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# Genetic parameters and selection of black bean lines for resistance to fusarium wilt and yield

Abstract – The objective of this work was to estimate genetic and phenotypic parameters of black bean (Phaseolus vulgaris) lines for reaction to fusarium wilt (RFW), yield, and 100-seed weight (100SW) under conditions of a field naturally infested by Fusarium oxysporum f. sp. phaseoli, as well as to select lines that combine the desirable phenotypes for the three traits simultaneously. For this, 116 lines obtained from two segregating populations and five check cultivars were evaluated using an 11×11 triple lattice experimental design, in the winter crop seasons of 2015 and 2016, with sowing in May. The obtained heritability estimates were high: 91, 75, and 92% for RFW, yield, and 100SW, respectively. Significant genetic correlations of -0.93 were detected between RFW and yield and of -0.28 between RFW and 100SW, indicating that more resistant lines have a higher yield and a larger grain size. Direct selection for each trait led to increases of 34% in resistance to FW, 11% in yield, and 9.0% in 100SW. Simultaneous selection for the three traits led to high gains of 22.1% for RFW, 6.6% for yield, and 7.7% for 100SW. Therefore, there is genetic variability and a high possibility of success from selection. Five lines - CNFP 19237, CNFP 19346, CNFP 19320, CNFP 19291, and CNFP 19306 show a higher genetic potential.

**Index terms**: *Fusarium oxysporum* f. sp. *phaseoli*, *Phaseolus vulgaris*, genetic gain, heritability, plant breeding.

## Parâmetros genéticos e seleção de linhagens de feijão-preto para resistência à murcha-de-fusário e produtividade

Resumo – O objetivo deste trabalho foi estimar parâmetros genéticos e fenotípicos em linhagens de feijão-preto (Phaseolus vulgaris) para reação à murcha-de-fusário (RMF), produtividade e massa de 100 grãos (M100), em condições de campo naturalmente infestado por Fusarium oxysporum f. sp. phaseoli, bem como selecionar linhagens que combinem os fenótipos desejáveis para as três características simultaneamente. Para tanto, 116 linhagens obtidas de duas populações segregantes e cinco cultivarestestemunha foram avaliadas em delineamento experimental látice triplo 11×11, nas safras de inverno de 2015 e 2016, com semeadura em maio. As estimativas de herdabilidade obtidas foram altas: 91, 75 e 92% para RMF, produtividade e M100, respectivamente. Correlações genéticas significativas de -0.93 foram detectadas entre RMF e produtividade e de -0,28 entre RMF e M100, o que indica que linhagens mais resistentes apresentam maior produtividade e maior tamanho de grão. A seleção direta para cada uma das características levou a aumentos de 34% na resistência à MF, 11% na produtividade e 9,0% na M100. A seleção simultânea para as três características também levou a altos ganhos de 22,1% para RMF, 6,6% para produtividade e 7,7% para M100. Assim, há variabilidade genética e alta possibilidade de sucesso com a seleção. Cinco linhagens – CNFP 19237, CNFP 19346, CNFP 19320, CNFP 19291, and CNFP 19306 – apresentam maior potencial genético.

**Termos para indexação**: *Fusarium oxysporum* f. sp. *phaseoli, Phaseolus vulgaris*, ganho genético, herdabilidade, melhoramento vegetal.

#### Introduction

Common bean (*Phaseolus vulgaris* L.), also known as dry bean, is one of the main leguminous species used for human consumption worldwide because it is a rich source of proteins, carbohydrates, fiber, and minerals at a low cost (Batista et al., 2017). In Brazil, the production of common bean was 2.5 million metric tons in 2020, making the country one of the largest producers in the world (FAO, 2020; Embrapa Arroz e Feijão, 2021). However, black bean, the second most produced and consumed in Brazil, corresponds only to approximately 20% of the country's production, and around 120,000 tons of this bean type still must be imported annually (Conab, 2021), showing the need to increase production.

Although Brazil has a prominent role in bean production worldwide, the average yield of 1,500 kg ha-1 is considered only intermediate (Embrapa Arroz e Feijão, 2021) and much below the crop's yield potential. The main factor that contributes to a low bean yield is the high incidence of pests and diseases. Of the diseases, fusarium wilt, caused by the fungus Fusarium oxysporum f. sp. phaseoli, is among the main ones that attack the common bean crop, with negative impacts on worldwide production (Niño-Sánchez et al., 2015). Despite being present in nearly the entire Brazilian territory, the disease causes more damage in areas irrigated with a center pivot system, in which the crop is normally grown in a successive manner (Torres et al., 2021). In this scenario, the most effective, economic, and safest way to combat the disease is through genetic resistance, which has the lowest negative impact on humans and on the environment (Cândida et al., 2009; Pereira et al., 2019).

Genetic variability has been reported for resistance to fusarium wilt (Pastor-Corrales & Abawi, 1987; Azevedo et al., 2015; Leitão et al., 2020; Pereira et al., 2011, 2020), indicating the possibility of selection of resistant genotypes and of genetic gain for this trait. However, in general, there is little information on the genetic resistance to this disease and few black bean cultivars are resistant to fusarium wilt in Brazil (Pereira et al., 2016, 2018), which shows the need to obtain new cultivars with resistance to the causative pathogen.

Genetic parameters allow the breeder to obtain information on the genetic aspects of the population under study and to predict the success of the selection of the best genotypes (Coelho et al., 2002). However, in the literature, the estimates of genetic parameters for resistance to fusarium wilt are restricted to studies conducted in controlled environments, with pathogen inoculation (Cândida et al., 2009; Musoni et al., 2010; Pereira et al., 2011; Leitão et al., 2020). The results obtained in these researches have shown heritability ranging from 76 to 99%, with a predominance of high values (Pereira et al., 2009, 2011; Musoni et al., 2010), and estimates of expected gain from selection from 26.8 to 35.5% (Cândida et al., 2009). The estimation of these parameters and the evaluation of different lines under field conditions is, therefore, essential for cultivar selection and recommendation (Resende & Duarte, 2007).

A new cultivar must meet market demands, such as resistance to diseases and other desirable phenotypes, which, in the Brazilian black bean market, currently include a high yield and a great 100-seed weight, which are related to grain size. Although there are several reports of estimates of genetic parameters for these traits (Coelho et al., 2002; Alvares et al., 2016; Okii et al., 2018), the greatest challenge is to obtain lines that combine the phenotypes for these traits simultaneously.

The objective of this work was to estimate the genetic and phenotypic parameters of black bean lines for reaction to fusarium wilt, yield, and 100-seed weight under conditions of a field naturally infested by *Fusarium oxysporum* f. sp. *phaseoli*, as well as to select lines that combine the desirable phenotypes for the three traits simultaneously.

### **Materials and Methods**

The experiments were conducted in the experimental field of Embrapa Arroz e Feijão, in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil (16°30'17"S, 49°16'53"W, at 819 m of altitude). The

region has an Aw, tropical savanna, megathermal climate, according to Köppen-Geiger's classification. The predominant soil is a Latossolo Vermelho-Ácrico, according to Brazilian soil classification system (Santos et al., 2018), which corresponds to a positively charged Oxisol. The experimental area is characterized by a high natural infestation of the pathogen, confirmed in other studies on the reaction of bean lines to fusarium wilt (Pereira et al., 2018, 2018, 2019, 2020).

The used lines were obtained from the two following segregating populations of black bean from the  $F_5$  generation: 'BRS Esplendor' / 'BRS Expedito' and 'BRS Expedito' / CNFP 15867, which were selected on the basis of the results of a previous study by Pereira et al. (2019). These populations were selected from 28 populations obtained from a complete diallel cross design, due to their high resistance to fusarium wilt, high yield, and greater 100-seed weight in an area with a high natural occurrence of the pathogen.

In the 2014 winter crop season, 58 plants from the F<sub>5</sub> generation, chosen at random, were harvested and threshed individually from each selected population, resulting in 116 lines. These lines, together with five black bean cultivars used as check cultivars, were evaluated. The experiment was conducted in the winter crop season of 2015, with sowing on 5/25/2015 and harvest on 8/25/2015, in an 11×11 triple lattice design, in an area infested by the pathogen. Plots were formed by two 3.0 m length rows, spaced at 0.5 m, totalizing 1.5 m<sup>2</sup>. At sowing, 12 seed per linear meter were used, totaling 72 plants per plot. Fertilization was carried out with 200 kg ha-1 monoammonium phosphate (10% N and 50% P<sub>2</sub>O<sub>5</sub>) at sowing and 178 kg ha<sup>-1</sup> urea (80 kg ha<sup>-1</sup> N) as topdressing at 20 days after planting. Irrigation was carried out by center pivot. Other cultural practices, such as weed plant and insect control, were performed whenever necessary; however, no pesticides were applied for disease control. The seeds harvested in this experiment were used to set up a similar experiment in the winter crop season of 2016, with sowing on 5/20/2016 and harvest on 8/20/2016. BRS FP403, BRS Esplendor, and BRS Expedito were used as check cultivars resistant to fusarium wilt, and BRS Esteio and BRS Supremo as check cultivars susceptible to the disease (Pereira et al., 2016).

The evaluated traits were: reaction to fusarium wilt, yield, and 100-seed weight (100SW). A scale ranging

from 1 to 9, adapted from Pastor-Corrales & Abawi (1987), was used to score the reaction to fusarium wilt in the plots, as follows: 1, 0% of susceptible plants in the plot; 2, 0.1 to 5.0%; 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%. For yield evaluation, all plants of the plots were harvested, and grain weight was obtained in grams per plot and then converted into kilogram per hectare. To determine 100-seed weight, a random sample of 100 seeds was taken from each plot and weighed.

The data for each trait in each environment were subjected to individual analyses of variance. Residual variances were evaluated by Hartley's test, at 5% probability, and, after checking for homoscedasticity, joint analyses were carried out considering the effect of treatments as random and that of environments as fixed. The experimental coefficient of variation (CV) and selective accuracy were estimated to determine experimental accuracy (Resende & Duarte, 2007).

The variance components were estimated from analyses of variance as proposed by Cruz et al. (2012). Afterwards, estimates were made of genetic variance; variance of the interaction between lines and years; heritability; expected gain from direct selection (in percentage) for each trait, with a selection intensity of 26.7%; and gain from simultaneous selection for the evaluated traits (Cruz et al., 2012). Estimates of genetic and phenotypic correlations were also obtained for the studied traits according to Cruz et al. (2012).

For simultaneous selection, the method of independent culling levels was used, which consists in establishing maximum and/or minimum values for each trait in the lines. All lines that did not reach the proposed level for at least one trait were eliminated. Then, the following criteria were used for the selection of the lines: reaction to fusarium wilt, with mean scores below 3; mean yield greater than 2,614 kg ha<sup>-1</sup>; and mean 100-seed weight greater than 21.9 g per 100 seeds. All statistical analyses were performed with the aid of the GENES software (Cruz, 2013).

### **Results and Discussion**

In the individual analyses, the estimates of the environmental CVs for each year were 15.8 and 19.5% for yield and 4.4 and 5.9% for 100-seed weight, indicating a good experimental accuracy (Okii et

al., 2018; Pereira et al., 2018; Torres et al., 2021). For reaction to fusarium wilt, the estimates were higher – 28.9 and 36.8% –, probably because the experiment was carried out in the field under conditions in which the disease occurs naturally and the distribution of the fungus is not as homogeneous (Pereira et al., 2019, 2020). These higher estimates may also be attributed to the low mean values found, despite the increase in the CV.

The estimates of selective accuracy were 0.77 and 0.80 for yield, considered high ( $\geq$  0.70 and < 0.90); and 0.90 and 0.96 for 100-seed weight and 0.91 and 0.94 for reaction to fusarium wilt, considered very high ( $\geq$  0.90). These results confirm the good experimental accuracy in the winter crop season of 2015 and 2016, which is essential for obtaining reliable genetic parameters, indicating that the selection of superior lines is possible. As selective accuracy is not affected by the mean, the breeder is able to know if there is

a correlation between the true genotypic value of the treatment and the one predicted from the information of the experiment (Resende & Duarte, 2007).

Significant differences were found among the studied lines for all traits, on the basis of the joint analyses (Table 1), showing that there is variability among the lines and also among the lines of each population separately. Therefore, there is the possibility of the selection of superior genotypes for the three traits in each population. The differences among the lines confirm the high infestation of the experimental area with the pathogen, as reported in other studies (Pereira et al., 2016, 2018, 2019, 2020; Torres et al., 2021).

Differences were also observed between years for all traits (Table 1), which is an indicative that the climate conditions, such as temperature and moisture, in the two study years had varying effects on the evaluated traits. This is commonly noted and has also been reported by other authors for 100-seed weight

**Table 1.** Summary of the joint analyses of variance for reaction to fusarium wilt, grain yield, and 100-seed weight of black bean (*Phaseolus vulgaris*) lines evaluated in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil, in the winter crop seasons of 2015 and 2016.

Source of variation <sup>(1)</sup>	DF <sup>(2)</sup>	Fusari	um wilt	Grain yield	l (kg ha-1)	100-seed weight (g)		
	_	MS <sup>(3)</sup>	p-value	MS <sup>(3)</sup>	p-value	MS <sup>(3)</sup>	p-value	
Genotypes	120	10.5	0.001	897,985	0.001	17.5	0.001	
Check cultivars (C)	4	35.7	0.001	474,727	0.100	38.0	0.001	
Lines (L)	115	8.8	0.001	926,429	0.001	16.8	0.001	
L1	57	5.8	0.001	634,156	0.001	20.4	0.001	
L2	57	11.9	0.001	1,234,861	0.001	13.0	0.001	
L1 vs L2	1	2.79	0.068	5,307	1.000	25.2	0.001	
C vs L	1	93.4 0.001		1,756,484	0.007	23.6	0.002	
Years (Y)	1	66.0	0.001	151,191,447	0.001	367.6	0.001	
Genotypes $\times$ Y	120	0.9	0.113	322,229	0.006	2.9	0.001	
$\mathbf{C} \times \mathbf{Y}$	4	3.9	0.001	357,825	0.208	1.4	0.364	
$\boldsymbol{L}\times\boldsymbol{Y}$	115	1.0	0.178	336,487	0.001	3.3	0.001	
$L1 \times Y$	57	1.1	0.056	345,510	0.027	3.7	0.001	
$L2 \times Y$	57	0.8	1.000	326,649	0.053	2.8	0.001	
$(L1 \text{ vs } L2) \times Y$	1	1.7	0.158	382,957	0.209	8.1	0.013	
$(C vs L) \times Y$	1	0.1	1.000	359	1.000	10.6	0.001	
Residue	420	0.8	-	226,844	-	1.3	-	
Overall mean	-	-	2.8	-	2743	-	21.8	
Mean for 2015	-	-	2.5	-	2287	-	22.5	
Mean for 2016	-	-	3.1	-	3199	-	21.1	
CV <sup>(4)</sup> (%)	-	-	31.8	-	17.4	-	5.2	

<sup>(1)</sup>L1, lines obtained from population 'BRS Esplendor' / 'BRS Expedito'; and L2, lines obtained from population 'BRS Expedito' / CNFP 15867. <sup>(2)</sup>Degrees of freedom. <sup>(3)</sup>Mean square. <sup>(4)</sup>Experimental coefficient of variation. and yield (Ribeiro et al., 2013), as well as for reaction to fusarium wilt (Pereira et al., 2020).

The effect of the interaction between lines and years was significant for grain yield and 100-seed weight (Table 1), indicating that the lines responded differently to the experimental years, as found in the literature (Di Prado, 2017). Grain yield, being a trait of quantitative inheritance, with a low heritability, is highly affected by the environment, as concluded by Torga et al. (2013). For 100-seed weight, the obtained results are in alignment with those of Alvares et al. (2016) and Okii et al. (2018).

However, for reaction to fusarium wilt, there was no significant effect of the interaction between lines and years, as observed in their decompositions. This is an indicative that the lines responded similarly in the two years, which facilitates the selection of resistant lines. Therefore, years and not lines affect the mean expression of the trait, as confirmed by the genetic correlation of 0.99 between the lines in the both years, considered high and significant. Pereira et al. (2019) and Torres et al. (2021) reported similar results.

It is likely that only one or a few races were prevalent in the infected area, since, in the presence of various races, the evaluated lines would probably have had a differentiated reaction from one year to another, with a consequent significance of the interaction. The obtained result may also be an indicative that the expression of reaction to fusarium wilt is controlled by a few genes or by quantitative trait loci of great effect, as observed by Cândida et al. (2009) and Batista et al. (2017) in studies conducted under controlled conditions. Currently, at least seven races of the disease's pathogen are described (Henrique et al., 2015). However, the systems used to define these races vary, with different forms of evaluation and series for differentiating cultivars (Henrique et al., 2015), which makes it difficult to understand the pathogenic variability of this pathogen (Cruz et al., 2018). For this reason, there are few studies on the prevalence of races in the main bean producing regions, which hinders the development of new cultivars with broad resistance.

For all evaluated traits, the estimates of genetic variance and of heritability were considered high (Table 2). For the estimates of genetic variance, the obtained values were always higher than those of the interaction, which confirms that the lines were little affected by the interaction with the environment. For heritability for reaction to fusarium wilt, 90% of the variation is of a genetic nature; this high value was similar to that found by Musoni et al. (2010) and Pereira et al. (2009) but higher than that reported by Pereira et al. (2011), all under controlled conditions. Therefore, the phenotypic selection for this trait will be effective due to the high correlation between the phenotype and the genotype. In each population, heritability ranged from 86.2% for 'BRS Esplendor' / 'BRS Expedito' to 93.3% for 'BRS Expedito' / CNFP 15867, indicating that both populations have potential for selection of lines resistant to fusarium wilt.

The estimate of heritability for yield, based on the joint analyses, was 75.5% in the two populations, ranging from 64.2% for 'BRS Esplendor' / 'BRS Expedito' to 81.6% for 'BRS Expedito' / CNFP 15867. These values are considered high since this trait is controlled by several genes, which usually make it highly affected by the environment (Torga et al., 2013). For 100-seed weight, the estimate of joint heritability was 92.3%, ranging from 90% for 'BRS Esplendor' / 'BRS Expedito', confirming that the genetic components showed high values and that the selection of superior

**Table 2.** Estimates of genetic variance  $(\sigma_g^2)$ , herdability (h<sup>2</sup>), and variance of lines by year interaction  $(\sigma_{LY}^2)$  for reaction to fusarium wilt, yield, and 100 seed weight, based on the joint analyses of black bean (*Phaseolus vulgaris*) lines evaluated in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil, in the winter crop seasons of 2015 and 2016.

Genotype	Fusarium wilt				Yield			100 seed weight		
	$\sigma_{g}^{2}$	h²	$\sigma_{\scriptscriptstyle LY}^2$	$\sigma_{g}^{2}$	h²	$\sigma_{\rm LY}^2$	$\sigma_{g}^{2}$	h²	$\sigma_{\scriptscriptstyle LY}^2$	
Lines (L)	1.33	90.9	0.03	116,597	75.5	18,274	2.58	92.3	0.33	
L from Pop1 <sup>(1)</sup>	0.83	86.2	0.05	67,885	64.2	19,778	3.18	93.6	0.40	
L from Pop2 <sup>(2)</sup>	1.85	93.3	0.00	168,003	81.6	16,634	1.95	90.0	0.25	

(1)'BRS Esplendor' / 'BRS Expedito'. (2)'BRS Expedito' / CNFP 15867.

genotypes on the basis of the observed phenotype will be efficient (Alvares et al., 2016; Okii et al., 2018).

The joint variation of traits, also known as phenotypic correlation, can occur through environmental and genetic factors. Through genetic factors, it is called genetic correlation and is explained by the occurrence of gene linkage and/or pleiotropy, being considered the only heritable correlation. Therefore, in breeding programs aiming at simultaneous selection, knowledge of the estimates of the genetic correlation between traits of economic interest is fundamental. In the present study, the estimates of genetic correlation and phenotypic correlation between reaction to fusarium wilt and yield were significant, negative, and of considerable magnitude, being of -0.93 and -0.72, respectively (Table 3), indicating that the lower the score for resistance to fusarium wilt, i.e., the greater the resistance, the greater the yield. This is shows that, as expected, the damage caused by the disease is expressive and is reflected in a decline in yield.

Between reaction to fusarium wilt and 100-seed weight, the estimates of genetic and phenotypic correlations were -0.28 and -0.26, respectively, both considered significant (Table 3), negative, and of low magnitude, indicating an inverse relationship between these traits. This result is an indicative that the plants that did not die by infection from the pathogen had altered vegetative and reproductive physiological stages, which led to a reduction in pod filling and in seed weight. However, no genetic correlation was detected between yield and 100-seed weight, differently from in the study of Coelho et al. (2002), who found negative and significant genetic correlations.

In relation to the selection of lines, the direct selection of the 31 most resistant to fusarium wilt led to gains of 33.7% (Table 4), confirming the possibility of increase in the frequency of the favorable alleles that control this trait for the next generation. Among these lines, 22 originated from 'BRS Expedito' / CNFP 15867, indicating the greater potential of this population for the extraction of lines resistant to fusarium wilt. This was confirmed by the high estimate of 34.6% for the

**Table 3.** Estimates of genetic  $(r_g)$  and phenotypic  $(r_p)$  correlations between reaction to fusarium wilt, yield, and 100-seed weight of black bean (*Phaseolus vulgaris*) lines evaluated in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil, in the winter crop seasons of 2015 and 2016.

Variable	r <sub>g</sub>	r <sub>p</sub>
Fusarium wilt × yield	-0.93++	-0.72**
Fusarium wilt $\times$ 100-seed weight	-0.28+	-0.26**
Yield × 100-seed weight	0.24	0.17

\* and \*\*Significant by the t-test, at 5 and 1% probability, respectively. <sup>+</sup> and <sup>++</sup>Significant by the bootstrap resampling method, with 10,000 simulations, at 5 and 1% probability, respectively.

**Table 4.** Mean values of the 31 black bean (*Phaseolus vulgaris*) lines selected independently from the population of origin and of the 16 lines selected from each population, expected gain from direct and simultaneous selection (GS), and number of lines selected from each population (NL) among the 31 best ones for reaction to fusarium wilt (scores from 1 to 9), grain yield, and 100-seed weight, based on the joint analyses carried out in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil, in the winter crop seasons of 2015 and 2016.

	General gain from direct selection and by population											
Genotype	Fusarium wilt				Grain yield (kg ha <sup>-1</sup> )				100-seed weight (g)			
	Mean	GS (%)	NL1 <sup>(1)</sup>	NL2 <sup>(2)</sup>	Mean	GS (%)	NL1 <sup>(1)</sup>	NL2 <sup>(2)</sup>	Mean	GS (%)	NL1 <sup>(1)</sup>	NL2 <sup>(2)</sup>
Lines	1.70	33.7	9	22	3,145	10.8	15	16	23.8	8.8	12	19
L1 <sup>(1)</sup>	1.84	29.3	16	0	3,259	4.8	16	0	23.8	9.7	16	0
L2 <sup>(2)</sup>	1.64	34.6	0	16	2,770	9.9	0	16	23.8	7.5	0	16
						Simulta	neous gain					
Genotype	Fusarium wilt Gr				Grain yield	d (kg ha-1)	kg ha <sup>-1</sup> ) 100-seed weight (g)					
	М	ean	GS	(%)	Mean GS (%)		Mean		GS (%)			
Lines	2	2.0	2	2.1	2,994 6.6		23.6		7.7			
Overall mean	2	2.7			2,	2,752 21.7						

<sup>(1)</sup>Lines obtained from population 'BRS Esplendor' / 'BRS Expedito'. <sup>(2)</sup>Lines obtained from population 'BRS Expedito' / CNFP 15867.

expected gain from selection of the 16 best lines in this population. These results are similar to those obtained by Cândida et al. (2009), who estimated genetic gain in two  $F_{2:3}$  populations ('Milionário 1732' / 'Macanudo' and 'FT Tarumã' / 'Macanudo') under controlled conditions, finding expected gains of 26.8 and 35.5%, respectively.

For 100-seed weight, the expected gain was 8.8% from the selection of the 31 best lines for this trait, considering both studied populations (Table 4). Of these lines, 12 came from population 'BRS Esplendor' / 'BRS Expedito' and 19 from 'BRS Expedito' / CNFP 15867. However, there was a greater expected gain of 9.7% from selection for population 'BRS Esplendor' / 'BRS Expedito', which can be explained by the high estimates of genetic variance and heritability found for this population. According to Faria et al. (2014), the annual genetic progress for this trait, considering elite lines of black bean, was of 0.65% over a period of 22 years, which confirms the considerable potential for gain from selection for 100-seed weight in the present study.

For grain yield, the direct selection of the 31 best lines, considering the two evaluated populations, led to a genetic gain of 10.8% (Table 4). Of these lines, 16 came from the 'BRS Expedito' / CNFP 15867 population, which also showed a greater gain from selection of 9.9%. These estimates are similar to those reported in the literature for common bean (Alvares et al., 2016).

Considering the estimates of expected gain from selection for the three traits in an isolated manner, population 'BRS Expedito' / CNFP 15867 stood out for reaction to fusarium wilt and grain yield, whereas 'BRS Esplendor' / 'BRS Expedito' showed better results for 100-seed weight. However, a superior performance for only one trait is not sufficient for the selection of lines aiming at the recommendation of new cultivars. From simultaneous selection, the expected gain for the 31 best lines was 22.1% for reaction to fusarium wilt, 6.6% for yield, and 7.7% for 100-seed weight (Table 4), indicating that this type of selection was effective in increasing the frequency of the favorable alleles of the genes that control these traits. Although the estimates for the three traits simultaneously are lower than those obtained by direct gain, they are considered high when compared with those reported in the literature (Alvares et al., 2016).

Of the 31 selected lines, 14 came from 'BRS Esplendor'/'BRS Expedito' and 17 from 'BRS Expedito' / CNFP 15867 (Table 5), indicating that both of these populations have potential for the extraction of lines that simultaneously show resistance to fusarium wilt, a high yield, and a greater 100-seed weight. All 31 lines showed a resistance to fusarium wilt greater than that of 3.5 observed for 'BRS FP403' (Table 5), which was recently recommended due to its high resistance to fusarium wilt, high yield, and 100-seed weight greater than that of the cultivars available on the market (Pereira et al., 2016). In addition, 19 lines were more resistant than the most resistant check cultivar, BRS Expedito, confirming their high level of resistance to fusarium wilt.

For grain yield, the 31 selected lines showed a mean performance superior to that of 'BRS Supremo' (2,185 kg ha<sup>-1</sup>) and 'BRS Esteio' (2,374 kg ha<sup>-1</sup>), which are susceptible to fusarium wilt, and to that of 'BRS Expedito' (2,483 kg ha<sup>-1</sup>), which is resistant (Table 5). Of these lines, 29 also showed a yield superior to that of 'BRS FP403' (2,721 kg ha<sup>-1</sup>), whereas 22 were superior to the highest yielding check cultivar, BRS Esplendor (2,898 kg ha<sup>-1</sup>), confirming the high yield potential of these lines and, consequently, the possibility of them being transformed into cultivars.

The 31 selected lines had a 100-seed weight greater than that of 'BRS Esplendor' (19.6 g) and 'BRS Supremo' (20.6 g) (Table 5). However, no line had seeds larger than those of 'BRS FP403', whereas 15 lines had seeds larger than those of 'BRS Esteio', which is currently consolidated in the market as a reference due to its optimal bean grain size. Therefore, the studied lines have grains that meet high commercial standards.

Of the 31 lines, five – CNFP 19237, CNFP 19346, CNFP 19320, CNFP 19291, and CNFP 19306 – proved to be superior to the check cultivars (Table 5), showing, simultaneously, a resistance to fusarium wilt greater than that of the most resistant check cultivar BRS Expedito (2.2), a yield higher than that of the highest yielding cultivar BRS Esplendor (2,898 kg ha<sup>-1</sup>), and a 100-seed weight greater than that of cultivar BRS Esteio (23.2 g). These results are indicative of the high potential of these lines for use in multiple environment evaluations aiming at future recommendations of new cultivars. **Table 5.** Mean values based on the joint analyses of the check cultivars and of the 31 black bean (*Phaseolus vulgaris*) lines selected simultaneously for reaction to fusarium wilt (scores from 1 to 9), grain yield, and 100-seed weight, evaluated in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil, in the winter crop seasons of 2015 and 2016.

Line	Fusarium wilt	Grain yield (kg ha <sup>-1</sup> )	100-seed weight (g)
CNFP 19347 <sup>(2)</sup>	1.4	3,101	22.2
CNFP 19322 <sup>(2)</sup>	1.4	2,924	22.7
CNFP 19319 <sup>(2)</sup>	1.5	2,666	25.5
CNFP 19318 <sup>(2)</sup>	1.5	2,828	23.4
CNFP 19346 <sup>(2)</sup>	1.5	2,965	24.8
CNFP 19296 <sup>(2)</sup>	1.6	2,847	22.8
CNFP 19311 <sup>(2)</sup>	1.7	2,887	23.9
CNFP 19248 <sup>(1)</sup>	1.7	2,795	26.7
CNFP 19307 <sup>(2)</sup>	1.7	2,614	24.4
CNFP 19286 <sup>(1)</sup>	1.7	2,818	22.5
CNFP 19237 <sup>(1)</sup>	1.8	3,057	26.1
CNFP 19324 <sup>(2)</sup>	1.8	3,385	21.9
CNFP 19320 <sup>(2)</sup>	1.8	3,066	23.6
CNFP 19266 <sup>(1)</sup>	1.9	3,035	22.8
CNFP 19310 <sup>(2)</sup>	1.9	2,943	22.9
CNFP 19334 <sup>(2)</sup>	2.0	3,237	22.4
CNFP 19331 <sup>(2)</sup>	2.0	2,967	22.6
CNFP 19253 <sup>(1)</sup>	2.0	2,934	22.5
CNFP 19288 <sup>(1)</sup>	2.1	2,772	26.3
CNFP 19291 <sup>(1)</sup>	2.2	2,944	23.2
CNFP 19306 <sup>(2)</sup>	2.2	3,057	23.5
BRS Expedito(3)	2.2	2,483	23.8
CNFP 19349 <sup>(2)</sup>	2.3	3,373	24.8
CNFP 19263 <sup>(1)</sup>	2.3	3,168	24.6
CNFP 19236 <sup>(1)</sup>	2.4	2,956	24.5
CNFP 19325 <sup>(2)</sup>	2.5	3,468	23.1
CNFP 19271 <sup>(1)</sup>	2.5	3,050	23.8
CNFP 19245 <sup>(1)</sup>	2.5	2,968	22.8
CNFP 19290 <sup>(1)</sup>	2.6	3,037	22.4
CNFP 19278 <sup>(1)</sup>	2.7	3,040	22.5
BRS Esplendor <sup>(3)</sup>	2.7	2,898	19.6
CNFP 19339(2)	2.8	3,062	22.3
CNFP 19249 <sup>(1)</sup>	2.9	2,858	23.2
BRS FP403(3)	3.5	2,721	25.9
BRS Supremo <sup>(3)</sup>	6.4	2,185	20.6
BRS Esteio <sup>(3)</sup>	7.6	2,374	23.2

<sup>(1)</sup>Line originated from population 'BRS Esplendor' / 'BRS Expedito'. <sup>(2)</sup>Line originated from population 'BRS Expedito' / CNFP 15867. <sup>(3)</sup>Check cultivar.

#### Conclusions

1. There is genetic variability and a high possibility of success from selection among the evaluated black bean (*Phaseolus vulgaris*) lines for reaction to fusarium wilt, yield, and 100-seed weight, as shown by the high estimates of heritability and expected gain from selection.

2. Thirty-one lines of black bean combine high resistance to fusarium wilt, yield, and 100-seed weight, whereas the most resistant lines show a higher yield and a larger grain size, among which CNFP 19237, CNFP 19346, CNFP 19320, CNFP 19291, and CNFP 19306 stand out with mean values for these traits higher than those of the cultivars currently available on the market.

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#### References

ALVARES, R.C.; SILVA, F.C; MELO, L.C.; MELO, P.G.S.; PEREIRA, H.S. Estimation of genetic parameters and selection of high-yielding, upright common bean lines with slow seedcoat darkening. **Genetics and Molecular Research**, v.15, gmr15049081, 2016. DOI: https://doi.org/10.4238/gmr15049081.

AZEVEDO, C.V.G.; RIBEIRO, T.; SILVA, D.A. da; CARBONELL, S.A.M.; CHIORATO, A.F. Adaptabilidade, estabilidade e resistência a patógenos em genótipos de feijoeiro. **Pesquisa Agropecuária Brasileira**, v.50, p.912-922, 2015. DOI: https://doi.org/10.1590/S0100-204X2015001000007.

BATISTA, R.O.; SILVA, L.C.; MOURA, L.M.; SOUZA, M.H.; CARNEIRO, P.C.S.; CARVALHO FILHO, J.L.S.; CARNEIRO, J.E. de S. Inheritance of resistance to fusarium wilt in common bean. **Euphytica**, v.213, art.133, 2017. DOI: https://doi.org/10.1007/ s10681-017-1925-1.

CÂNDIDA, D.V.; COSTA, J.G.C.; RAVA, C.A.; CARNEIRO, M.S. Controle genético da murcha do fusário (*Fusarium oxysporum*) em feijoeiro comum. **Tropical Plant Pathology**, v.34, p.379-384, 2009.

COELHO, A.D.F.; CARDOSO, A.A.; CRUZ, C.D.; ARAÚJO, G.A. de A.; FURTADO, M.R.; AMARAL, C.L.F. Herdabilidades e correlações da produção do feijão e dos seus componentes primários, nas épocas de cultivo da primavera-verão e do verão-outono. **Ciência Rural**, v.32, p.211-216, 2002. DOI: https://doi.org/10.1590/S0103-84782002000200005.

CONAB. Companhia Nacional de Abastecimento. **Boletim da** safra de grãos: 4º levantamento: safra 2020/21. Available at: <https://www.conab.gov.br/info-agro/safras/graos/boletim-dasafra-de-graos>. Accessed on: Mar. 12 2021.

CRUZ, A.F.; SILVA, L.F.; SOUSA, T.V.; NICOLI, A.; PAULA JUNIOR, T.J. de; CAIXETA, E.T.; ZAMBOLIM, L. Molecular diversity in *Fusarium oxysporum* isolates from common bean fields in Brazil. **European Journal of Plant Pathology**, v.152, p.343-354, 2018. DOI: https://doi.org/10.1007/s10658-018-1479-7.

CRUZ, C.D. Genes: a software package for analysis in experimental statistics and quantitative genetics. Acta Scientiarum. Agronomy, v.35, p.271-276, 2013. DOI: https://doi.org/10.4025/actasciagron.v35i3.21251.

CRUZ, C.D.; REGAZZI, A.J.; CARNEIRO, P.C.S. **Modelos biométricos aplicados ao melhoramento genético**. 4.ed. Viçosa: Ed. da UFV, 2012. v.1, 514p.

EMBRAPA ARROZ E FEIJÃO. **Feijão**: dados conjunturais do feijão (área, produção e rendimento) - Brasil - 1985 a 2020. Sócioeconomia. Available at: <a href="http://www.cnpaf.embrapa.br/">http://www.cnpaf.embrapa.br/</a> apps/socioeconomia/index.htm>. Accessed on: Mar. 12 2021.

DI PRADO, P.R.C. Melhoramento genético para altos teores de ferro e zinco em feijoeiro-comum. 2017. 133p. Tese (Doutorado) - Universidade Federal de Goiás, Goiânia.

FAO. Food and Agriculture Organization of the United Nations. Faostat. 2020. Available at: <a href="http://www.fao.org/faostat/en/#data/QC">http://www.fao.org/faostat/en/#data/QC</a>. Accessed on: Mar. 12 2021.

FARIA, L.C. de; MELO, P.G.S.; PEREIRA, H.S.; WENDLAND, A.; BORGES, S.F.; PEREIRA FILHO, I.A.; DIAZ, J.L.C.; CALGARO, M.; MELO, L.C. Genetic progress during 22 years of black bean improvement. **Euphytica**, v.199, p.261-272, 2014. DOI: https://doi.org/10.1007/s10681-014-1135-z.

HENRIQUE, F.H.; CARBONELL, S.A.M.; ITO, M.F.; GONÇALVES, J.G.R.; SASSERON, G.R.; CHIORATO, A.F. Classification of physiological races of *Fusarium oxysporum* f. sp. *phaseoli* in common bean. **Bragantia**, v.74, p.84-92, 2015. DOI: https://doi.org/10.1590/1678-4499.0265.

LEITÃO, S.T.; MALOSETTI, M.; SONG, Q.; van EEUWIJK, F.; RUBIALES, D.; PATTO, M.C.V. Natural variation in Portuguese common bean germplasm reveals new sources of resistance against *Fusarium oxysporum* f. sp. *phaseoli* and resistanceassociated candidate genes. **Phytopathology**, v.110, p.633-647, 2020. DOI: https://doi.org/10.1094/PHYTO-06-19-0207-R.

MUSONI, A.; KIMANI, P.; NARLA, R.D.; BURUCHARA, R.; KELLY, J. Inheritance of fusarium wilts (*Fusarium oxysporum* F. sp. *phaseoli*) resistance in climbing beans. **African Journal of Agricultural Research**, v.5, p.399-404, 2010. DOI: https://doi.org/10.5897/AJAR.9000435.

NIÑO-SÁNCHEZ, J.; TELLO, V.; CASADO-DEL CASTILLO, V.; THON, M.R.; BENITO, E.P.; DÍAZ-MÍNGUEZ, J.M. Gene expression patterns and dynamics of the colonization of common bean (*Phaseolus vulgaris* L.) by highly virulent and weakly virulent strains of *Fusarium oxysporum*. Frontiers in **Microbiology**, v.6, art.234, 2015. DOI: https://doi.org/10.3389/fmicb.2015.00234.

OKII, D.; MUKANKUSI, C.; SEBULIBA, S.; TUKAMUHABWA, P.; TUSIIME, G.; TALWANA, H.; ODONG, T.; NAMAYANJA, A.; PAPARU, P.; NKALUBO, S.; OTIM, M.; UGEN, M.; BUAH, S.; GEPTS, P. Genetic variation, heritability estimates and GXE effects on yield traits of Mesoamerican common bean (*Phaseolus vulgaris* L) germplasm in Uganda. **Plant Genetic Resources: Characterization and Utilization**, v.16, p.237-248, 2018. DOI: https://doi.org/10.1017/s1479262117000259.

PASTOR-CORRALES, M.A.; ABAWI, G.S. Reactions of selected bean germ plasms to infection by *Fusarium oxysporum* f. sp. *phaseoli*. **Plant Disease**, v.71, p.990-993, 1987. DOI: https://doi.org/10.1094/PD-71-0990.

PEREIRA, D.G.; FARIA, L.C.; SOUZA, T.L.P.O.; MELO, L.C.; PEREIRA, H.S. Selection of parents and segregating populations of black bean resistant to fusarium wilt with high yield and seed weight. **Genetics and Molecular Research**, v.18, gmr18276, 2019. DOI: https://doi.org/10.4238/gmr18276.

PEREIRA, D.G.; FARIA, L.C.; TORGA P.P.; SOUZA, T.L.P.O.; MELO, L.C.; PEREIRA, H.S. Genetic potential of fusarium wilt-resistant elite common bean lines assessed in multiple environments. **Genetics and Molecular Research**, v.19, gmr18617, 2020. DOI https://doi.org/10.4238/gmr18617.

PEREIRA, H.S.; FARIA, L.C.; WENDLAND, A.; COSTA, J.G.C.; SOUZA, T.L.P.O.; MELO, L.C. Genotype by environment interaction for disease resistance and other important agronomic traits supporting the indication of common bean cultivars. **Euphytica**, v.214, art.12, 2018. DOI: https://doi.org/10.1007/s10681-017-2093-z.

PEREIRA, H.S.; MELO, L.C.; SOUZA, T.L.P.O. de; FARIA, L.C. de; WENDLAND, A.; MAGALDI, M.C. de S. Resistance to fusarium wilt in common bean cultivars and lines in precommercial stage. **Annual Report of the Bean Improvement Cooperative**, v.59, p.103-104, 2016.

PEREIRA, M.J.Z.; RAMALHO, M.A.P.; ABREU, A. de F.B. Inheritance of resistance to *Fusarium oxysporum* f. sp. *phaseoli* Brazilian race 2 in common bean. Scientia Agricola, v.66, p.788-792, 2009. DOI: https://doi.org/10.1590/s0103-90162009000600010.

PEREIRA, M.J.Z.; RAMALHO, M.A.P.; ABREU, A. de F.B. Reação de linhagens de feijoeiro ao fungo *Fusarium oxysporum* f. sp. *phaseoli* em condições controladas. **Ciência e Agrotecnologia**, v.35, p.940-947, 2011. DOI: https://doi.org/10.1590/S1413-70542011000500011.

RESENDE, M.D.V. de; DUARTE, J.B. Precisão e controle de qualidade em experimentos de avaliação de cultivares. **Pesquisa** Agropecuária Tropical, v.37, p.182-194, 2007.

RIBEIRO, N.D.; MAMBRIN, R.B.; STORCK, L.; PRIGOL, M.; NOGUEIRA, C.W. Combined selection for grain yield, cooking quality and minerals in the common bean. **Revista Ciência Agronômica**, v.44, p.869-877, 2013. DOI: https://doi.org/10.1590/ s1806-66902013000400025.

SANTOS, H.G. dos; JACOMINE, P.K.T.; ANJOS, L.H.C. dos; OLIVEIRA, V.Á. de; LUMBRERAS, J.F.; COELHO, M.R.;

ALMEIDA, J.A. de; ARAÚJO FILHO, J.C. de; OLIVEIRA, J.B. de; CUNHA, T.J.F. **Sistema brasileiro de classificação de solos**. 5.ed. rev. e ampl. Brasília: Embrapa, 2018. 356p.

TORGA, P.P.; MELO, P.G.S.; PEREIRA, H.S.; FARIA, L.C. de; DEL PELOSO, M.J.; MELO, L.C. Interaction of common beans cultivars of the black group with years, locations and

sowing seasons. **Euphytica**, v.189, p.239-248, 2013. DOI: https://doi.org/10.1007/s10681-012-0793-y.

TORRES, M.H.R.M.; SOUZA, T.L.P.O. de; MELO, L.C.; PEREIRA, H.S. Combining ability for resistance to Fusarium wilt and yield in black bean. **Pesquisa Agropecuária Brasileira**, v.56, e02591, 2021. DOI: https://doi.org/10.1590/S1678-3921.pab2021. v56.02591.