

Selection of carioca common bean lines for fusarium wilt resistance, yield, and grain quality

Abstract – The objective of this work was to estimate genetic parameters for the selection of carioca common bean lines resistant to fusarium wilt, with a high yield, an optimal 100-seed weight, and a desirable grain color. Two experiments were conducted during the 2019 and 2020 winter seasons in areas under a high natural pathogen infestation, using a randomized complete block design with three replicates. Sixty lines derived from the cross between cultivars BRS FC402 (resistant) and BRS FC406 (susceptible), plus four checks, were evaluated for fusarium wilt, yield, 100-seed weight, and grain color. Analyses of variance were carried out, and estimates of heritability, expected selection gains, and trait correlations were obtained. Significant differences were observed among lines for all traits. Heritability estimates were 74, 73, 91, and 52% for fusarium wilt, yield, 100-seed weight, and grain color, respectively, indicating a high selection potential. In addition, the reaction to fusarium wilt showed a negative correlation with yield (-0.60) and 100-seed weight (-0.52). Simultaneous selection identified 15 promising lines, generating gains of 13.3, 7.9, 2.4, and 3.5% for fusarium wilt, yield, 100-seed weight, and grain color, respectively. Among these lines, CNFC 20188, CNFC 20134, CNFC 20160, and CNFC 20142 combine all four desirable traits, standing out as promising candidates for the release of new cultivars resistant to fusarium wilt, with a high yield, an optimal 100-seed weight, and a desirable grain color.

Index terms: *Fusarium oxysporum* f. sp. *phaseoli*, *Phaseolus vulgaris*, heritability, selection gain.

Seleção de linhagens de feijão-carioca para resistência à murcha-de-fusário, alta produtividade e qualidade de grãos

Resumo – O objetivo deste trabalho foi estimar parâmetros genéticos para seleção de linhagens de feijão-carioca resistentes à murcha-de-fusário, com elevada produtividade, massa de 100 grãos ideal e coloração de grãos desejável. Foram conduzidos dois experimentos durante as safras de inverno de 2019 e 2020, em áreas com alta infestação natural do patógeno, tendo-se utilizado delineamento em blocos ao acaso, com três repetições. Sessenta linhagens provenientes do cruzamento entre as cultivares BRS FC402 (resistente) e BRS FC406 (susceptível), além de quatro testemunhas, foram avaliadas quanto à reação à murcha-de-fusário, produtividade, massa de 100 grãos e coloração de grãos. Foram realizadas análises de variância, tendo-se obtido estimativas de herdabilidade, ganhos esperados com a seleção e correlações entre caracteres. Observou-se diferença significativa entre as linhagens para todos os caracteres. As estimativas de herdabilidade foram 74, 73, 91 e 52% para murcha-de-fusário, produtividade, massa de 100 grãos e coloração de grãos, respectivamente, o que indica alto potencial de seleção. Além disso, a

Angelina Harmyans Ciappina 
Centro Universitário Araguaia, Goiânia, GO,
Brazil. E-mail: angelinaciappina@gmail.com

Nayana Valéria Costa 
Embrapa Arroz e Feijão, Santo Antônio de
Goiás, GO, Brazil.
E-mail: nayanavcosta@gmail.com

Leonardo Cunha Melo 
Embrapa Arroz e Feijão, Santo Antônio de
Goiás, GO, Brazil.
E-mail: leonardo.melo@embrapa.br

Thiago Lívio Pessoa Oliveira de Souza 
Limagrains Brasil S.A., Curitiba, PR, Brazil.
E-mail: tlposouza@gmail.com

Helton Santos Pereira 
Embrapa Arroz e Feijão, Santo Antônio de
Goiás, GO, Brazil.
E-mail: helton.pereira@embrapa.br

✉ Corresponding author

Received
October 17, 2025

Accepted
February 11, 2026

How to cite
CIAPPINA, A.H.; COSTA, N.V.; MELO, L.C.;
SOUZA, T.L.P.O. de; PEREIRA, H.S. Selection
of carioca common bean lines for fusarium wilt
resistance, yield, and grain quality. **Pesquisa
Agropecuária Brasileira**, v.61, e04282, 2026.
DOI: <https://doi.org/10.1590/S1678-3921.pab2026.v61.04282>.

reação à murcha-de-fusário apresentou correlação negativa com produtividade (-0,60) e massa de 100 grãos (-0,52). A seleção simultânea identificou 15 linhagens promissoras, com ganhos de 13,3, 7,9, 2,4 e 3,5% para murcha-de-fusário, produtividade, massa de 100 grãos e coloração de grãos, respectivamente. Entre estas linhagens, CNFC 20188, CNFC 20134, CNFC 20160 e CNFC 20142 combinaram os quatro caracteres desejáveis, tendo-se destacado como candidatas promissoras para o lançamento de novas cultivares resistentes à murcha-de-fusário, com elevada produtividade, massa de 100 grãos ideal e coloração de grãos desejável.

Termos para indexação: *Fusarium oxysporum* f. sp. *phaseoli*, *Phaseolus vulgaris*, herdabilidade, ganho de seleção.

Introduction

Common bean (*Phaseolus vulgaris* L.) is a legume of great economic, nutritional, and social relevance, being the main source of plant protein for many families and a key source of income for numerous farmers (Izquierdo et al., 2018). However, the production of common bean can be affected by several factors, including inadequate crop management, the use of uncertified and low-quality seeds, unfavorable climatic conditions, and the incidence of diseases (Karavidas et al., 2022).

Fusarium wilt, caused by the fungus *Fusarium oxysporum* f. sp. *phaseoli*, stands out among the most important diseases, leading to yield losses of up to 80% (Cavalheiro et al., 2023a). The infection process begins in roots, followed by colonization and obstruction of xylem vessels, resulting in leaf wilting, vascular discoloration, chlorosis, stunting, and premature plant death (Benchimol-Reis et al., 2023).

The use of resistant cultivars is the most efficient control method, as it is not only effective and cost-efficient but also environmentally sustainable (Guimarães & Souza, 2019). The development of these cultivars starts with the identification of resistant plants, followed by the assessment of the nature and magnitude of the genetic effects involved in the observed resistance. In this context, the estimation of genetic parameters is essential to quantify the available variability and to predict the expected gain from selection, guiding breeders in defining optimal selection strategies (Ramalho et al., 2012).

In the literature, several studies have reported the existence of genetic variability for reaction to fusarium wilt (Pereira et al., 2011, 2020; Torres et al., 2021, 2022, 2024; Cavalheiro et al., 2023a, 2023b). Regarding genetic control, some works have indicated that the inheritance of resistance may be oligogenic (Cândida et al., 2009; Batista et al., 2017; Cavalheiro et al., 2023a), while others suggest a polygenic basis (Torres et al., 2022, 2024; Chiwina et al., 2023), reflecting the complexity of the host-pathogen interaction.

For common bean, there are registers of high heritability estimates, ranging from 77 to 94% for resistance to fusarium wilt (Cândida et al., 2009; Pereira et al., 2011; Torres et al., 2022, 2024; Cavalheiro et al., 2023a), as well as of expected selection gains, varying from 23 to 37% (Cândida et al., 2009; Torres et al., 2022, 2024; Cavalheiro et al., 2023a). However, most estimates were calculated under controlled conditions, where resistance expression is less influenced by environmental factors. Therefore, the estimation of genetic parameters under diverse field environments remains limited, restricting the ability of breeding programs to predict selection response and to develop cultivars with a durable resistance. In this scenario, estimating genetic parameters and evaluating resistance under representative conditions are critical steps toward improving selection efficiency.

In the case of carioca-type common bean, in addition to pathogen resistance, cultivars must exhibit market-preferred traits such as a high yield, an optimal 100-seed weight, and a very light-colored beige seed coat with light brown stripes (Cavalheiro et al., 2023a). The greatest challenge for breeding programs lies in developing lines that combine all desirable traits in a single phenotype.

The objective of this work was to estimate genetic parameters for the selection of carioca common bean lines resistant to fusarium wilt, with a high yield, an optimal 100-seed weight, and a desirable grain color.

Materials and Methods

The experiments were conducted at the experimental area of Embrapa Arroz e Feijão, located in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil (16°30'17"S, 49°16'53"W, at an altitude 819 m). The local climate is Aw, a tropical savanna in the megathermal zone, according to Köppen, and

the soil is classified as a Latossolo Vermelho-Escuro (Santos et al., 2025), corresponding to a positively charged Oxisol (Soil Survey Staff, 2022). The area, used in several previous studies, is characterized by a high natural infestation of *Fusarium oxysporum* f. sp. *phaseoli* (Pereira et al., 2018, 2019, 2020; Torres et al., 2021, 2022, 2024; Cavaleiro et al., 2023a, 2023b).

To obtain the breeding lines, a segregating population was derived from the cross between the BRS FC402 and BRS FC406 carioca-type cultivars. Cultivar BRS FC402 has a high resistance to fusarium wilt and anthracnose, a high yield, and a 100-seed weight of 26 g (Melo et al., 2017). Comparatively, cultivar BRS FC406 presents a high yield, resistance to anthracnose and angular leaf spot, and a 100-seed weight of 28 g, but is susceptible to fusarium wilt (Pereira et al., 2021). The population was advanced up to the F₄ generation by the bulk method, between 2015 and 2017, in an experimental area naturally infested with the pathogen.

In the F₅ generation, during the 2018 winter season, 60 individual plants were randomly harvested from the population. The lines originating from these plants were evaluated in the first field trial in the 2019 winter season (sowing in May), in addition to four carioca-type check cultivars. Seeds harvested from this trial were used for a second experiment, in the same design, in the 2020 winter season (sowing also in May). Cultivars BRS FC402 and BRS Notável were used as resistant checks for fusarium wilt, while BRS Cometa and BRS FC406 were the susceptible checks (Melo et al., 2017; Pereira et al., 2016, 2018, 2021).

The trials were arranged in a randomized complete block design, with plots consisting of three rows, each 3.0 m long, spaced 0.50 m apart. The evaluated traits were: grain yield, 100-seed weight, reaction to fusarium wilt, and grain color after harvest. Grain yield (grams per plot), adjusted to 13% moisture, was obtained by weighing the grains harvested from all plants in the three rows, being later converted to kilogram per hectare. The trait 100-seed weight (grams) was determined by weighing a random sample of 100 seeds from each plot. Reaction to fusarium wilt was assessed 80 days after emergence using the rating scale adapted from Pastor-Corrales & Abawi (1987), which ranged from 1 to 9, representing 0, 0.1–5.0, 5.1–10, 10.1–20, 20.1–40, 40.1–60, 60.1–80, 80.1–90, and 90.1–100% susceptibility in the plot, respectively

(Torres et al., 2022). Grain color was evaluated 30 days after harvest using the scale adapted from Silva et al. (2008), which ranged from 1 (very light beige grain coat with light brown stripes) to 5 (dark beige grain coat with dark brown stripes).

The data were subjected to individual and combined analyses of variance, considering only the environment effect as fixed. Prior to both analyses of variance, the assumptions of normality of residuals and homogeneity of variances were verified. Coefficients of variation and selective accuracy were calculated to assess the informativeness of the experiments (Resende & Duarte, 2007). From the analyses of variance, the components of phenotypic variance, genetic variance, genotype $\times$ environment interaction variance, and heritability were estimated for all traits, according to the models described by Ramalho et al. (2012). Expected genetic gain was calculated for each trait using a selection intensity of 25%. In addition, the expected gain from the simultaneous selection of traits, at the same intensity, was obtained using the method of independent culling levels (Hazel & Lush, 1942), considering the following selection criteria: fusarium wilt reaction score ≤ 3 , grain color score ≤ 3 , yield above the mean of 2,089 kg ha⁻¹ of the lines, and 100-seed weight above 29 g. Phenotypic correlations among the evaluated traits were estimated as described by Ramalho et al. (2012), whereas statistical analyses were performed using the GENES software (Cruz, 2013).

Results and Discussion

The estimates of the coefficients of variation obtained in the individual analyses in 2019 and 2020 were: 20 and 18.7% for grain yield, 2.8 and 3.9% for 100-seed weight, and 20.7 and 14.9% for grain color after harvest, respectively (Table 1). These values indicate an adequate experimental precision, consistent with reports in the literature for the same traits (Pereira et al., 2021; Silva et al., 2023). Specifically for reaction to fusarium wilt, the estimates of the coefficients of variation reached higher values of 29.4 and 24.1% in each year, as expected in field evaluations due to a naturally heterogeneous pathogen distribution in the soil (Cavaleiro et al., 2023a, 2023b; Torres et al., 2021, 2022, 2024). In both years, selective accuracy estimates were high (>0.85), showing a good

experimental informativeness and strong correlation between genotypic and phenotypic values (Resende & Duarte, 2007).

The combined analysis of variance revealed significant differences among lines for all traits, indicating the presence of genetic variability. In the

case of reaction to fusarium wilt, the differences among lines confirmed the high disease pressure in the experimental area, consistent with the findings of previous studies conducted at the same site (Pereira et al., 2016, 2018, 2019, 2020; Torres et al., 2021, 2022, 2024; Cavaleiro et al., 2023a, 2023b). These results

Table 1. Summary of individual and combined analyses of variance for grain yield (GY), 100-seed weight (100SW), reaction to fusarium wilt (FOP), and grain color after harvest (GC) of carioca common bean (*Phaseolus vulgaris*) lines evaluated in 2019 and 2020, in the municipality of Santo Antônio de Goiás, in the state of Goiás, Brazil.

Individual analyses									
Source of variation	DF ⁽¹⁾	GY (kg ha ⁻¹)		100SW (g)		FOP (Score 1–9)		GC (Score 1–5)	
		MS ⁽²⁾	p-value	MS ⁽²⁾	p-value	MS ⁽²⁾	p-value	MS ⁽²⁾	p-value
2019									
Block	2	17,890	0.932	16.65	0.000	0.66	0.550	0.31	0.336
Genotype	63	1,031,682	0.000	10.76	0.000	3.92	0.000	0.97	0.000
Control (C)	3	691,322	0.047	6.73	0.000	14.89	0.000	4.53	0.000
Line (L)	59	1,050,059	0.000	7.19	0.000	2.48	0.000	0.61	0.000
C x L	1	968,550	0.053	233.42	0.000	56.39	0.000	11.57	0.000
Residual	126	253,791	-	0.63	-	1.10	-	0.29	-
CVe ⁽³⁾	-	20.0		2.8		29.4		20.7	
Selective accuracy	-	0.87		0.97		0.85		0.85	
Overall mean	-	2516		28.4		3.6		2.6	
2020									
Block	2	665,130	0.001	23.77	0.000	7.22	0.000	1.63	0.003
Genotype	63	174,287	0.002	8.73	0.000	1.84	0.000	0.46	0.005
Control (C)	3	232,515	0.063	7.53	0.001	4.11	0.000	0.67	0.061
Line (L)	59	170,926	0.002	6.25	0.000	1.35	0.000	0.44	0.008
C x L	1	197,889	0.148	158.86	0.000	23.65	0.000	0.61	0.131
Residual	126	93,318	-	1.36	-	0.46	-	0.27	-
CVe ⁽³⁾	-	18.7		3.9		24.1		14.9	
Selective accuracy	-	0.68		0.92		0.87		0.65	
Overall mean	-	1636		29.9		2.8		3.4	
Combined analyses									
Source of variation	DF ⁽¹⁾	GY		100SW		FOP		GC	
		MS ⁽²⁾	p-value	MS ⁽²⁾	p-value	MS ⁽²⁾	p-value	MS ⁽²⁾	p-value
Block/Years	4	341,510	0.144	20.2	0.000	3.9	0.008	1.0	0.032
Genotype (G)	63	653,852	0.000	17.3	0.000	4.8	0.000	0.8	0.000
Line (L)	59	641,721	0.000	11.4	0.000	3.0	0.000	0.6	0.000
Control (C)	3	770,038	0.005	9.3	0.000	15.8	0.000	3.7	0.000
C x L	1	1,021,015	0.016	388.7	0.000	76.5	0.000	8.7	0.000
Years (A)	1	74,312,483	0.000	236.4	0.015	55.5	0.005	62.9	0.000
G x A	63	552,116	0.000	2.2	0.000	1.0	0.115	0.6	0.000
L x A	59	579,263	0.000	2.0	0.000	0.8	0.379	0.5	0.000
C x A	3	153,798	0.415	4.9	0.002	3.2	0.007	1.5	0.001
(C x L) x A	1	145,423	0.435	3.6	0.059	3.5	0.035	3.4	0.000
Residual	252	173,554	-	1.0	-	0.8	-	0.3	-
CVe ⁽³⁾	-	20.1		3.4		27.7		17.2	
Overall mean	-	2076		29.2		3.2		3.0	

⁽¹⁾Degrees of freedom. ⁽²⁾Mean square. ⁽³⁾Experimental coefficient of variation.

are important since variability is a prerequisite for breeding, enabling the selection of superior genotypes for fusarium wilt resistance, optimal yield, and ideal grain size and appearance.

The effect of year was significant for all traits, with a considerable variation between means in 2019 and 2020, as follows: 2,516 and 1,636 kg ha⁻¹ for yield, 28.4 and 29.9 g for 100-seed weight, 3.6 and 2.8 for reaction to fusarium wilt, and 2.6 and 3.4 for grain color after harvest, respectively. These results suggest that, although both experiments were carried out at the same site and cropping season, climatic variations across years strongly influenced pathogen behavior and the phenotypic expression of the studied lines.

A significant interaction between lines and years was observed for yield, 100-seed weight, and grain color, which is expected for quantitative traits under a strong environmental influence (Batista et al., 2017). In contrast, reaction to fusarium wilt showed no significant line $\times$ year interaction ($p>0.05$), as reported by Pereira et al. (2019) and Torres et al. (2022), indicating that genotypes classified as superior for resistance remain stable across years and can be reliably selected. This stability may reflect a relatively uniform disease pressure in the experimental area, possibly due to the predominance of a single or limited number of *Fusarium oxysporum* f. sp. *phaseoli* races. This information is not yet known since there are still gaps regarding the distribution of the pathogen (Benchimol-Reis et al., 2023), specifically of its physiological races reported worldwide, confirming its wide genetic variability (Henrique et al., 2015). Furthermore, the consistent response observed may suggest resistance controlled by major-effect loci, as proposed by Batista et al. (2017).

In both individual and combined analyses, genetic variance accounted for a large proportion of phenotypic variance across all evaluated traits (Table 2), indicating that most of the observed variation was predominantly genetic in origin. In the joint analysis, genetic variance consistently exceeded the genotype $\times$ environment interaction variance for all traits, suggesting that the performance of the lines was only slightly influenced by environmental variation across years. Similar results have been obtained for common bean, especially regarding reaction to fusarium wilt, indicating a consistent resistance expression across environments, while highlighting genetic variance

as the main driver of phenotypic differences among lines (Torres et al., 2022; Cavaleiro et al., 2023a). Estimates of phenotypic, genetic, and environmental variance are fundamental for breeding programs, as they allow quantifying the relative contribution of genetic and environmental factors to trait expression, guiding selection strategies (Ramalho et al., 2012).

For reaction to fusarium wilt, the heritability estimates in each environment were lower than those of the combined analysis, indicating a more reliable selection when data from both years are considered jointly (Table 2). Cavaleiro et al. (2023a) also reported a high heritability of 76.6% for resistance to fusarium wilt in carioca bean. Torres et al. (2022) obtained even higher estimates of 90.9% for black bean genotypes, which tend to show higher resistance levels than carioca genotypes according to Pereira et al. (2016).

Grain yield showed a high heritability in the combined analysis (Table 2), which is particularly notable since this trait is quantitatively inherited and strongly influenced by environmental fluctuations. The variation observed between years reinforces the importance of multi-environment evaluations to improve selection accuracy for yield in common bean breeding programs (Ramalho et al., 2012). The trait 100-seed weight also presented a consistently high heritability, indicating a strong genotype-phenotype association and a greater predictability of selection response. For grain color after harvest, the estimates were moderate as in previous reports, reflecting the combined influence of genetic control and environmental effects during grain maturation and storage (Cavaleiro et al., 2023a). These results are especially relevant because they were obtained under field conditions, confirming that genetic variance remains sufficiently high to support a consistent selection across years.

Due to the expected gain from direct selection, the 15 selected lines, at a 25% selection intensity, reduced the mean score for reaction to fusarium wilt by 0.58 in the joint analysis, which corresponds to an 18% gain (Table 2). The obtained value was lower than those reported in the literature of 26.8 to 35.5% under controlled conditions (Cândida et al., 2009), likely due to the greater environmental variability in the experimental field, which provides a more realistic estimate of selection response for breeding programs. These findings are important because selection gain represents the targeted shift in the mean of a trait

toward desirable levels, maximizing the frequency of favorable alleles that control it (Ramalho et al., 2012).

Among the 60 lines evaluated, 40 had mean scores below 3 (Table 3), being classified as resistant (Pastor-Corrales & Abawi, 1987). This probably occurred because the population was advanced using the bulk method during five generations in a field naturally infested with the pathogen, which may have facilitated the elimination of the most susceptible plants in the early segregating generations. This result reflects the high standard of the studied population, which reduces the likelihood of highly expressive gains from selection, given the high frequency of favorable alleles conferring resistance.

The direct selection gains obtained for grain yield, 100-seed weight, and grain color in the joint

analysis are highly relevant for breeding programs (Table 2). This is meaningful considering that yield and grain-quality traits have a complex inheritance, being controlled by multiple genes subject to epistatic interactions, pleiotropic effects, multiple allelism, and linkage, which hinder their selection (Ramalho et al., 2012). The aforementioned result is an indicative that the obtained gains represent a greater alignment of the selected lines with market requirements, favoring product commercialization.

The gains obtained through simultaneous selection, although lower than those resulting from direct selection, were satisfactory for all traits in the joint analysis (Table 2). This favored an increase in the frequency of favorable alleles for multiple traits, which will reduce the expended time and costs of

Table 2. Estimates of the genetic parameters and simultaneous selection gain, at a 25% selection intensity, for grain yield (GY), 100-seed weight (100SW), reaction to fusarium wilt (FOP), and grain color after harvest (GC) of carioca common bean (*Phaseolus vulgaris*) lines in 2019 and 2020.

2019				
Parameter	GY (kg ha ⁻¹)	100SW (g)	FOP (Score 1–9)	GC (Score 1–5)
Genetic variance	265,422	2.19	0.46	0.12
Phenotypic variance	350,019	2.40	0.82	0.21
Heritability	75.8	91.2	55.5	55.9
Selection gain	534	1.89	-0.61	-0.30
Percent of selection gain	21.2	6.7	-17.1	-11.4
2020				
Parameter	GY (kg ha ⁻¹)	100SW (g)	FOP (Score 1–9)	GC (Score 1–5)
Genetic variance	25,869	1.63	0.30	0.06
Phenotypic variance	56,975	2.08	0.45	0.15
Heritability	45.4	78.2	66.3	40.3
Selection gain	133	1.36	-0.48	-0.22
Percent of selection gain	8.2	4.5	-16.9	-6.3
Joint analysis				
Parameter	GY (kg ha ⁻¹)	100SW (g)	FOP (Score 1–9)	GC (Score 1–5)
Genetic variance	78,027	1.74	0.37	0.05
Genotype × year interaction variance	67,618	0.16	0.01	0.04
Phenotypic variance	106,959	1.90	0.50	0.09
Heritability	72.9	91.3	74.1	51.9
Selection gain	294	1.54	-0.58	-0.40
Percent of selection gain	14.2	5.3	-18.0	-12.6
Simultaneous selection				
Parameter	GY (kg ha ⁻¹)	100SW (g)	FOP (Score 1–9)	GC (Score 1–5)
Overall mean	2,076	29.2	3.2	3.0
Mean of selected lines	2,301	29.9	2.6	2.9
Selection gain	164	0.69	-0.42	-0.10
Percent of selection gain	7.9	2.4	-13.3	-3.2

breeding programs. Similar results were reported by Cavalheiro et al. (2023a), who observed gains of 12.9% for resistance to fusarium wilt, 5.6% for grain yield, 3.4% for 100-seed weight, and 6.1% for grain color. Torres et al. (2022) found higher gains of 22.1 and 7.7% for resistance to fusarium wilt and 100-seed weight, respectively, and similar results of 6.6% for yield.

For reaction to fusarium wilt, all 60 lines were superior to the two susceptible check cultivars, BRS Cometa and BRS FC406 (Table 3), confirming the success of natural selection during generational

advancement. In relation to the BRS Notável and BRS FC402 resistant checks, 58 and 39 lines, respectively, achieved equal or lower scores.

The BRS FC402 parental cultivar carries the same quantitative trait loci (QTL) associated with resistance to fusarium wilt identified in BRS FP403 (Torres et al., 2024; Ciappina et al., 2026), a black bean cultivar recognized for its resistance to the disease. This QTL, designated FOP2.3^{403H} and located on chromosome 2, explained 40.5% of phenotypic variance (Torres et al., 2024). The studied cultivar, however, does not carry

Table 3. Means based on the joint analysis of 60 common bean lines (*Phaseolus vulgaris*) and 4 checks for grain yield (GY), 100-seed weight (100SW), reaction to fusarium wilt (FOP), and grain color after harvest (GC)⁽¹⁾.

Genotype (Line)	GY (kg ha ⁻¹)	100SW (g)	FOP (Score 1–9)	GC (Score 1–5)	Genotype (Line)	GY (kg ha ⁻¹)	100SW (g)	FOP (Score 1–9)	GC (Score 1–5)
CNFC 20153	1788	30.3	2.2	2.7	CNFC 20154	1876	29.4	3.0	3.0
CNFC 20134	2204	29.6	2.3	2.7	CNFC 20156	2593	30.0	3.0	3.3
CNFC 20151	1607	29.7	2.3	2.8	CNFC 20169	2186	29.0	3.0	3.3
CNFC 20152	1597	29.7	2.3	2.7	CNFC 20174	2412	29.6	3.0	3.1
CNFC 20165	1776	29.2	2.3	2.8	CNFC 20178	1643	32.3	3.0	3.2
CNFC 20173	2554	29.7	2.3	3.2	CNFC 20184	2408	29.5	3.0	3.2
CNFC 20135	2229	29.8	2.5	3.0	CNFC 20185	2446	29.6	3.0	3.0
CNFC 20140	2381	29.2	2.5	3.0	BRS FC402 ⁽²⁾	2121	25.1	3.0	2.5
CNFC 20144	2398	29.9	2.5	2.8	CNFC 20139	1870	29.0	3.2	3.0
CNFC 20160	2183	30.1	2.5	2.7	CNFC 20147	2125	29.3	3.2	2.7
CNFC 20168	2435	30.6	2.5	3.2	CNFC 20149	2280	32.0	3.2	2.2
CNFC 20179	2182	30.1	2.5	3.0	CNFC 20159	2119	30.0	3.2	2.8
CNFC 20181	2157	30.1	2.5	2.8	CNFC 20192	2414	29.3	3.2	2.8
CNFC 20183	1874	31.3	2.5	2.8	CNFC 20166	2203	29.2	3.3	2.7
CNFC 20188	2160	32.1	2.5	2.5	CNFC 20141	1472	30.6	3.5	3.7
CNFC 20190	2362	29.0	2.5	3.2	CNFC 20157	1941	29.2	3.5	3.2
CNFC 20136	2105	29.2	2.7	2.8	CNFC 20158	2138	29.4	3.5	3.2
CNFC 20142	2367	29.1	2.7	2.7	CNFC 20167	2295	29.1	3.7	2.7
CNFC 20145	2506	29.2	2.7	2.8	CNFC 20172	2070	28.7	3.7	3.0
CNFC 20150	2061	30.5	2.7	3.0	CNFC 20175	1966	28.8	3.7	2.5
CNFC 20155	2271	29.7	2.7	3.2	CNFC 20148	1625	29.4	3.8	2.8
CNFC 20161	2049	29.7	2.7	3.0	CNFC 20143	1710	24.4	4.0	3.5
CNFC 20189	1970	29.6	2.7	3.3	CNFC 20186	1762	28.6	4.0	3.2
CNFC 20137	2444	29.8	2.8	3.2	CNFC 20187	1742	27.5	4.0	4.0
CNFC 20138	2559	29.1	2.8	2.8	CNFC 20146	1249	27.0	4.2	3.2
CNFC 20162	2236	29.9	2.8	2.8	CNFC 20164	1831	30.9	4.2	3.5
CNFC 20163	2010	29.4	2.8	3.0	CNFC 20170	1811	32.3	4.2	3.3
CNFC 20176	1853	28.2	2.8	2.7	BRS Notável ⁽²⁾	1985	23.9	4.2	3.8
CNFC 20177	2653	29.9	2.8	3.0	CNFC 20171	1919	25.6	5.5	3.3
CNFC 20180	2629	30.0	2.8	3.0	CNFC 20191	1328	25.8	5.7	3.5
CNFC 20182	2021	28.9	2.8	3.2	BRS Cometa ⁽²⁾	1345	25.3	6.0	4.3
CNFC 20133	2307	28.9	3.0	3.2	BRS FC406 ⁽²⁾	2053	26.9	6.5	3.8

⁽¹⁾Bold values correspond to genotypes selected using the independent culling level method at a 25% selection intensity. ⁽²⁾Checks used in the experiment.

the QTLs associated with resistance in other sources, including: FOP7.1^{NS}, on chromosome 7 in the BRS Notável resistant cultivar check, explaining 45 of phenotypic variance (Cavalheiro, 2021); and FOP8.1^{EH}, on chromosome 8 in the BRS Esplendor black bean cultivar (Ciappina et al., 2026), explaining 66%. These results underscore the value of the selected lines as promising material for resistance-allele pyramiding and for the development of common bean cultivars with a stable resistance to fusarium wilt.

Regarding yield traits, 14 lines surpassed the highest-yielding check cultivar, BRS FC402, showing a high yield potential (Table 3). For 100-seed weight, the minimum value for the selected lines was 29.1 g, exceeding that of all checks and meeting the commercial standards of a grain weight above 25 g (Pereira et al., 2012).

For grain color after harvest, the selected line with the highest score of 3.0 produced lighter grains than three checks (cultivars BRS Notável, BRS Cometa, and BRS 406), indicating conformity with commercial standards (Table 3). However, the grains produced by these cultivars presented a light beige background and dark brown stripes, while the market has increasingly preferred grains with a very light beige background but light brown stripes (Cavalheiro et al., 2023a). Considering these standards, lines CNFC 20188, CNFC 20149, and CNFC 20175 stood out for color selection, with a score equal to or lower than that of the BRS FC402 resistant check cultivar, which has light beige grains with light brown stripes, in line with market values and industry preferences (Melo et al., 2017).

Overall, line CNFC 20188 stood out from the others, surpassing all checks for the four traits evaluated. Lines CNFC 20134, CNFC 20160, and CNFC 20142 also showed a high potential, outperforming cultivar BRS FC402 for fusarium wilt resistance, yield, and 100-seed weight, with a 2.7 score for grain color. In the future, it is essential to evaluate these lines across multiple environments to validate their potential for release as commercial cultivars.

The correlation estimates indicated that the scores for reaction to fusarium wilt were associated with a yield of -0.60 and 100-seed weight of -0.52. These associations were negative and significant ($p < 0.01$), showing that plants with a higher disease incidence, i.e., higher scores, exhibited lower yields. Conversely,

plants with a better health contributed to higher yields and a consequent heavier seed weight. Cavalheiro et al. (2023a) and Torres et al. (2022) also reported negative correlations of -0.58 and -0.72 between yield and reaction to fusarium wilt, respectively, which are close to the values obtained in the present study. For 100-seed weight and reaction to fusarium wilt, other authors found estimates of -0.36 (Cavalheiro et al., 2023a) and -0.28 (Torres et al., 2022), both lower than those presented here.

Conclusions

1. Carioca common bean (*Phaseolus vulgaris*) lines present genetic variability among themselves, as well as high heritability estimates and expected selection gains for reaction to fusarium wilt, grain yield, 100-seed weight, and grain color after harvest.

2. Fifteen lines combine resistance to fusarium wilt, high yield, heavier 100-seed weight, and grain color meeting market requirements, among which CNFC 20188, CNFC 20134, CNFC 20160, and CNFC 20142 are the most outstanding.

References

- 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, p.133, 2017. DOI: <https://doi.org/10.1007/s10681-017-1925-1>.
- 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>.
- BENCHIMOL-REIS, L.L.; BUENO, C.J.; CARBONELL, S.A.M.; CHIORATO, A.F. Fusarium wilt-common bean pathosystem: pathogen variability and genetic control. *Crop Science*, v.63, p.2609-2622, 2023. DOI: <https://doi.org/10.1002/csc2.21063>.
- 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.
- CAVALHEIRO, S.B. **Seleção de genótipos e mapeamento de QTLs para resistência à murcha-de-fusário em feijão carioca**. 2021. 108p. Tese (Doutorado) – Universidade Federal de Goiás, Goiânia.
- CAVALHEIRO, S.B.; MELO, L.C.; SOUZA, T.L.P.O. de; PEREIRA, H.S. Genetic parameters and selection of carioca common bean lines resistant to Fusarium wilt. *Pesquisa*

- Agropecuária Brasileira**, v.58, e03313, 2023a. DOI: <https://doi.org/10.1590/S1678-3921.pab2023.v58.03313>.
- CAVALHEIRO, S.B.; MELO, L.C.; SOUZA, T.L.P.O. de; PEREIRA, H.S. Selection of parents and segregating populations of carioca common bean resistant to Fusarium wilt. **Semina: Ciências Agrárias**, v.44, p.499-514, 2023b. DOI: <https://doi.org/10.5433/1679-0359.2023v44n2p499>.
- CHIWINA, K.; XIONG, H.; BHATTARAI, G.; DICKSON, R.W.; PHIRI, T.M.; CHEN, Y.; ALATAWI, I.; DEAN, D.; JOSHI, N.K.; CHEN, Y.; RIAZ, A.; GEPTS, P.; BRICK, M.; BYRNE, P.F.; SCHWARTZ, H.; OGG, J.B.; OTTO, K.; FALL, A.; GILBERT, J.; SHI, A. Genome-wide association study and genomic prediction of Fusarium wilt resistance in common bean core collection. **International Journal of Molecular Sciences**, v.24, art.15300, 2023. DOI: <https://doi.org/10.3390/ijms242015300>.
- CIAPPINA, A.H.; VIANELLO, R.P.; COSTA, N.V.; MARTINS, S.M.; GOMES-MESSIAS, L.M.; MELO, L.C.; SOUZA, T.L.P.O. de; PEREIRA, H.S. Identification of QTLs and validation of markers associated with Fusarium wilt response in the common bean cultivar BRS Esplendor. **Euphytica**, v.222, art.25, 2026. DOI: <https://doi.org/10.1007/s10681-025-03667-5>.
- 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>.
- GUIMARÃES, E.P.; SOUZA, T.L.P.O. de. Feijão comum: o uso de sementes certificadas na cadeia produtiva. **Seed News**, v.23, p.30-35, 2019.
- HAZEL, L.N.; LUSH, J.L. The efficiency of three methods of selection. **Journal of Heredity**, v.33, p.393-399, 1942. DOI: <https://doi.org/10.1093/oxfordjournals.jhered.a105102>.
- 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>.
- IZQUIERDO, P.; ASTUDILLO, C.; BLAIR, M.W.; IQBAL, A.M.; RAATZ, B.; CICHY, K.A. Meta-QTL analysis of seed iron and zinc concentration and content in common bean (*Phaseolus vulgaris* L.). **Theoretical and Applied Genetics**, v.131, p.1645-1658, 2018. DOI: <https://doi.org/10.1007/s00122-018-3104-8>.
- KARAVIDAS, I.; NTATSI, G.; VOUGELEKA, V.; KARKANIS, A.; NTANASI, T.; SAITANIS, C.; AGATHOKLEOUS, E.; ROPOKIS, A.; SABATINO, L.; TRAN, F.; IANNETTA, P.P.M.; SAVVAS, D. Agronomic practices to increase the yield and quality of common bean (*Phaseolus vulgaris* L.): a systematic review. **Agronomy**, v.12, art.271, 2022. DOI: <https://doi.org/10.3390/agronomy12020271>.
- MELO, L.C.; PEREIRA, H.S.; FARIA, L.C. de; SOUZA, T.L.P.O. de; WENDLAND, A.; CABRERA DÍAZ, J.L.; CARVALHO, H.W.L. de; MELO, C.L.P. de; COSTA, A.F. da; MAGALDI, M.C. de S.; COSTA, J.G.C. da. BRS FC402: high-yielding common bean cultivar with carioca grain, resistance to anthracnose and fusarium wilt. **Crop Breeding and Applied Biotechnology**, v.17, p.67-71, 2017. DOI: <https://doi.org/10.1590/1984-70332017v17n1c11>.
- PASTOR-CORRALES, M.A.; ABAWI, G.S. Reactions of selected bean germplasms 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.
- 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.
- PEREIRA, H.S.; ALMEIDA, V.M. de; MELO, L.C.; WENDLAND, A.; FARIA, L. C. de; Del PELOSO, M.J.; MAGALDI, M.C. de S. Influência do ambiente em cultivares de feijoeiro-comum em cerrado com baixa altitude. **Bragantia**, v.71, p.165-172, 2012. DOI: <https://doi.org/10.1590/S0006-87052012005000024>.
- 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 pre-commercial stage. **Annual Report of the Bean Improvement Cooperative**, v.59, p.103-104, 2016.
- PEREIRA, H.S.; SOUZA, T.L.P.O. de; FARIA, L.C. de; AGUIAR, M.S.; WENDLAND, A.; COSTA, J.G.C. da.; CABRERA DÍAZ, J.L.; MAGALDI, M.C. de S.; SOUZA, N.P. de; CARVALHO H.W.L. de; COSTA, A.F. da; MELO, C.L.P. de; ALMEIDA, V.M. de; MELO, L.C. BRS FC406: Common bean cultivar with high yield in the rainy season in central Brazil. **Functional Plant Breeding Journal**, v.3, art.10, 2021. DOI: <https://doi.org/10.35418/2526-4117/v3n2a10>.
- PEREIRA, M.J.Z.; RAMALHO, M.A.P.; ABREU, Â. 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>.
- RAMALHO, M.A.P.; ABREU, Â. de F.; SANTOS, J.B. dos; NUNES, J.A.R. **Aplicações da genética quantitativa no melhoramento de plantas autógamas**. Lavras: UFLA, 2012. 522p.
- 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.
- 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; LIMA, H.N.; MARQUES, F.A.; OLIVEIRA, J.B. de; CUNHA, T.J.F. **Sistema brasileiro de classificação de solos**. 6.ed. rev.e ampl. Brasília: Embrapa, 2025. 393p.

SILVA, F. de C.; MARTINS, S.M.; PEREIRA, H.S.; MELO, P.G.S.; MELO, L.C. Strategies for the selection of common bean lines for yield and commercial grain quality. **Pesquisa Agropecuária Brasileira**, v.58, e03403, 2023. DOI: <https://doi.org/10.1590/S1678-3921.pab2023.v58.03403>.

SILVA, G.S. da; RAMALHO, M.A.P.; ABREU, Â. de F.B.; SILVA, F.B. Genetic control of early grain darkening of carioca common bean. **Crop Breeding and Applied Biotechnology**, v.8, p.299-304, 2008.

SOIL SURVEY STAFF. **Keys to soil taxonomy**. 13th ed. Washington: USDA, NRCS, 2022. 401p.

TORRES, M.H.R.M.; SOUZA, T.L.P.O. de; FARIA, L.C. de; MELO, L.C.; PEREIRA, H.S. Genetic parameters and selection of black bean lines for resistance to fusarium wilt and yield.

Pesquisa Agropecuária Brasileira, v.57, e02846, 2022. DOI: <https://doi.org/10.1590/S1678-3921.pab2022.v57.02846>.

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>.

TORRES, M.H.R.M.; VIANELLO, R.P.; SOUZA, T.L.P.O. de; MELO, L.C.; MARTINS, S.M.; GOMES-MESSIAS, L.M.; PEREIRA, H.S. Identification of QTLs and validation of molecular markers associated with reaction to Fusarium wilt in the common bean cultivar BRS FP403. **Crop Science**, v.64, p.1729-1742, 2024. DOI: <https://doi.org/10.1002/csc2.21218>.

Author contributions

Angelina Harmyans Ciappina: data curation (equal), formal analysis (equal), investigation (equal), methodology (equal), software (equal), supervision (equal), validation (equal), visualization (equal), writing – original draft (equal), writing – review & editing (equal); **Nayana Valéria Costa**: conceptualization (equal), data curation (equal), investigation (equal), visualization (equal), writing - original draft (equal), writing - review & editing (equal); **Leornado Cunha Melo**: conceptualization (equal), data curation (equal), funding acquisition (equal), investigation (equal), project administration (equal), resources (equal), supervision (equal), validation (equal), writing - review & editing (equal); **Thiago Lívio Pessoa Oliveira de Souza**: conceptualization (equal), data curation (equal), funding acquisition (equal), investigation (equal), methodology (equal), resources (equal), supervision (equal), validation (equal), writing - review & editing (equal); **Helton Santos Pereira**: conceptualization (equal), data curation (equal), formal analysis (equal), funding acquisition (equal), investigation (equal), methodology (equal), software (equal), supervision (equal), validation (equal), visualization (equal), writing - original draft (equal), writing - review & editing (equal).

Chief editor: Edemar Corazza

Edited by: Mírian Baptista

Data availability statement

Data available upon request: research data are only available upon reasonable request to the corresponding author.

Declaration of use of AI technologies

No generative artificial intelligence (AI) was used in this study.

Conflict of interest statement

The authors declare no conflicts of interest.

Acknowledgments

To Embrapa Arroz e Feijao and its partners for providing infrastructure and labor support; to Coordenacao de Aperfeiçoamento de Pessoal de Nivel Superior (CAPES), for granting a doctoral scholarship to AHC (grant no. 88882.386276/2019-01), and to Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), for granting a technological and industrial development scholarship to NVC (grant no. 384993/2025-7), as well as for granting scholarships for technological development and innovative extension to HSP and LCM authors.

Disclaimer/Publisher's note:

The statements, opinions, and data contained in all texts published in Pesquisa Agropecuária Brasileira (PAB) are solely those of the individual author(s) and not of the journal's publisher, editor, and editorial team, who disclaim responsibility for any injury to people or property resulting from any referred ideas, methods, instructions, or products.

The mention of specific chemical products, machines, and commercial equipment in the texts published in this journal does not imply their recommendation by the publisher.