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*ARTICLE*

# Inheritance of resistance to Fusarium wilt in the carioca grain type common bean

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**Renata Oliveira Batista[1]*, Leila Lourenço Furtado[2], José Eustáquio Carneiro[3], Pedro Crescêncio Souza Carneiro[3], Alessandro Nicoli[1], Larissa Barbosa de Sousa[4] and Anderson Barbosa Evaristo[1]**

***Corresponding author:**
E-mail: renata.o.batista@gmail.com
*ORCID: 0000-0002-2082-0351*

[1] Universidade Federal dos Vales do Jequitinhonha e Mucuri, Avenida Universitária, 1000, Universitários, 38610-971, Unaí, MG, Brazil
[2] Universidade de Brasília, Campus Universitário Darcy Ribeiro, Asa Norte, 70910-900, Brasília, DF, Brazil
[3] Universidade Federal de Viçosa, Avenida Peter Henry Rolfs, s/n, Campus Universitário, 36570-900, Viçosa, MG, Brazil
[4] Universidade Federal de Uberlândia, BR 050, km 78, Campus do Glória, 38410-337, Uberlândia, MG, Brazil

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**Abstract:** *Carioca grains are the most cultivated commercial group of common bean and Fusarium oxysporum f. sp. phaseoli (Fop) is an important disease under field conditions. Genetic resistance is the most effective control strategy. Thus, our objective was to study the inheritance of Fop resistance in the carioca grain type common bean. Lines CNFC 11965 (S) and CVIII 8511 (R) were crossed to obtain* $F_1$ *and* $F_2$ *generations and backcrosses, inoculated with the isolate FOP UFV 01, and severity grades used to estimate genetic parameters. Segregation of resistant and susceptible plants in the* $F_2$ *generations and backcrosses resulted in dominant monogenic inheritance of Fop resistance. The high values of heritability emphasized the probability of success in the selection processes because environmental factors were not significant. The carioca grain line CVIII 8511 is promising, and its Fop resistance gene can be transferred to commercial cultivars of this group using the backcross method.*

**Keywords:** Phaseolus vulgaris *L.,* Fusarium oxysporum *f. sp.* phaseoli*, plant breeding, genetic control.*

## INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is a cultivated species with socioeconomic relevance and is a major source of vegetable proteins and nutrients worldwide, mainly in the Americas and parts of Africa (Ribeiro et al. 2020, Zeffa et al. 2020, FAOSTAT 2021). In Brazil, the carioca grain type accounts for approximately 70% of national bean consumption (Pereira et al. 2019); however, few commercial cultivars of this group exhibit high yield potential, upright plant architecture, and disease resistance when considered simultaneously.

Common bean hosts a wide variety of pathogens that cause significant losses in yield and affect the commercial quality of grains. Fusarium wilt is caused by the soil-borne pathogen *Fusarium oxysporum* (Schlecht.) f. sp. *phaseoli* (Kendrick and Snyder 1942) (*Fop*) and is one of the most important diseases of the common bean. Its control depends almost entirely on genetic and cultural management (Batista et al. 2016, Jha et al. 2020, Sasseron et al. 2020). Thus, introgression of resistance genes is the most effective and sustainable control strategy, in terms of both economics and ease of adoption by farmers (Miklas et al. 2006, Gonçalves-Vidigal et al. 2013, Batista et al. 2017, Leitão et al. 2020).

After the selection and recombination of genitors, the method to conduct segregating populations is a determining factor for when to obtain a new cultivar and the costs of the program (Batista et al. 2017). Thus, knowledge of genetic parameters, such as inheritance of resistance to Fusarium wilt, contributes significantly to the rapid transfer of resistance genes. In studies with the carioca grain type, Batista et al. (2016) and Batista et al. (2017) reported that common bean resistance to Fusarium wilt is dominant and governed by few major genes, and the presence of polygenes was also identified (Batista et al. 2017). The presence of dominance in the genetic control of this disease was observed in a study involving three resistant genitors from the carioca grain type in different crosses (Pereira et al. 2009).

After studying contrasting crosses, Batista et al. (2016) concluded that the segregating population derived from line CVIII 8511 was promising for bean improvement aimed toward grain yield and resistance to Fusarium wilt, with a lower frequency of alleles for growth reduction caused by the pathogen than the others parents used in the research. Therefore, introgression of resistant alleles from resistant lines into commercial cultivars is an important strategy for common bean breeding. The objective of this study was to investigate the inheritance of *Fop* resistance in the carioca grain type common bean.

## MATERIAL AND METHODS

Cultivars and elite lines of the carioca grain type common bean CNFC 11965, Dama, Pérola, Madrepérola, BRS Estilo, BRS Uai, Agronorte, Star and CVIII 8511 and the black grain type Meia Noite were evaluated for *Fop* resistance under greenhouse conditions. Isolate FOP UFV 01, which was used in this assay**,** was collected in Coimbra (Minas Gerais, Brazil) from plants of the black type grain cultivar Meia Noite, which exhibited the typical symptoms of Fusarium wilt (Pereira et al. 2013). This isolate was chosen because it was previously identified using molecular markers (Cruz et al. 2018) and has been widely characterized and applied in common bean breeding programs owing to its aggressiveness (Batista et al. 2016, Batista et al. 2017, Cruz et al. 2018, Paulino et al. 2020, Sasseron et al. 2020, Paulino et al. 2021).

The inoculum was produced on potato dextrose agar discs containing mycelia that were transferred to Petri dishes containing fresh potato dextrose agar medium. The Petri dishes were incubated in a biochemical oxygen demand medium for 14 days at 25 ± 1 °C, under a 12h photoperiod. The spore suspension was prepared 1 h before inoculation at a concentration of $10^6$ conidia $mL^{-1}$ as recommended by Pastor-Corrales and Abawi (1987).

Inoculation of the genotypes was performed according to the method of immersion of roots in conidial suspension as proposed by Pastor-Corrales and Abawi (1987). The genotypes were sown in 128-cell polystyrene trays containing the vegetable substrate Tropstrato® (Viva Verde Company, SP, Brazil) and maintained in a greenhouse for seedling germination and growth. At the V2 stage (fully expanded primary leaf), the seedlings were carefully removed from the trays, their roots were washed and 1/3 of their length was cut. Immediately after cutting, the seedling roots were immersed in a conidium suspension of the isolate FOP UFV 01 for 5 min, transplanted into plastic pots containing Tropstrato ® substrate (2.5 L), and maintained in a greenhouse at 25 ± 4 °C. The plants were irrigated daily, and 10 days after inoculation, each pot received 1.0 g of urea as a source of nitrogen.

The reaction of genotypes to Fusarium wilt was evaluated using the scale of disease severity described by Pastor-Corrales and Abawi (1987), which is based mainly on disease intensity in the shoots. According to this scale, 1 = no visible symptoms; 3 = 1% to 10% symptomatic leaves (leaves with mild wilting and chlorosis); 5 = 11% to 25% symptomatic leaves (leaves with moderate wilting and chlorosis); 7 = 26% to 50% symptomatic leaves (leaves with severe wilting and chlorosis); and 9 = dead or severely infected plants. The evaluations were performed at 15, 18, and 21 days after inoculation, and the grade of severity of Fusarium wilt (SFW) in the last evaluation was used to classify the genotypes as resistant (mean grade of 1.0 to 3.0), intermediate reaction (mean grade of 3.1 to 6.0), or susceptible (mean grade of 6.1 to 9.0) to Fusarium wilt.

Among the genotypes evaluated, line CVIII 8511 was selected as resistant (R) and line CNFC 11965 as susceptible (S), two contrasting genotypes in their reaction to *Fop*. The seeds of these genitors were sown in trays containing Tropstrato® and kept in a greenhouse for germination and seedling growth. At the V2 stage, seedlings were transplanted into 5 L pots containing soil + manure + sand mixture (3:1:1) plus 10 g of N-P-K and kept in the greenhouse at 25 ± 4 °C. The plants were irrigated daily and 20 days after transplanting, each pot received 5.0 g of urea as the nitrogen source. At the reproductive stage R5 (emergence of the first flower bud), manual hybridization without emasculation was performed between the R and S genitors to obtain $F_1$ seeds, which were harvested at the R9 stage (harvest stage) and stored. To obtain backcrosses with resistant ($BC_R$) and susceptible ($BC_S$) genitors, hybridizations were performed between $F_1$ plants and the R and S genitors, respectively. Some of the flowers were conserved to obtain $F_2$ generation seeds by self-pollination. The seeds from backcrosses, $F_1$, and $F_2$ were harvested at R9 and stored.

Plants of the genitors, $F_1$ and $F_2$ generations, and $BC_R$ and $BC_S$ backcrosses were inoculated and evaluated for their reaction to *Fop*, as previously described. The plot consisted of one pot with three plants, totaling 15 plants for each genitor (R and S), 12 plants for the $F_1$ generation, 333 plants for the $F_2$ generation, 24 plants for $BC_R$, and 25 plants for $BC_S$. The inoculation methodology and evaluation of disease severity were performed as previously described. The grades of SFW attributed individually to plants of populations $P_1$, $P_2$, $F_1$, $F_2$, $BC_R$, and $BC_S$ were used to obtain the means and variances of each population in addition to estimation of other genetic parameters of bean resistance to *Fop*.

The environmental variance ($\sigma^2_E$) was estimated based on the variances in the $P_1$ ($\sigma^2_{P1}$), $P_2$ ($\sigma^2_{P2}$), and $F_1$ ($\sigma^2_{F1}$) generations:

$$\sigma^2_E = \frac{\sigma^2_{P1} + \sigma^2_{P2} + 2\sigma^2_{F1}}{4}$$

Genotypic variance ($\sigma^2_G$) and its additive ($\sigma^2_A$) and dominance ($\sigma^2_D$) components were estimated according to Mather and Jinks (1977). From these averages, the average degree of dominance was estimated to determine the allelic interaction of resistance. The heritability in the broad ($h^2_b$) and narrow ($h^2_n$) senses was calculated according to Allard (1960). Heterobeltiosis from susceptible and resistant parents were calculated using the following formulas:

$$h_{bS} = (\overline{F1}) - (\overline{P1})$$

$$h_{bR} = (\overline{F1}) - (\overline{P2})$$

The minimum number of genes (n) determining bean resistance to *Fop* was estimated using the method described by Castle (1921):

$$n = \frac{(\overline{P1}) - (\overline{P2})^2}{8\sigma^2_{G_{F2}}}$$

The frequencies of resistant, intermediate, and susceptible (R, I, and S) plants of the genitors, hybrids, and $F_2$ generation were grouped according to the disease severity grade. Based on the frequencies of R, I, and S plants of the $F_2$ generation, hypotheses of Mendelian inheritance of resistance were tested using the chi-square test at 5% probability with the aid of the software Genética Básica On-Line (GBOL) (Cruz 2011).

## RESULTS AND DISCUSSION

The cultivars CVIII 8511, Dama, Pérola, Madrepérola, Star, BRS Uai, Meia Noite, Agronorte, CNFC 11965, and BRS Estilo presented SFW values of 1.0, 1.2, 4.3, 4.6, 5.0, 6.2, 7.1, 8.7, 8.85, and 9.0, respectively. The line CNFC 11965, selected as a susceptible genitor (S), showed an SFW grade between 7 and 9, with an average of 8.85. This line was previously identified as susceptible to *Fop* with high grades, which resulted in the death of plants (Batista et al. 2016, Batista et al. 2017). In contrast, most plants of line CVIII 8511, selected as a resistant genitor (R), showed no symptoms of the disease in our study. This line was also characterized by the lowest values of general combining ability considering the severity of Fusarium wilt, indicating a high frequency of *Fop* resistance alleles to isolate FOP UFV 01 (Batista et al. 2016).

The plants of the $F_1$ generation from the cross CNFC 11965 (S) × CVIII 8511 (R) were resistant to Fusarium wilt, whereas in the $F_2$ generation, 249 resistant and 84 susceptible plants were observed. In backcrossing with line CVIII 8511 ($BC_R$), all plants were resistant, whereas in BCs, 11 resistant and 13 susceptible plants were observed, which revealed dominance towards Fusarium wilt resistance. The frequencies of resistant and susceptible plants in the segregating $F_2$ generation support the hypothesis that the inheritance of resistance is monogenic and dominant (3:1) (Table 1).

A 3:1 ratio of resistance:susceptibility to *Fop*, was also observed by Cross et al. (2000) when evaluating the segregating $F_2$ and $F_3$ progenies derived from Durango bean. In a study with cowpeas, Musoni et al. (2010) reported the inheritance of resistance as monogenic dominant to *Fop* and recommended the use of the backcrossing method for common bean improvement. When evaluating the $F_2$ generation of the BRSMG Talismã × BRS Estilo cross, 3:1 segregation was identified for carioca bean resistance to *Fop* (Batista et al. 2017). However, in other crosses between carioca bean genotypes,

***Table 1.*** Segregation analysis for reaction to Fusarium wilt in populations (F$_1$, F$_2$, BC$_R$, and BC$_S$) from the cross between susceptible (S) CNFC 11965 and resistant (R) CVIII 8511 lines, with number of plants of each generation, expected ratio, and probability of $\chi^2$

| **Genotype** | **Number of plants** | | **Expected ratio R: S** | $\chi^2$ | **Probability** (%) ($p < 0.05$) |
|---|---|---|---|---|---|
| | **R** | **S** | | | |
| CNFC 11965 (S) | 0 | 16 | 0:1 | | |
| CVIII 8511 (R) | 14 | 0 | 1:0 | | |
| F$_1$ | 12 | 0 | 1:0 | 0.02* | - |
| F$_2$ | 249 | 84 | 3:1 | 0.00* | 92.44 |
| BCs | 11 | 13 | 1:1 | 0.17* | 68.31 |
| BC$_R$ | 25 | 0 | 1:0 | 0.01* | - |

BC: Backross.

the 57:7 hypothesis for *Fop* resistance was observed (Batista et al. 2017) contrasting with the 3:1 result of the present study. Recently, nine single-nucleotide polymorphism markers associated with oligogenic resistance to *Fop* have been identified (Leitão et al. 2020). These data suggest that when studying the same crop, the difference between genotypes confers a variability in resistance genes, and inheritance is essential for the choice of the method of conducting the improvement program.

The SFW grades of CNFC 11965 (S), CVIII 8511 (R), F$_1$, and BC$_R$ generations (0.29, 0.56, 0.25, and 0.49, respectively) varied minimally in each population, resulting in low variance values, with all plants of P$_1$ being susceptible, whereas the P$_2$, F$_1$, and BC$_R$ generations were resistant (Table 2). In contrast, F$_2$ and BC$_S$ showed two phenotypes (resistant and susceptible), resulting in increased diversity of means and consequently variances of large magnitude (9.73 and 13.46). The difference between the variances of F$_2$ and BC$_S$ is owing to the different proportions between them, in which F$_2$ showed a ratio of 3:1 (¾:¼), whereas BC$_S$ showed a proportion of 1:1 (½:½). The lowest environmental variance (0.3361) indicated experimental precision under controlled conditions. Pereira et al. (2009) and Cândida et al. (2009) analyzed the inheritance of resistance to *Fop* and observed few environmental effects on the characteristics. This implies that the phenotypic variance (9.73) is mostly due to the genotypic variance (9.39) (Table 3).

***Table 2.*** Estimates of phenotypic variance, mean, and range of the severity Fusarium wilt (SFW) in F$_1$, F$_2$, BC$_R$ and BC$_S$ generations of the cross between susceptible (S) CNFC 11965 and resistant (R) CVIII 8511 lines

| **Generation** | **Phenotypic variance** | **Mean of SFW** | **Range of SFW** |
|---|---|---|---|
| CNFC 11965 (S) | 0.29 | 8.85 | 7 - 9 |
| CVIII 8511 (R) | 0.56 | 1.90 | 1 - 3 |
| F$_1$ | 0.25 | 1.54 | 1 - 2 |
| F$_2$ | 9.73 | 3.53 | 1 - 9 |
| BC$_S$ | 13.46 | 5.37 | 1 - 9 |
| BC$_R$ | 0.49 | 1.92 | 1 - 3 |

BC: Backross.

The variance owing to dominance deviations (3.89) was a considerable part of the genotypic variance, demonstrating the dominance effect verified by the 3:1 hypothesis. It is worth noting that the dominance of this trait is in the sense of conferring resistance, as low grades indicate plants with low disease severity (Cândida et al. 2009). However, the additive variance (5.50) shows a substantial value of the allele effect in contributing to resistance. In the pathosystem Bean × *Fop*, several previous studies have reported dominance, but with expressive additive effects (Cândida et al. 2009, Pereira et al. 2009, Batista et al. 2016).

Heritability is one of the parameters that helps in the selection procedure used by plant breeders, and indicates the proportion of genotypic variance in the total phenotypic variance (Cruz et al. 2012, Ramalho et al. 2021). The high broad-sense heritability estimates of 96%, as listed in Table 3, suggest a higher proportion of genetic variation in resistance and lower influence of environmental factors on disease severity. In addition to the low evidence of environmental

***Table 3.*** Estimates of genetics parameters of segregating F$_2$ generation of the cross between the susceptible (S) CNFC 11965 and resistant (R) CVIII 8511 lines

| **Parameter** | **Values** |
|---|---|
| Phenotypic variance | 9.73 |
| Environmental variance | 0.34 |
| Genotypic variance | 9.39 |
| Additive variance | 5.50 |
| Dominance variance | 3.89 |
| Broad heritability $h^2_b$ (%) | 96.55 |
| Narrow heritability $h^2_n$ (%) | 56.57 |
| Heterosis | -3.98 |
| Heterobeltiosis relation to S genitor | -7.31 |
| Heterobeltiosis relation to R genitor | -0.65 |
| Average degree of dominance (ADD) (based on averages) | -1.19 |
| Number of genes (based on variances) | 1.45 |

effects (0.34), the divergence between the genitors CNFC 11965 (S) and CVIII 8511 (R) also contributed to an increase in the genotypic variability of the cross and, consequently, the heritability values. Considering the narrow-sense heritability that only includes the effects of additive genetic variance, we observed a value of 56%. Pereira et al. (2009) observed broad-sense heritability of 76% and narrow-sense heritability of 34% for resistance to *Fop*. Higher heritability values indicate a greater possibility of obtaining gains through selection to enhance breeding program success, indicating that backcrossing is an appropriate method.

The heterosis effect, which refers to the superior performance of the average of the $F_1$ hybrid compared to the average of its genitors, was -3.98, whereas heterobeltiosis, which is manifested when an $F_1$ is superior to each genitor, was -0.64 and -7.31 in relation to CNFC 11965 (genitor S) and CVIII 8511 (genitor R), respectively. Similarly, an average degree of dominance of -1.19 determined that the average of the heterozygotes was close to the average of the resistant genitor (grade 1). The negative values of heterosis, heterobeltiosis, and average degree of dominance corroborate the effect of resistance alleles, leading to a reduction in the value of disease (disease severity grade) and confirming that the resistance is dominant.

The screening test was relevant to confirm that line CVIII8511 was resistant to *Fop* isolate FOP UFV 01 and was consequently used in contrasting crosses to study the inheritance of resistance in a new combination with another genitor. To continue the breeding program, especially for the carioca grain type with this line, the selection should start early to advance generation of only resistant plants. The $F_{2:3}$ families should be evaluated for agronomic traits such as yield potential, upright plant architecture, and commercial quality of grains. Considering the yield potential evaluated by mean and general combining ability (Batista et al. 2016), the resistance gene of line CVIII 8511 can be easily transferred to other genotypes of the carioca grain type by backcrossing, probably without a negative influence on the frequency of favorable alleles for grain yield.

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## REFERENCES

Allard RW (1960) **Principles of plant breeding**. Wiley, New York, 485p.

Batista RO, Oliveira AMC, Silva JLO, Nicoli A, Carneiro PCS, Carneiro JES, Paula Júnior TJ and Queiroz MV (2016) Resistance to Fusarium wilt in common bean. **Crop Breeding and Applied Biotechnology 16**: 226-233.

Batista RO, Silva LC, Moura LM, Souza MH, Carneiro PCS, Carvalho Filho JLS and Carneiro JES (2017) Inheritance of resistance to fusarium wilt in common bean. **Euphytica 213**: 1-12.

Cândida DV, Costa JGC, Rava CA and Carneiro MS (2009) Controle genético da murcha do fusário (*Fusarium oxysporum*) em feijoeiro comum. **Tropical Plant Pathology 34**: 379-384.

Castle WE (1921) An improved method of estimating the number of genetic factors concerned in cases of blending inheritance. **Science 54**: 223.

Cruz AF, Silva LF, Sousa TV, Nicoli A, Paula Junior TJ, Caixeta ET and Zambolim L (2018) Molecular diversity in Fusarium oxysporum isolates from common bean fields in Brazil. **European Journal of Plant Pathology 152:** 343-354.

Cruz CD, Viana JMS, Carneiro PCS and Bhering LL (2011) **GBOL - software para ensino e aprendizagem de genética**. Editora UFV, Viçosa, 326p.

Cruz CD, Regazzi AJ and Carneiro PCS (2012) **Modelos biométricos aplicados ao melhoramento genético.** Editora UFV, Viçosa, 514p.

FAO - Food and Agriculture Organization of the United Nations (2021) Faostat: Statistical databases. Available at <https://www.fao.org/faostat/en/#data/QCL>. Accessed on December 02, 2021.

Gonçalves-Vidigal MC, Cruz AS, Lacanallo GF, Vidigal Filho PS, Sousa LL, Pacheco CMNA, Gepts P and Pastor-Corrales MA (2013) Co-segregation analysis and mapping of the anthracnose co-10 and angular leaf spot Phg-on disease-resistance genes in the common bean cultivar Ouro Negro. **Theoretical and Applied Genetics 126**: 2245-2255.

Jha UC, Bohra A, Pandey S and Parida SK (2020) Breeding, genetics, and genomics approaches for improving fusarium wilt resistance in major grain legumes. **Frontiers in Genetics 11**: 1001.

Kendrick J and Snyder W (1942) Fusarium yellows of beans. **Phytopathology 32**: 1010-1014.

Leitão ST, Malosetti M, Song Q, Eeuwijk FV, Rubiales D and Patto MCV (2020) Natural variation in Portuguese common bean germplasm reveals new sources of resistance against *Fusarium oxysporum* f. sp. *phaseoli* and resistance-associated candidate genes. **Phytopathology 110 (3)**: 633-647.

Mather K and Jinks JL (1977) **Introduction to biometrical genetics**. Cornell University Press, New York, 231p.

Miklas PN, Kelly JD, Beebe SE and Blair MW (2006) Common bean breeding for resistance against biotic and abiotic stresses: From classical to MAS breeding. **Euphytica 147**: 105-131.

Musoni A, Kimani P, Narla RD, Buruchara R and Kelly JD (2010) Inheritance of fusarium wilt (*Fusarium oxysporum* f. sp. *phaseoli*) resistance in climbing beans. **African Journal of Agricultural Research 5**: 399-404.

Pastor-Corrales MA and Abawi GS (1987) Reactions of selected bean germplasms to infection by *Fusarium oxysporum* f. sp. *phaseoli*. **Plant Disease 71**: 990-993.

Paulino JFC, Almeida CP, Bueno CJ, Song Q, Fritsche-Neto R, Carbonell SAM, Chiorato AF and Benchimol-Reis LL (2021) Genome-wide association study reveals genomic regions associated with fusarium wilt resistance in common bean. **Genes 12**: 765.

Paulino JFC, Almeida CP, Gonçalves GMC, Bueno CJ, Carbonell SAM, Chiorato AF and Bechimol-Reis LL (2020) Assessment of resistance in common bean to *Fusarium oxysporum* f. sp. *phaseoli* using different inoculation and evaluation methods. **Crop Breeding and Applied Biotechnology 20**: e337620311.

Pereira AC, Cruz MFA, Paula Junior TJ, Rodrigues FA, Carneiro JES, Vieira RF and Carneiro PCS (2013) Infection process of *Fusarium oxysporum* f. sp. *phaseoli* on resistant, intermediate and susceptible bean cultivars. **Tropical Plant Pathology 38**: 323-328.

Pereira HS, Mota APS, Rodrigues LA, Souza TLPO and Melo LC (2019) Genetic diversity among common bean cultivars based on agronomic traits and molecular markers and application to recommendation of parent lines. **Euphytica 215**: 1-16.

Pereira MJZ, Ramalho MAP and Abreu AFB (2009) Inheritance of resistance to *Fusarium oxysporum* f. sp. *phaseoli* Brazilian race 2 in common bean. **Scientia Agricola 66**: 788-792.

Ramalho MAP, Santos JB, Pinto CABP, Souza EA, Gonçalves FMA and Souza JC (2021) **Genética na Agropecuária**. UFLA, Lavras, 508p.

Ribeiro ND, Steckling SDM, Maziero SM and Klasener GR (2020) Higher-precision experimental statistics for the selection of early and upright common bean lines. **Acta Scientiarum Agronomy 42**: e42725.

Sasseron GR, Benchimol-Reis LL, Perseguini JMKC, Paulino JFC, Bajay MM, Carbonell SAM and Chiorato AF (2020) *Fusarium oxysporum* f. sp. *phaseoli* genetic variability assessed by new developed microsatellites. **Genetics and Molecular Biology 43**: e20190267.

Zeffa DM, Moda-Cirino V, Medeiros IA, Freiria GH, Santos Neto J, Ivamoto-Suzuki ST, Delfini J, Scapim CA and Gonçalves LSA (2020) Genetic progress of seed yield and nitrogen use efficiency of Brazilian carioca common bean cultivars using Bayesian approaches. **Frontiers in Plant Science 11**: 1-14.