-0.43
'BRS Supremo'	6.3d	-	1,574d	-	20.9h	-
'BRS Esteio'	6.8d	-	1,897c	-	21.9f	-
σ ($\hat{s}_{ij}$)[3]	-	0.24	-	82	-	0.26

[1]Values followed by equal letters, in the columns, do not differ statistically from each other using the Scott-Knott means test, at 10% probability. [2]Fusarium wilt scores according to Pastor-Corrales & Abawi (1987). [3]Mean standard deviation of $\hat{s}_{ij}$.

yield, with a high and significant g_i estimate of 218 (Table 2). Among the parents of Group II, line CNFP 11995 and cultivar BRS Esteio stood out, showing positive and significant estimates of 132 and 94, respectively, in the joint analysis. Therefore, these genotypes are most recommended for generating populations with a higher yield.

The mean values for grain yield ranged from 1,574 kg ha^{-1} for 'BRS Supremo' to 2,553 kg ha^{-1} for the 'BRS FP403'/CNFP 11995 population (Table 3), based on the joint analysis. The evaluated genotypes formed four groups of means. The first was composed of the 'BRS FP403'/CNFP 11995, 'BRS FP403'/VP 22, and 'BRS FP403'/'BRS Esteio' populations, as well as by 'BRS FP403', indicating a high grain yield, superior to that of the other populations. The second group was formed by 14 other populations, with a greater yield than that of cultivars BRS Supremo (1,574 kg ha^{-1}), which is susceptible, and BRS Esteio (1,897 kg ha^{-1}), which is susceptible but has a very high yield potential (Pereira et al., 2013). Those populations were also considered to have a good potential. Among the superior populations, six had positive and significant estimates of $\hat{s}_{ij}$ associated with higher mean values: 'BRS Esplendor'/CNFP 11976, CNFP 15207/VP 22, 'BRS Esplendor'/'BRS Supremo', 'BRS FP403'/VP 22, CNFP 15194/'BRS Esteio', and 'BRS Campeiro'/'BRS Esteio'. These populations have yields that cannot be explained only by the mean of the parents.

For 100-seed weight, the BRS FP403 cultivar and the CNFP 15194 line were prominent in Group I, with positive and significant $\hat{g}_i$ estimates of 1.46 and 0.69, respectively, in the joint analysis and in all years/generations (Table 2), indicating that they have a high frequency of alleles for increase in 100-seed weight. In Group II, lines VP 22 and CNFP 11995 also had positive and significant $\hat{g}_i$ estimates, respectively, of 0.64 and 0.87 in the joint analysis.

Considering the mean values, based on the joint analysis, cultivar BRS FP403 had the greatest 100-seed weight, in isolation (Table 3). The second group of means was composed of two populations: 'BRS FP403'/VP 22 and 'BRS FP403'/CNFP11995. Eighty percent of the populations had larger bean seeds than those of the BRS Esteio cultivar, which is currently the market standard for black bean, indicating a high potential for the extraction of lines with a great 100-seed weight. The populations that had seeds larger than those of 'BRS

Esteio' were considered to have a good performance. The CNFP 15207/VP 22, 'BRS Campeiro'/CNFP 11995, and 'BRS FP403'/VP 22 populations stood out for 100-seed weight, with positive and significant estimates of $\hat{s}_{ij}$, along with high mean values and a parent with positive and significant estimates of $\hat{g}_i$, indicating that these populations have a concentration of alleles that allows an increase in the trait.

Considering the three traits simultaneously, no population was superior to the BRS FP403 cultivar. However, a cultivar is the final result of a breeding study and, therefore, has already passed through the selection process necessary for fixing alleles of the loci that control the traits of interest, furthering the homozygosity of this genotype, resulting in a similar performance among plants. Furthermore, the cited cultivar was recently released to combine resistance to Fusarium wilt, high yield, and great 100-seed weight compared with the cultivars available in the market (Souza et al., 2019). In contrast, the segregating populations assessed here are still in the initial phase of the breeding process, with the possibility of the selection of lines superior even to 'BRS FP403'.

The 'BRS FP403'/CNFP 11995 population proved to have the greatest potential, as it is in the group of greatest resistance to Fusarium wilt and a high yield, as well as in the second group for 100-seed weight. In addition, it is formed by at least one parent with significant and favorable estimates of $\hat{g}_i$ for all traits (Table 3). Five other populations also proved to be promising: CNFP 15194/CNFP 11976, CNFP 15194/CNFP 11995, CNFP 15207/CNFP 11976, CNFP 15207/CNFP 11995, and 'BRS FP403'/CNFP11976. Although they were not grouped simultaneously in the best groups for yield and 100-seed weight, they have satisfactory mean values for these traits, along with high resistance to Fusarium wilt, significant and favorable estimates of $\hat{s}_{ij}$ for at least one trait, and at least one parent with favorable estimates of $\hat{g}_i$. Therefore, these six populations are recommended for obtaining lines with greater resistance to Fusarium wilt, high yield, and great 100-seed weight simultaneously.

Conclusions

1. There is a predominance of additive effects in the genetic control of the reaction to Fusarium wilt,

yield, and 100-seed weight in black bean (*Phaseolus vulgaris*).

2. In black bean breeding programs, the BRS Esplendor cultivar and the CNFP 15207 line are the best parents to form black bean populations that have greater resistance to Fusarium wilt, the CNFP 15194 line is the best parent to form black bean populations with greater resistance to Fusarium wilt and 100-seed weight, and the BRS FP403 cultivar is the best parent to increase yield and 100-seed weight.

3. The 'BRS FP403'/CNFP 11995, CNFP 15194/CNFP 11976, CNFP 15194/CNFP 11995, CNFP 15207/CNFP 11976, CNFP 15207/CNFP 11995, and 'BRS FP403'/CNFP11976 populations are the most promising for extracting black bean lines that combine resistance to Fusarium wilt, high yield, and great 100-seed weight.

Acknowledgments

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