Soybean genotypes selection with resistance to White Mold and agronomic performance from moderately resistant parents

Lorraine Cristina Polloni-Barros1*, Osvaldo Toshiyuki Hamawaki2, Lorena Polloni1, Heber Leão Silva Barros3, Tâmara Prado de Morais4, Raphael Lemes Hamawaki2, Cristiane Divina Lemes Hamawaki2, Fernando Cezar Juliatti2, Heber Leão Silva Barros3, Ana Paula Oliveira Nogueira1

1Universidade Federal de Uberlândia/Instituto de Biotecnologia, Av. Pará, 1720 – 38400-90 – Uberlândia, MG – Brasil.
2Universidade Federal de Uberlândia/Instituto de Ciências Agrárias, BR-050, km 78, s/n – 38410-337 – Uberlândia, MG – Brasil.
3Universidade Federal de Uberlândia/Instituto de Ciências Biomédicas, Av. Maranhão, 1783 – 38405-318 – Uberlândia, MG – Brasil.
4Instituto Federal de Educação, Ciência e Tecnologia do Sul de Minas Gerais, Rod. Machado-Paraguaçu, km 3, s/n – 37750-000 – Machado, MG – Brasil.

*Corresponding author <lorrainepolloni@gmail.com>

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Abstract: White Mold (WM) is a yield-limiting disease found in soybean. However, up to now no cultivars have been genetically resistant to this disease. Given this context, the present study aimed to develop superior soybean lines with resistance to WM, while maintaining other desirable agronomic traits. Two early maturing soybean cultivars (i.e., EMGOPA 316 and MG/BR 46–Conquista), moderately resistant to WM were used for biparental crosses from which the analyzed population was derived. Therefore, we assessed the resistance to WM in early generation testing of this population. Additionally, we determined the agronomic traits, genetic parameters and selection gains. From 348 F1 genotypes, 35 transgressive genotypes moderately resistant to WM were identified, amongst which 22 genotypes showed desirable agronomic traits for early cycle and grain yield. Moreover, 69 lines were selected as the most promising genotypes for each agronomic trait (i.e. based on the number of days to flowering and maturity, plant height at flowering and maturity, number of nodes on main stem at flowering and maturity, number of pods, grain yield, etc.). Among these selected lines, ten progenies emerged as the superior genotypes for grain yield and early cycle. All together, these results demonstrated that the cross between EMGOPA 316 x MG/BR 46 (Conquista) revealed promising progenies with moderate resistance to WM and/or desirable agronomic traits. Thus, these lines could be used as future resources for breeding efforts aimed at improving resistance to WM.

Keywords: Glycine max, generation analysis, genetic parameters, disease resistance, plant breeding

Introduction

Soybean [Glycine max (L.) Merr] is one of the most important commodities of international agricultural trading (Gale et al., 2019), with 361 million metric tons produced globally in 2020/21. Currently, Brazil is the world’s top producer followed by the United States and Argentina (USDA, 2021).

Importantly, one of the main factors that can limit soybean production worldwide is the occurrence of diseases (Martins et al., 2018). Soybean white mold (WM), caused by Sclerotinia sclerotiorum [Lib.] de Bary, is a yield-limiting disease found in soybean that causes reductions in productivity as high as 60% to growers when environmental conditions are favorable (Cunha et al., 2010; McCaghey et al., 2017). This necrotrophic and polyphagous fungus is capable of infecting up to 400 different species (Boland and Hall, 1994).

Currently, no cultivars genetically resistant to S. sclerotiorum are available (Kandel et al., 2018). However, several studies have demonstrated that individual cultivars can differ in susceptibility, which represent a key element for breeding programs (Juliatti et al., 2014; Kandel et al., 2018; Roth et al., 2020).

Indeed, the main objective of any breeding program is to identify among the segregating populations the few lines with the best genetic combinations, including grain quality, grain yield, adaptation and disease resistance. This decision to select the most promising lines should be vested in the earliest possible generations (Ribeiro et al., 2009). In this regard, an efficient estimation of genetic parameters such as variance components, heritability and selection gain can result in a more efficient selection process to obtain promising genotypes from segregating populations (Hamawaki et al., 2012; Silva et al., 2014).

Therefore, in this study, the main purpose was to develop a segregant soybean population, from parents with moderate resistance to WM, that exhibit favorable agronomics traits such as high yields and disease resistance. This would allow for the use of these lines in breeding programs as a source of WM resistance to accelerate the development of elite cultivars.

Materials and Methods

All the experiments were carried out throughout the seasons 2017–2019, in the municipality of Uberlândia, in the state of Minas Gerais, Brazil [19°52’ S, 48°20’ W, altitude of 805 m].

Plant materials

Two early maturing soybean cultivars moderately resistant to the fungus S. sclerotiorum [i.e. EMGOPA 316 (maturity group: 7.5) and MG/BR 46 – Conquista (maturity group: 8.1)] were used for biparental crosses from which the analyzed population was derived. The cultivar EMGOPA 316 is a result of the crossing...
between FT 79–2564 × Emgopa 302 cultivars, carried out in Goiânia, in the state of Goiás, Brazil. MG/BR 46 (Conquistã) is a cultivar resulting from the crossing of Lo 76–4484 × Numbaíra, carried out in Uberaba, in the state of Minas Gerais, Brazil.

**F₁ segregating generations**

To obtain the first generation of hybridization (F₁), parental materials were sown in four plastic pots every 4 days in a greenhouse for 4 months, starting Jan/2017, where each plastic pot contained two plants. The plants were grown in 17.5 cm × 17.5 cm × 20 cm (Height × Width × Length) plastic pots containing substrate (1/3 organic matter and 2/3 soil), with daily irrigation, and fertilized with NPK (8:28:16) every 15 days, in accordance with the manufacturer’s recommendations. A sulphur fungicide treatment was used once a week to control mildew, also in accordance with the manufacturer’s recommendations. The temperature was measured daily. During vegetative growth, at the V5 stage (Fehr and Caviness, 1977), the meristems were removed to favor the branch structure. Artificial hybridizations were made using EMGOPA 316 as the female genitor (P1) and MG/BR 46 (Conquistã) as the male genitor (P2). Temperatures ranged from 19 °C to 40 °C during the experimental period. Subsequently, to obtain the second generation (F₂), F₁ seeds were sown and the hybrids were self-polinated. Artificial hybridizations P1 × P2 were crossed again to obtain more F₂ seeds. For this experimental stage, three pots of P1, P2 and F₁ were sown every 5 days over two months, starting June/2017, and each plastic pot contained two plants. Sowing and management were carried out as previously described in this section. Confirmation of the hybridization of the F₁ plants was obtained by comparing the female parental, using the hypocotyl and flower colors as markers (Arantes, 1996; Nunes Júnior et al., 2001). The temperature inside the greenhouse during the experimental period varied from 11 °C to 40 °C.

**Genetic and phenotypic parameters**

In order to evaluate the resistance to WM, the agronomic traits and the genetic parameters of this population, five seeds from P2, F₁ and F₂ generations were sown in plastic pots (17.5 cm × 17.5 cm × 20 cm – Height × Width × Length) containing substrate (1/3 organic matter and 2/3 soil). A total of 20 P2 pots, 12 F₁ pots and 174 F₂ pots were sown in a greenhouse in Jan/2018. Two plants were placed in each plastic pot and tutored with bamboo sticks. Plants were irrigated daily. Fertilization was carried out with NPK (8:28:16) every 15 days, in accordance with the manufacturer’s recommendations. A sulphur fungicide treatment was used once a week to control mildew, in accordance with the manufacturer’s recommendations. Temperatures were measured daily, and ranged from 21 °C to 35 °C during the experimental period.

Aiming to evaluate the resistance to WM, fungal inoculum was prepared from the sclerotia in the laboratory, according to the methodology defined by Juliatti et al. (2014). The isolate was obtained from commercial fields in Jataí, in the state of Goiás – Brazil. The sclerotia were previously disinfected in 70 % ethanol and 0.5 % sodium hypochlorite diluted in sterile distilled water during 30 and 60 sec, respectively. After that, they were transferred to Petri dishes containing Potato Dextrose Agar (PDA) medium and incubated at 22 ± 3 °C in 12 h of photoperiod for the mycelium formation. For the inoculation, PDA medium plugs (8 mm in diameter) containing 5 day–old fungal mycelia were used. In the greenhouse, at the R1 stage of the plants (Fehr and Caviness, 1977), the lateral stem of the first trifoliate axillary bud was cut horizontally. An inoculation with a 200 microliter pipette tip containing fungal mycelium was given, with the mycelial side towards the plant (Chawla et al., 2013; Hüller et al., 2016). The severity of disease development was evaluated 5 days after inoculation, based on the proportion of the stem lesion length in comparison with the total stem length (both measured with a ruler). F₁ plants with greater resistance were considered transgressive segregates and were selected for further evaluation as F₂ genotypes.

The following agronomic traits were evaluated in the greenhouse: 1) number of days to flowering (NDF): corresponding to the period between emergence (VE stage) and the opening of the first flower (R1 stage); 2) number of days to maturity (NDM): corresponding to the period between the VE stage to the day on which approximately 95 % of the pods appeared to be mature (R8 stage); 3) plant height at flowering (PHF): which corresponds to the distance in centimeters measured between the soil level and the most distal inflorescence insertion on the main stem, assessed at the R1 stage; 4) plant height at maturity (PHM): which corresponds to the distance (cm) measured from the soil surface and the farthest flower bud on the main stem, evaluated at the R8 stage; 5) number of nodes on the main stem at flowering (NNF): all visible nodes were counted in the main stem at the R1 stage; 6) number of nodes on the main stem at maturity (NNM): all visible nodes were counted on the main stem at the R8 stage; 7) number of pods with 1 grain (PN1G), 8) number of pods with 2 grains (PN2G), 9) number of pods with 3 grains (PN3G) and 10) total number of pods (TNP): after harvest, all pods of each plant were counted; 11) number of seeds per pod (SNP): after harvesting and processing, seeds from each plant were counted; 12) one hundred seed weight (HSW): weight of one hundred grains of each plant, with three replications, was determined; and 13) grain yield (GY): the total weight of grains of each plant, with three replications, was also determined. The plant stage was defined according to Fehr and Caviness (1977).
Genetic parameters

The averages and variances were estimated by the phenotypic data obtained from parental (P2), hybrid (F1) and segregating populations (F2). The variances were estimated by the expression: \( \sigma^2_P = \sigma^2_P + \sigma^2_e \), in which the environmental variance \( \sigma^2_e \) was calculated using the following expression: \( \sigma^2_e = \sigma^2_{P2} \), where \( \sigma^2_{P2} \) is the phenotypic variance of P2. Genetic variance \( \sigma^2_G \) was estimated by the equation: \( \sigma^2_G = \sigma^2_{P2} - \sigma^2_e \). Broad sense heritability \( h^2 \) was calculated using the following equation:

\[
h^2 = \frac{\sigma^2_G}{\sigma^2_P} \times 100.
\]

The average degree of dominance \( K_m \) was calculated according to the equation:

\[
K_m = \frac{2F_1 - (F_1 + P_2)}{F_1 - P_2},
\]

where: \( F_1 \) is the phenotypic average of parental one, \( P_2 \) the phenotypic average of parental two, and \( F_1 \) the phenotypic average of \( F_2 \) generation. The number of genes involved in determining trait \( n \) was calculated by the equation:

\[
n = \frac{R^2(1 + 0.5K^2)}{8\sigma^2_{DF}}\]

where \( R \) is the amplitude between parent averages \( (R = F_1 - P_2) \). The selection gain rates \( GS \) were determined by the following expression: \( GS = DS \cdot h^2 \) and \( GS\% = \frac{GS}{X_o} \),

where: \( GS \) is the selection gain, \( DS \) is the differential selection \( (DS = X_o - X_o) \), is the observed average and \( X_o \) is the average of selected individuals. The genetic parameters were estimated using the GENES software program.

Resistance of transgressive segregation

To assess the resistance of the \( F_{2:3} \) genotypes, fungal inocula were prepared as aforementioned [Julia et al., 2014]. During Sept/2019, five seeds of P1, P2, BMX Desafio, BRSGO-7560 and F2:3 genotypes were sown in polystyrene trays (72-cells), containing substrate, each individual cell with one plant. A randomized complete block design was used, with three replications under greenhouse conditions. The soybean cultivars BMX Desafio and BRSGO-7560 were used as a susceptible standard. Temperatures were measured daily at the greenhouse (18 °C - 36 °C). At V2-V3 stage [Fehr and Cavinness, 1977], the main stem of the plants was cut horizontally. Inoculation was given according to Julia et al. [2014]. Subsequently, plants were kept at 22 ± 2 °C in a Bio-chemical Oxygen Demand (B.O.D) incubator with a photoperiod of 12 h. The severity of disease development was evaluated ten days after inoculation, based on the proportion of the stem lesion length in comparison with the total stem length (both measured with a ruler). The heritability and resistance trait were estimated using the GENES software program. The data for resistance trait were normalized by the equation \( \sqrt{k + x} \), and the values were compared by the Scott–Knott test \( p \leq 0.05 \). The estimation of heritability was calculated using analysis of variance (ANOVA).

Results and Discussion

Disease severity evaluations

The resistance of 348 \( F_2 \) genotypes was tested in the greenhouse inoculation test [Lateral Stem]. All genotypes exhibited different levels of symptoms and signs of WM. The severity in the \( F_2 \) generation ranged from 17 % to 100 % (Table 1). From among these genotypes, 50 lines with phenotype for resistance to WM (severity levels < 50 %) were identified (Table 2). These transgressive genotypes were tested by the Main Stem method, and all genotypes showed typical symptoms and signs of WM (severity ranged from 28 % to 75 % – Tables 1 and 2).

Soybean breeding programs for resistance to white mold (WM) still face a challenge as the majority of methods have low to moderate correlation values between field and laboratory tests for resistance [Boland and Hall, 1987; Kim and Diers, 2000; Kandel et al., 2018]. However, several studies have shown that the inoculation methods bear a strong relationship with the field results. Furthermore, compared to the cotyledon and detached leaf methods, the inoculation methods were found to be more precise [Kull et al., 2003; Koga et al., 2014; Martins et al., 2018].

The use of the Main Stem method allowed for discriminating different resistance levels of this population, based on the reactions to WM. Necrotic lesions and white fluffy mycelia were distinctly visible on the apical meristems and main stems. The development and progress of the disease occurred very

Table 1 – Severity range assigned based on the assessments of the inoculation methods of Sclerotinia sclerotiorum (%) in \( F_2 \) and \( F_{2:3} \) genotypes from the cross EMGOPA 316 × MG/BR46 (Conquista).

| Generation | \( N \) | Severities Lateral Stem method | \( N \) | Severities Main Stem method |
|------------|-------|-------------------------------|-------|-----------------------------|
|            |       | %                            |       | %                            |
| P1         | –     | –                            | 15    | 13.4 – 28.7                  |
| P2         | 40    | 15.5 – 36.6                  | 15    | 14.4 – 25.7                  |
| \( F_2 \)  | 348   | 17.6 – 100                  | –     | –                            |
| \( F_{2:3} \) | –    | –                            | 750   | 27.53 – 74.77                |
| BMX Desafio | –    | –                            | 15    | 86.0 – 96.1                  |
| BRSGO–7560 | –    | –                            | 15    | 85.6 – 92.3                  |

P1 = EMGOPA 316; P2 = MG/BR46 (Conquista); \( F_2 \) = self-pollination of \( F_2 \) plants; \( F_{2:3} \) = self-pollination of \( F_{2:3} \) plants; \( N \) = number of individuals inoculated in the Lateral Stem method; \( N \) = number of individuals inoculated in the Main Stem method.
rapidly in susceptible plants, whereas in resistant plants, disease progress was limited to the apical meristem.

As shown in Table 3, the results revealed the existence of genetic variance between soybean progenies for severity to WM ($p \leq 0.05$). Furthermore, $h^2$ was 47 %, thus indicating that most of the phenotypic variance of the resistance to WM is environmentally controlled. Nevertheless, this should not infer that genetic components are necessarily negligible. However, according to the findings of this study and others reported in the literature (Guo et al., 2008; Kim and Dias, 2000; Kandel et al., 2018), WM resistance has a low to moderate $h^2$ estimate. Kandel et al. (2018) stated that the development of resistant genotypes has proven to be difficult due to the highly polygenic nature of inheritance, and the low heritability of the trait. Thus, there is still a need to identify cultivars that sustain heritable resistance both across environments, and with multiple isolates of S. sclerotiorum.

Therefore, in order to compare the averages of the severity of WM on genotypes, the Scott–Knott test was performed. Table 2 shows the formation of two response groups to WM: group “a” with incidence scores between 45 % and 90 %, composed of 24 F$_{2:3}$ genotypes, including the soybean cultivars BMX Desafio and BRSGO–7560 as a susceptibility standard commercial cultivars; group “b” with incidence ranging from 20 % to 45 %, consisting of 26 genotypes and two commercial cultivars, EMGOPA 316 and MG/BR 46 (Conquista).

We also observed that 15 F$_{2:3}$ evaluated genotypes were classified as susceptible and 35 were moderately resistant to the WM (Table 2). The rank of each genotype varied according to each experiment (Lateral Stem method and Main Stem method) (Table 1).

### Table 2 – Averages of severity and resistance classification to white mold in transgressive genotypes from the cross EMGOPA 316 × MG/BR46 (Conquista).

| Genotypes     | Severity | Resistance Classification |
|---------------|----------|---------------------------|
| BMX DESAFIO   | 90.10 a  | S                         |
| BRSGO–7560    | 88.73 a  | S                         |
| UFUA7P1       | 74.77 a  | S                         |
| UFUA160P1     | 70.90 a  | S                         |
| UFUA155P4     | 67.20 a  | S                         |
| UFUA104P1     | 60.90 a  | S                         |
| UFUA158P1     | 60.00 a  | S                         |
| UFUA134P2     | 58.77 a  | S                         |
| UFUA148P1     | 57.30 a  | S                         |
| UFUA142P3     | 53.97 a  | S                         |
| UFUA150P1     | 53.00 a  | S                         |
| UFUA10P2      | 52.53 a  | S                         |
| UFUA78P3      | 52.43 a  | S                         |
| UFUA107P2     | 51.80 a  | S                         |
| UFUA33P1      | 51.57 a  | S                         |
| UFUA156P1     | 51.40 a  | S                         |
| UFUA7P2       | 50.53 a  | S                         |
| UFUA113P2     | 49.27 a  | MR                        |
| UFUA96P1      | 48.00 a  | MR                        |
| UFUA86P1      | 47.33 a  | MR                        |
| UFUA105P2     | 47.07 a  | MR                        |
| UFUA48P1      | 46.73 a  | MR                        |
| UFUA138P3     | 45.57 a  | MR                        |
| UFUA134P3     | 45.50 a  | MR                        |
| UFUA43P3      | 45.23 a  | MR                        |
| UFUA84P2      | 45.17 b  | MR                        |
| UFUA14P1      | 44.27 b  | MR                        |
| UFUA46P1      | 43.67 b  | MR                        |
| UFUA83P1      | 42.83 b  | MR                        |
| UFUA106P1     | 42.77 b  | MR                        |
| UFUA12P2      | 42.73 b  | MR                        |
| UFUA20P1      | 42.43 b  | MR                        |
| UFUA143P1     | 41.60 b  | MR                        |
| UFUA144P2     | 39.59 b  | MR                        |
| UFUA94P1      | 39.10 b  | MR                        |
| UFUA79P1      | 38.70 b  | MR                        |
| UFUA38P2      | 38.40 b  | MR                        |
| UFUA140P1     | 37.70 b  | MR                        |
| UFUA136P3     | 37.03 b  | MR                        |
| UFUA145P2     | 36.00 b  | MR                        |
| UFUA91P1      | 35.97 b  | MR                        |
| UFUA28P1      | 35.57 b  | MR                        |
| UFUA27P2      | 35.03 b  | MR                        |
| UFUA93P2      | 34.50 b  | MR                        |
| UFUA25P1      | 34.47 b  | MR                        |
| UFUA86P3      | 33.97 b  | MR                        |
| UFUA82P1      | 33.63 b  | MR                        |
| UFUA36P1      | 32.90 b  | MR                        |
| UFUA81P1      | 32.67 b  | MR                        |
| UFUA96P2      | 29.47 b  | MR                        |
| UFUA85P2      | 27.53 b  | MR                        |
| EMGOPA 316    | 20.53 b  | R                         |
| CONQUISTA     | 20.07 b  | R                         |

$S$ = susceptible; $MS$ = moderately susceptible; $MR$ = moderately resistant; $R$ = resistant; $\bar{X}$ = averages of severity followed by different letters are statistically different according to the Scott-Knott test ($p \leq 0.05$). 1According to Garcia and Juliatti (2012).

### Table 3 – Summary of analysis of variance and heritability ($h^2$) of segregating soybean progenies inoculated with Sclerotinia sclerotiorum from the cross EMGOPA 316 × MG/BR46 (Conquista).

| Source of Variation | DF | MS     | $F_{value}$ |
|---------------------|----|--------|-------------|
| Blocks              | 2  | 0.567878 |             |
| Genotypes           | 53 | 0.270026 | 1.899**     |
| Residual            | 106| 0.142191 |             |
| CV (%)              | 10.03 |        |             |
| $h^2$ (%)           | 47.34 |        |             |

$VS$ = variation source; $DF$ = degree of freedom; $MS$ = mean square; $CV$ = coefficient of variation; $h^2$ = heritability; **Probability (%) = 0.27.
The results herein suggested that both methods are capable of promoting the reaction of soybean genotypes to WM. Nevertheless, when the two methods were compared, despite different developmental stages, the responses of the genotypes to the pathogen varied. A number of studies have described the reproductive growth stages as the most appropriate for inoculations in controlled environments because it reproduces the natural conditions of infection (Huzar–Novakowiski and Dorrance, 2018; Peltier et al., 2009). On the other hand, other scientific evidence claims that the vegetative growth stages are more convenient as they provide results more quickly, thus accelerating the stages of the breeding program (Castro et al., 2016; Willbur et al., 2017). The presence of susceptible soybean genotypes reiterates the highly polygenic nature of the inheritance and the moderate heritability of the trait, as shown in Table 3. These findings indicate that low–intensity selection in the first generations should be used for this trait, so that in later generations the truly superior individuals or progenies may be identified.

Cycle and production from the moderately resistant genotypes

Certain traits are critical for all cultivars in order to enter the market such as high yield potential and tolerance and/or resistance to the major diseases. According to Table 4, it was possible to identify superior genotypes in this population. In addition to reporting moderate resistance to WM, the transgressive genotypes showed an early cycle (NDM = 96 days to 116 days) and, for the most part, high production levels.

Several studies have shown that partial resistance to WM in soybean has been identified, but current resistance sources of commercial cultivars are limited and do not prevent significant crop yield loss (Andrade et al., 2018; Kim and Diers, 2000). Based on the grain yield (GY), 11 transgressive genotypes stood out in this population for their higher grain yield (GY = 31.74 to 52.50 grams) (Table 4). The results demonstrated the potential of these transgressive genotypes to become resistance sources to WM in breeding programs.

These findings indicate that early selection may be efficient in soybeans, as long as it is applied with moderate intensity. Numerous studies reported favorable results with early generation testing (Friedrichs et al., 2016; Hegstad et al., 2019; Saint–Martin and Geraldi, 2002). It is noteworthy that eliminating low potential progenies is an important strategy since it enables efforts and resources to be concentrated in those with high potential for desirable traits.

Agronomic trait statistics in the segregating population

The average and variability parameters are useful statistical tools for breeders, since they allow for inferring the genetic potential of the segregating population (Bhering, 2017). As shown in Table 5, no significant average difference was found in most of the agronomic traits between the parental and the generations, but variability was identified between the traits. This variability is an important aspect since sufficient variability must be available to successfully develop high–yielding cultivars in breeding programs.

### Table 4 – Cycle and production in transgressive genotypes from the cross EMGOPA 316 × MG/BR46 (Conquista).

| Genotype | Trait | NDF | NDM | HSW | GY  |
|----------|-------|-----|-----|-----|-----|
| UFUA113P2 | NDF | 42  | 98  | 15.62 | 16.98 |
| UFUA96P1 | NDM | 47  | 108 | 21.91 | 24.82 |
| UFUA86P1 | HSW  | 44  | 98  | 17.23 | 25.84 |
| UFUA105P2 | GY  | 43  | 116 | 15.47 | 19.91 |
| UFUA48P1 | NDF | 44  | 108 | 26.01 | 38.42 |
| UFUA138P3 | NDM | 39  | 100 | 10.28 | 15.36 |
| UFUA138P3 | HSW  | 40  | 109 | 14.79 | 21.44 |
| UFUA38P2 | GY  | 41  | 100 | 13.85 | 35.11 |
| UFUA85P1 | NDF | 44  | 110 | 19.64 | 36.93 |
| UFUA94P1 | NDM | 45  | 104 | 18.82 | 35.27 |
| UFUA94P1 | HSW  | 45  | 100 | 9.69  | 13.86 |
| UFUA79P1 | GY  | 47  | 100 | 9.69  | 13.86 |
| UFUA38P2 | NDF | 47  | 103 | 7.53  | 12.34 |
| UFUA136P3 | NDM | 42  | 105 | 31.72 | 34.23 |
| UFUA136P3 | HSW  | 38  | 97  | 9.16  | 9.35  |
| UFUA145P2 | GY  | 42  | 105 | 13.94 | 25.65 |
| UFUA27P2 | NDF | 42  | 105 | 20.85 | 36.91 |
| UFUA143P1 | NDM | 42  | 101 | 5.51  | 13.44 |
| UFUA143P1 | HSW  | 40  | 109 | 16.59 | 32.35 |
| UFUA85P2 | GY  | 40  | 109 | 16.59 | 32.35 |
| UFUA93P1 | NDF | 40  | 112 | 18.19 | 33.84 |
| UFUA92P1 | NDM | 40  | 108 | 15.18 | 20.90 |
| UFUA86P3 | HSW  | 40  | 108 | 14.97 | 31.74 |
| UFUA81P1 | GY  | 48  | 112 | 14.79 | 51.92 |
| UFUA86P2 | NDF | 48  | 106 | 25.27 | 28.71 |
| UFUA85P2 | NDM | 40  | 105 | 16.13 | 16.46 |
| UFUA106P1 | HSW  | 41  | 104 | 8.64  | 16.61 |
| UFUA142P1 | GY  | 41  | 104 | 27.70 | 29.12 |

NDF = number of days to flowering; NDM = number of days to maturity; HSW = one hundred seed weight (grams); GY = grain yield (grams).
Table 5 – Estimation of averages and variability of agronomic traits obtained in the generations P2, F1 and F2 in soybean grown in greenhouse in 2018 harvested in Uberlândia, Minas Gerais State, Brazil.

| Trait         | P2  | F1  | F2  |
|---------------|-----|-----|-----|
| NDF           | 41.37 | 40.50 | 38.68 |
| NDM           | 109.05 | 109.29 | 107.03 |
| PHF           | 83.07 | 81.00 | 83.26 |
| PHM           | 115.00 | 123.25 | 123.37 |
| NNF           | 10.00 | 11.21 | 9.24 |
| NNM           | 15.27 | 17.83 | 15.63 |
| NP1G          | 2.40  | 11.66 | 5.12  |
| NP2G          | 18.00 | 33.73 | 22.44 |
| NP3G          | 36.02 | 31.75 | 23.18 |
| TNP           | 56.42 | 80.75 | 50.74 |
| NSP           | 0.26  | 0.22  | 0.23  |
| HSW           | 16.13 | 17.72 | 16.49 |
| GY            | 26.14 | 33.07 | 20.62 |

The number of nodes on the main stem is a critical yield component, since it is associated with the processes that determine the number of pods and seeds [Egli, 2005; Egli, 2013]. The average for NNF (number of nodes on the main stem at flowering) and NNM (number of nodes on the main stem at maturity) were similar among P2 (NNF = 10.00 nodes and NNM = 15.27 nodes), F1 (NNF = 11.21 nodes and NNM = 17.83 nodes), and F2 (NNF = 9.24 nodes and NNM = 15.63 nodes) (Table 5). Accordingly, a greater number of nodes on a soybean plant usually means more pods and seeds. The variable number of pods per plant (TNP), number of seeds per pod (NSP) and one hundred seed weight (HSW) are pivotal components for the yield. The average values for TNP and NSP were 56.42 pods and 2.62 seeds, respectively, for P2, 80.75 pods and 2.25 seeds for F1, and 50.74 pods and 2.36 seeds for F2 (Table 5).

It is known that the higher the number of pods with three grains (NP3G), the greater will be the yield. The P2 averages for NP1G, NP2G and NP3G were 2.4, 11.66 and 36.02 pods, respectively. These results were slightly better than those found in F1 (NP1G = 11.66; NP2G = 37.33 and NP3G = 31.37) and F2 (NP1G = 5.12; NP2G = 22.44 and NP3G = 23.18) generations, since P2 showed a lower number of NP1G and NP2G and a higher number of NP3G (Table 5).

The one hundred seed weight (HSW) trait exhibits wider variation in ranges [Xin et al., 2016]. The modern elite soybean cultivars report HSW above 18 grams [Yan et al., 2015]. We observed that HSW average values were similar in P2 (16.13 grams), F1 (17.72 grams), and F2 (16.42 grams) (Table 5). All generations revealed HSW close to the minimum limit of 18 grams.

There were differences in GY (grain yield) averages between the P2 (26.14 grams), F1 (33.07 grams), and F2 (16.42 grams) generations. The highest GY value observed for the F1 generation can be attributed to the heterosis or hybrid vigor phenomenon, since heterosis is defined as the superiority of individuals from the F1 generation compared to its parents (Fehr, 1987).

We evaluated the variance components for heritability, average degree of dominance, and number of genes to agronomic traits, which play a pivotal role for the conduct of a breeding program, as well as for decision-making. As shown in Table 5, phenotypic variance oscillated from 0.04 (SNP) to 1000.41 (TNP), and genetic variance had an amplitude from 0.03 (SNP) to 431.75 (TNP). Variation in genotype is an important tool for determining the likelihood of success in breeding selection.

The environmental variance ranged from 0.01 (SNP) to 568.66 (TNP). The predominance of genetic variance higher than the environmental variance was observed in the traits NDF, PHM, NNF, NNM, PN1G, PN2G, SNP and HSW (Table 6). Selection was favorable for these traits, as indicated by the high values of genetic variance. The phenotype reflects the genotype once the genotypic variance, in absolute values, had exceeded the environmental variance.
In the current study, the heritability for the agronomic traits ranged from zero to 82%. The traits NDF (80%), PHM (75%), NNF (67%), NNM (82%), PN1G (83%), PN2G (69%), NSP (71%) and HSW (74%) reported high $h^2$ estimates (Table 6). These findings indicate that most of the phenotypic variance of these agronomic traits were genetically controlled. Moreover, high heritability makes the selection of individuals in the initial generations of self-fertilization viable. In agreement with our results, various studies have described high $h^2$ for the same traits studied herein (Leite et al., 2016; Volpato et al., 2019; Zhang et al., 2015). In turn, PHF (41%), TNP (43%), and GY (29%) presented lower $h^2$ values (Table 6), which means that the selection for these traits should be practiced in advanced generations (trials conducted in various locations and years) for the identification of superior genotypes as a result of the influence of the environmental interaction.

We also investigated the selection gain once it had highlighted the superior individuals in a base population. Furthermore, the variable is considered an efficient guide to breeders. In order to obtain selection gain, the existence of genetic variability inside a base population is necessary, and the magnitude of the effects that it masks (environmental components and interaction) (Hamawaki et al., 2012). With the objective of selecting the best individuals, considering the reduction in the vegetative cycle and increase in the other traits, a selection intensity of 20% was applied in various locations and years) for the identification of superior genotypes as a result of the influence of the environmental interaction.

Finally, it was possible to select ten genotypes for the traits NDM and GY (UFUA22P2, UFUA70P3, UFUA74P1, UFUA103P2, UFUA104P1, UFUA114P2, UFUA116P1, UFUA117P1, UFUA130P1 and UFUA142P3). These genotypes were the most productive and early cycle. The individuals UFUA9P1, UFUA11P2, UFUA12P1, UFUA12P2, UFUA13P1, UFUA22P2, UFUA24P2, UFUA34P2, UFUA40P2, UFUA43P3, UFUA44P3, UFUA52P3, UFUA53P2, UFUA63P1, UFUA65P1, UFUA104P1, UFUA110P2, UFUA117P1, UFUA126P2, and UFUA132P2 showed an earlier cycle. However, they are not among the most productive genotypes. The genotypes UFUA38P1 and UFUA48P1 were selected most for the traits, except for the NDM, SNP, and GY (Tables 7 and 8).
Table 7 – Selected individuals in F2 soybean population from the cross EMGOPA 316 × MG/BR46 (Conquista), average of selected individuals (Xsi) and selection gain (GSi) of agronomic characters.

| SI      | NDM | SI | NNF | SI | NNM |
|---------|-----|----|-----|----|-----|
| UFUA1P1 | 92  | UFUA7P1 | 100 | UFUA2P1 | 155 | UFUA2P1 | 12  |
| UFUA5P2 | 93  | UFUA11P3 | 74  | UFUA2P2 | 144 | UFUA14P1 | 11  |
| UFUA8P3 | 97  | UFUA29P2 | 84  | UFUA7P1 | 145 | UFUA19P1 | 13  |
| UFUA9P1 | 97  | UFUA31P1 | 104 | UFUA13P1 | 180 | UFUA20P1 | 11  |
| UFUA9P2 | 97  | UFUA33P1 | 95  | UFUA33P1 | 158 | UFUA21P1 | 11  |
| UFUA9P3 | 97  | UFUA36P1 | 106 | UFUA34P1 | 141 | UFUA22P1 | 12  |
| UFUA11P2 | 92  | UFUA38P1 | 98  | UFUA36P1 | 143 | UFUA25P1 | 12  |
| UFUA12P1 | 96  | UFUA38P2 | 102 | UFUA36P2 | 174 | UFUA29P1 | 11  |
| UFUA12P2 | 96  | UFUA42P1 | 118 | UFUA38P1 | 151 | UFUA29P2 | 11  |
| UFUA13P1 | 97  | UFUA42P2 | 116 | UFUA42P2 | 152 | UFUA31P1 | 12  |
| UFUA16P2 | 97  | UFUA46P2 | 104 | UFUA42P2 | 152 | UFUA33P1 | 11  |
| UFUA20P2 | 97  | UFUA46P3 | 98  | UFUA43P1 | 152 | UFUA33P1 | 11  |
| UFUA21P2 | 97  | UFUA47P2 | 94  | UFUA44P1 | 147 | UFUA34P1 | 12  |
| UFUA22P2 | 97  | UFUA48P1 | 107 | UFUA44P1 | 165 | UFUA34P2 | 11  |
| UFUA24P2 | 97  | UFUA49P1 | 98  | UFUA45P1 | 141 | UFUA36P1 | 13  |
| UFUA34P2 | 97  | UFUA49P2 | 103 | UFUA46P1 | 157 | UFUA38P1 | 12  |
| UFUA40P2 | 93  | UFUA51P1 | 101 | UFUA47P2 | 140 | UFUA40P1 | 11  |
| UFUA43P3 | 97  | UFUA53P1 | 97  | UFUA48P1 | 151 | UFUA40P2 | 15  |
| UFUA44P3 | 97  | UFUA58P1 | 111 | UFUA49P2 | 150 | UFUA41P1 | 13  |
| UFUA46P2 | 93  | UFUA58P2 | 106 | UFUA51P1 | 140 | UFUA42P1 | 12  |
| UFUA52P3 | 99  | UFUA62P2 | 100 | UFUA51P2 | 153 | UFUA42P1 | 12  |
| UFUA53P2 | 92  | UFUA64P2 | 96  | UFUA52P1 | 162 | UFUA45P1 | 15  |
| UFUA55P1 | 97  | UFUA66P1 | 97  | UFUA53P1 | 146 | UFUA48P1 | 11  |
| UFUA55P2 | 97  | UFUA66P2 | 105 | UFUA54P1 | 162 | UFUA57P1 | 14  |
| UFUA63P1 | 96  | UFUA68P1 | 100 | UFUA58P1 | 142 | UFUA58P1 | 13  |
| UFUA64P1 | 97  | UFUA68P2 | 106 | UFUA58P2 | 157 | UFUA58P2 | 12  |
| UFUA64P2 | 97  | UFUA69P2 | 106 | UFUA61P1 | 151 | UFUA60P1 | 12  |
| UFUA65P1 | 97  | UFUA70P2 | 98  | UFUA64P1 | 156 | UFUA69P1 | 12  |
| UFUA65P2 | 97  | UFUA70P3 | 104 | UFUA66P2 | 153 | UFUA73P1 | 11  |
| UFUA65P3 | 97  | UFUA72P2 | 108 | UFUA66P4 | 150 | UFUA75P1 | 13  |
| UFUA67P2 | 97  | UFUA74P1 | 94  | UFUA68P1 | 147 | UFUA76P1 | 14  |
| UFUA69P2 | 97  | UFUA76P1 | 95  | UFUA69P1 | 144 | UFUA77P1 | 11  |
| UFUA70P3 | 95  | UFUA78P2 | 95  | UFUA70P1 | 143 | UFUA78P1 | 12  |
| UFUA72P2 | 93  | UFUA85P1 | 112 | UFUA70P2 | 150 | UFUA78P2 | 12  |
| UFUA74P1 | 97  | UFUA91P1 | 102 | UFUA73P1 | 150 | UFUA80P1 | 11  |
| UFUA79P2 | 97  | UFUA93P1 | 97  | UFUA80P2 | 162 | UFUA82P1 | 14  |
| UFUA79P3 | 97  | UFUA95P1 | 94  | UFUA85P1 | 141 | UFUA85P1 | 12  |
| UFUA86P2 | 97  | UFUA98P1 | 94  | UFUA85P1 | 141 | UFUA85P1 | 12  |
| UFUA102P2 | 97  | UFUA99P1 | 104.5 | UFUA105P1 | 166 | UFUA91P1 | 12  |
| UFUA103P2 | 97  | UFUA103P2 | 94  | UFUA107P2 | 156 | UFUA92P1 | 14  |
| UFUA104P1 | 97  | UFUA107P2 | 115 | UFUA110P1 | 145 | UFUA93P1 | 12  |
| UFUA104P2 | 97  | UFUA110P1 | 110 | UFUA112P2 | 145 | UFUA94P1 | 12  |
| UFUA110P2 | 93  | UFUA111P1 | 105.5 | UFUA112P3 | 161 | UFUA96P1 | 12  |
| UFUA111P2 | 97  | UFUA114P2 | 96  | UFUA113P2 | 145 | UFUA96P3 | 12  |
| UFUA114P2 | 95  | UFUA116P1 | 104 | UFUA113P3 | 169 | UFUA98P1 | 13  |
| UFUA116P1 | 97  | UFUA116P2 | 98  | UFUA115P1 | 153 | UFUA99P1 | 12  |
| UFUA117P1 | 92  | UFUA120P2 | 96  | UFUA116P2 | 148 | UFUA101P1 | 12  |
| UFUA120P2 | 93  | UFUA121P3 | 105 | UFUA117P1 | 141 | UFUA106P1 | 13  |
| UFUA120P3 | 93  | UFUA122P1 | 95  | UFUA123P1 | 141 | UFUA109P2 | 12  |
| UFUA121P2 | 97  | UFUA122P2 | 101 | UFUA124P1 | 143 | UFUA110P1 | 13  |
| UFUA126P2 | 93  | UFUA124P1 | 103 | UFUA129P2 | 143 | UFUA111P1 | 14  |
| UFUA128P1 | 97  | UFUA124P3 | 108 | UFUA134P1 | 165 | UFUA117P1 | 12  |
| UFUA128P2 | 97  | UFUA131P1 | 100 | UFUA135P1 | 141 | UFUA123P1 | 13  |
| UFUA128P3 | 96  | UFUA135P1 | 103 | UFUA135P2 | 142 | UFUA125P1 | 13  |
| Continue... | | | | | | |
## Table 7 – Continuation.

|        |         |         |         |         |         |         |         |
|--------|---------|---------|---------|---------|---------|---------|---------|
| UFUA130P1 | UFUA135P3 | UFUA136P1 | UFUA137P2 | UFUA127P2 | UFUA137P1 | UFUA120P1 | UFUA139P1 |
| 97     | 105     | 142     | 12      | 20      | 19      | 22      |
| UFUA130P2 | UFUA136P2 | UFUA139P2 | UFUA131P1 | UFUA130P1 | UFUA139P2 | UFUA130P1 | UFUA139P2 |
| 97     | 100     | 158     | 12      | 20      | 19      | 22      |
| UFUA130P3 | UFUA137P3 | UFUA140P2 | UFUA131P1 | UFUA130P1 | UFUA140P2 | UFUA131P1 | UFUA139P2 |
| 94     | 97      | 151     | 13      | 22      | 21      | 20      |
| UFUA132P2 | UFUA138P1 | UFUA148P2 | UFUA138P3 | UFUA138P3 | UFUA140P2 | UFUA138P3 | UFUA140P2 |
| 97     | 96      | 153     | 12      | 20      | 19      | 22      |
| UFUA135P3 | UFUA138P3 | UFUA149P1 | UFUA141P2 | UFUA141P2 | UFUA141P2 | UFUA141P2 | UFUA141P2 |
| 96     | 101     | 172     | 13      | 21      | 21      | 20      |
| UFUA136P2 | UFUA139P2 | UFUA152P2 | UFUA141P2 | UFUA141P2 | UFUA141P2 | UFUA141P2 | UFUA141P2 |
| 97     | 114     | 142     | 13      | 21      | 21      | 20      |
| UFUA137P2 | UFUA140P2 | UFUA153P3 | UFUA141P2 | UFUA141P2 | UFUA141P2 | UFUA141P2 | UFUA141P2 |
| 97     | 95      | 181     | 13      | 21      | 21      | 20      |
| UFUA138P1 | UFUA137P1 | UFUA154P3 | UFUA142P1 | UFUA142P1 | UFUA142P1 | UFUA142P1 | UFUA142P1 |
| 95     | 103     | 141     | 12      | 21      | 21      | 20      |
| UFUA142P2 | UFUA155P2 | UFUA156P2 | UFUA144P1 | UFUA144P1 | UFUA144P1 | UFUA144P1 | UFUA144P1 |
| 95     | 98      | 151     | 12      | 21      | 21      | 20      |
| UFUA145P3 | UFUA156P1 | UFUA157P3 | UFUA158P1 | UFUA158P1 | UFUA158P1 | UFUA158P1 | UFUA158P1 |
| 93     | 97      | 154     | 13      | 21      | 21      | 20      |
| UFUA146P3 | UFUA157P1 | UFUA157P2 | UFUA159P1 | UFUA159P1 | UFUA159P1 | UFUA159P1 | UFUA159P1 |
| 93     | 111     | 146     | 12      | 23      | 23      | 22      |
| UFUA147P3 | UFUA157P2 | UFUA157P3 | UFUA157P2 | UFUA157P2 | UFUA157P2 | UFUA157P2 | UFUA157P2 |
| 96     | 104     | 151     | 12      | 23      | 23      | 22      |
| UFUA155P2 | UFUA162P3 | UFUA163P3 | UFUA162P3 | UFUA162P3 | UFUA162P3 | UFUA162P3 | UFUA162P3 |
| 96     | 93      | 149     | 12      | 19      | 19      | 18      |
| UFUA157P3 | UFUA162P3 | UFUA163P2 | UFUA162P3 | UFUA162P3 | UFUA162P3 | UFUA162P3 | UFUA162P3 |
| 95     | 94      | 144     | 12      | 19      | 19      | 18      |
| SI     | GS%     | SI     | GS%     | SI     | GS%     | SI     | GS%     |
| 95.59  | 14.68   | 101.62 | 9.04    | 151.59 | 17.32   | 12.25  | 21.90   |

SI = Selected individuals; NDF = number of days to flowering; NDM = number of days to maturity; PHF = plant height at flowering; PHM = plant height at maturity; NNF = number of nodes on the main stem at flowering; NNM = number of nodes on the main stem at maturity; $\bar{x}_s$ = mean of selected individuals; $\bar{G}_s$% = selection gain.

## Table 8 – Selected individuals in F$_2$ soybean population from the cross EMGOPA 316 × MG/BR46 (Conquista), average of selected individuals ($\bar{x}_s$) and selection gains (GS%) of agronomic characters.

|        |         |         |         |         |         |         |
|--------|---------|---------|---------|---------|---------|---------|
| UFUA2P1 | UFUA2P2 | UFUA2P3 | UFUA2P4 | UFUA2P5 | UFUA2P6 | UFUA2P7 |
| 8      | 12      | 8       | 9       | 11      | 11      | 12      |
| UFUA10P1 | UFUA10P2 | UFUA10P3 | UFUA10P4 | UFUA10P5 | UFUA10P6 | UFUA10P7 |
| 10     | 12      | 8       | 9       | 11      | 11      | 12      |
| UFUA10P1 | UFUA10P2 | UFUA10P3 | UFUA10P4 | UFUA10P5 | UFUA10P6 | UFUA10P7 |
| 10     | 12      | 8       | 9       | 11      | 11      | 12      |
| UFUA10P1 | UFUA10P2 | UFUA10P3 | UFUA10P4 | UFUA10P5 | UFUA10P6 | UFUA10P7 |
| 10     | 12      | 8       | 9       | 11      | 11      | 12      |
| UFUA10P1 | UFUA10P2 | UFUA10P3 | UFUA10P4 | UFUA10P5 | UFUA10P6 | UFUA10P7 |
| 10     | 12      | 8       | 9       | 11      | 11      | 12      |
| UFUA10P1 | UFUA10P2 | UFUA10P3 | UFUA10P4 | UFUA10P5 | UFUA10P6 | UFUA10P7 |
| 10     | 12      | 8       | 9       | 11      | 11      | 12      |
| UFUA10P1 | UFUA10P2 | UFUA10P3 | UFUA10P4 | UFUA10P5 | UFUA10P6 | UFUA10P7 |
| 10     | 12      | 8       | 9       | 11      | 11      | 12      |
| UFUA10P1 | UFUA10P2 | UFUA10P3 | UFUA10P4 | UFUA10P5 | UFUA10P6 | UFUA10P7 |
| 10     | 12      | 8       | 9       | 11      | 11      | 12      |
| UFUA10P1 | UFUA10P2 | UFUA10P3 | UFUA10P4 | UFUA10P5 | UFUA10P6 | UFUA10P7 |
| 10     | 12      | 8       | 9       | 11      | 11      | 12      |
Table 8 – Continuation.

| UFUA77P1 | 26 | UFUA80P1 | 44 | UFUA77P1 | 144 | UFUA82P2 | 2.57 | UFUA80P2 | 20.05 | UFUA83P2 | 35.11 |
|----------|----|----------|----|----------|----|----------|----|----------|----|----------|----|
| UFUA80P2 | 9  | UFUA82P1 | 76 | UFUA82P2 | 165 | UFUA83P2 | 2.72 | UFUA84P1 | 19.56 | UFUA84P1 | 35.40 |
| UFUA81P1 | 15 | UFUA83P2 | 33 | UFUA84P1 | 97  | UFUA84P1 | 2.66 | UFUA87P1 | 21.55 | UFUA86P3 | 32.35 |
| UFUA82P1 | 34 | UFUA86P3 | 35 | UFUA85P1 | 79  | UFUA84P2 | 2.56 | UFUA91P2 | 20.38 | UFUA87P1 | 42.24 |
| UFUA89P1 | 24 | UFUA89P1 | 35 | UFUA89P1 | 145 | UFUA87P1 | 2.65 | UFUA95P1 | 24.09 | UFUA87P2 | 67.43 |
| UFUA93P1 | 12 | UFUA94P1 | 78 | UFUA91P1 | 82  | UFUA90P1 | 2.66 | UFUA96P1 | 21.91 | UFUA89P2 | 31.35 |
| UFUA94P1 | 18 | UFUA96P1 | 35 | UFUA92P1 | 89  | UFUA90P2 | 2.66 | UFUA96P2 | 25.27 | UFUA90P1 | 42.36 |
| UFUA96P1 | 8  | UFUA98P1 | 35 | UFUA94P1 | 128 | UFUA93P1 | 2.78 | UFUA97P3 | 19.84 | UFUA92P1 | 42.62 |
| UFUA101P2 | 10 | UFUA101P1 | 41 | UFUA95P1 | 94  | UFUA94P1 | 2.54 | UFUA110P1 | 30.71 | UFUA93P1 | 33.51 |
| UFUA105P1 | 13 | UFUA105P1 | 46 | UFUA96P1 | 110 | UFUA97P3 | 2.74 | UFUA114P1 | 36.16 | UFUA94P1 | 52.50 |
| UFUA107P1 | 12 | UFUA106P2 | 41 | UFUA98P1 | 82  | UFUA98P1 | 2.56 | UFUA116P3 | 21.48 | UFUA95P2 | 29.94 |
| UFUA113P2 | 8  | UFUA110P1 | 63 | UFUA99P1 | 118 | UFUA102P2 | 2.57 | UFUA112P1 | 26.06 | UFUA96P3 | 36.96 |
| UFUA113P3 | 11 | UFUA114P1 | 50 | UFUA105P1 | 127 | UFUA104P1 | 2.64 | UFUA132P2 | 27.78 | UFUA97P3 | 61.40 |
| UFUA114P1 | 10 | UFUA115P1 | 39 | UFUA107P1 | 85  | UFUA105P1 | 2.72 | UFUA133P1 | 25.55 | UFUA99P1 | 35.66 |
| UFUA115P1 | 17 | UFUA117P1 | 35 | UFUA110P1 | 146 | UFUA108P2 | 2.66 | UFUA134P1 | 24.88 | UFUA103P2 | 38.77 |
| UFUA117P1 | 11 | UFUA125P1 | 47 | UFUA114P1 | 92  | UFUA113P1 | 2.63 | UFUA134P1 | 28.37 | UFUA104P1 | 31.11 |
| UFUA119P1 | 18 | UFUA130P2 | 33 | UFUA115P1 | 81  | UFUA119P1 | 2.57 | UFUA138P1 | 20.09 | UFUA104P3 | 29.86 |
| UFUA119P2 | 10 | UFUA131P2 | 34 | UFUA117P1 | 122 | UFUA122P3 | 2.55 | UFUA140P1 | 31.72 | UFUA106P2 | 51.59 |
| UFUA122P2 | 8  | UFUA132P2 | 35 | UFUA119P1 | 115 | UFUA122P3 | 2.65 | UFUA141P1 | 20.04 | UFUA112P2 | 32.56 |
| UFUA122P3 | 8  | UFUA134P1 | 42 | UFUA125P1 | 114 | UFUA124P3 | 2.55 | UFUA144P1 | 19.29 | UFUA114P2 | 37.24 |
| UFUA125P1 | 11 | UFUA137P2 | 60 | UFUA131P1 | 98  | UFUA128P4 | 2.55 | UFUA144P2 | 27.70 | UFUA131P1 | 38.46 |
| UFUA130P2 | 8  | UFUA139P1 | 50 | UFUA132P2 | 89  | UFUA132P2 | 2.71 | UFUA145P1 | 24.72 | UFUA116P1 | 32.02 |
| UFUA132P2 | 14 | UFUA140P1 | 39 | UFUA134P1 | 99  | UFUA137P2 | 2.61 | UFUA147P3 | 22.67 | UFUA117P1 | 30.78 |
| UFUA134P1 | 19 | UFUA141P1 | 40 | UFUA137P2 | 96  | UFUA138P1 | 2.64 | UFUA148P1 | 22.29 | UFUA127P2 | 33.07 |
| UFUA134P3 | 15 | UFUA141P2 | 40 | UFUA139P1 | 99  | UFUA142P1 | 2.60 | UFUA148P2 | 21.24 | UFUA128P4 | 38.35 |
| UFUA144P1 | 12 | UFUA142P1 | 59 | UFUA140P2 | 75  | UFUA142P3 | 2.71 | UFUA148P3 | 19.80 | UFUA130P1 | 34.25 |
| UFUA144P1 | 11 | UFUA143P1 | 35 | UFUA141P2 | 77  | UFUA144P1 | 2.55 | UFUA152P2 | 35.55 | UFUA137P1 | 31.49 |
| UFUA144P1 | 20 | UFUA144P1 | 35 | UFUA142P1 | 102 | UFUA145P2 | 2.63 | UFUA153P3 | 23.60 | UFUA138P1 | 39.77 |
| SF  | 13.98 | SF  | 45.55 | SF  | 103.17 | SF  | 2.63 | SF  | 24.18 | SF  | 40.15 |
| G%  | 114.80 | G%  | 71.47 | G%  | 44.58 | G%  | 8.08 | G%  | 34.92 | G%  | 28.25 |

SI = Selected individuals; PN1G = number of pods with 1 grain; PN2G = number of pods with 2 grains; TNP = total number of pods; SNP = number of seeds per pod; HSW = one hundred seed weight; GY = grain yield; $\bar{x}$ = mean of selected individuals; GSI = selection gain.

As for the genotypes analyzed, the cross between EMGOPA 316 × MG/BR (Conquista) proved to be promising in the identification of WM resistance. The 22 lines selected with moderate resistance to WM also possessed additional desirable agronomic traits (i.e. early cycle and higher yield). The combination of early maturity with higher yield potential in a genotype that possesses WM tolerance can be decisive for the success of a cultivar among soybean growers.

Additionally, ten superior soybean lines were also selected due to their desirable traits of early maturity and higher yield. The significant expansion of off-season corn cultivation throughout the Cerrado region in Brazil has dramatically shortened the maturity time of the soybean cultivars preferred by growers. Therefore, the early maturity trait is now considered a prerequisite for a soybean genotype to be regarded as a promising line.

The data and findings presented in this work may be of substantial value and use by breeding programs seeking to improve soybean lines with WM resistance. Moreover, soybean lines that associate disease resistance with other desirable agronomic traits can considerably accelerate the development of elite cultivars. While the molecular mechanisms responsible for the resistance trait remain to be explored, further assessments of advanced generations of this population using molecular techniques can unveil regions in the genome linked to WM resistance.
Authors’ Contributions

Conceptualization: Polloni-Barros, L.C.; Juliatti, F.C.; Nogueira, A.P.O.; Hamawaki, O.T. Data acquisition: Polloni-Barros, L.C.; Polloni, L.; Barros, H.L.S.; Morais, T.P. Data analysis: Polloni-Barros, L.C.; Juliatti, F.C.; Nogueira, A.P.O.; Hamawaki, R.L.; Hamawaki, C.D.L. Design of methodology: Polloni-Barros, L.C.; Juliatti, F.C.; Nogueira, A.P.O.; Hamawaki, O.T. Software development: Polloni–Barros, L.C.; Nogueira, A.P.O. Writing and editing: Polloni–Barros, L.C.; Polloni, L.; Barros, H.L.S.; Juliatti, F.C.; Nogueira, A.P.O.

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