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Research Article

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

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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 F_2 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 × 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 interrnational 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 (18°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 Goias, Brazil. MG/BR 46 (Conquista) is a cultivar resulting from the crossing of Lo 76–4484 × Numbaíra, carried out in Uberaba, in the state of Minas Gerais, Brazil.

F_1 and segregating generations

To obtain the first generation of hybridization (F_1), 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 (Conquista) as the male genitor (P2). Temperatures ranged from 19 ºC to 40 °C during the experimental period. Subsequently, to obtain the second generation (F_2), F_1 seeds were sown and the hybrids were self–pollinated. Artificial hybridizations P1 × P2 were crossed again to obtain more F_1 seeds. For this experimental stage, three pots of P1, P2 and F_1 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 F_1 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 ºC to 40 ºC.

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, F_1 and F_2 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 F_1 pots and 174 F_2 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 ºC to 35 ºC 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). F_2 plants with greater resistance were considered transgressive segregates and were selected for further evaluation as $F_{2:3}$ 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 (F_1) and segregating populations (F_2). The variances were estimated by the expression: $\sigma_P^2 = \sigma_G^2 + \sigma_E^2$, in which the environmental variance (σ_E^2) was calculated using the following expression: $\sigma_E^2 = \sigma_{P2}^2$, where σ_{P2}^2 is the phenotypic variance of P2. Genetic variance (σ_G^2) was estimated by the equation: $\sigma_G^2 = \sigma_P^2 - \sigma_E^2$. Broad sense heritability (h^2) was calculated using the following equation:

$$h^2 = \frac{\sigma_G^2}{\sigma_P^2} \times 100 .$$

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

$$Km = \frac{2\bar{F}1 - (\bar{P}1 + \bar{P}2)}{\bar{P}1 - \bar{P}2} ,$$

where: $\bar{P}1$ is the phenotypic average of parental one, $\bar{P}2$ the phenotypic average of parental two, and $\bar{F}1$ the phenotypic average of F_1 generation. The number of genes involved in determining trait (n) was calculated by the equation:

$$n = \frac{R^2(1 + 0.5K^2)}{8\sigma_{GF2}^2} ,$$

where R is the amplitude between parent averages ($R = \bar{P}1 - \bar{P}2$). The selection gain rates (GS %) were determined by the following expression: $GS = DS \, . \, h^2$ and

$$GS\% = \frac{GS}{\bar{X}_O} ,$$

where: GS is the selection gain, DS is the differential selection ($DS = \bar{X}_S - \bar{X}_O$), is the observed average and $\bar{X}_S$ 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 (Juliatti et al., 2014). During Sept/2019, five seeds of P1, P2, BMX Desafio, BRSGO-7560 and $F_{2:3}$ 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 Caviness, 1977), the main stem of the plants was cut horizontally. Inoculation was given according to Juliatti 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 $\sqrt{x+k}$, 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[1]	Severities Lateral Stem method	N[2]	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_1 plants; $F_{2:3}$ = self-pollination of F_2 plants. N[1] = number of individuals inoculated in the Lateral Stem method; N[2] = number of individuals inoculated in the Main Stem method.

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

Genotypes	$\bar{X}$	Resistance Classification[1]
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	45.53 a	MR
UFUA34P3	45.50 a	MR
UFUA58P1	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	39.50 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 ($p \leq 0.05$). [1]According to Garcia and Juliatti (2012).

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).

Based on the severity of the reactions to WM, the genotypes were classified as immune (absence of the disease), highly resistant (HR = 0 to 11 %), resistant (R = 12 to 24 %), moderately resistant (MR = 25 to 50 %) and susceptible (S > 50 %) (Garcia et al., 2012) (Table 2). As for the Main Stem method, our results revealed that the parental materials were classified as resistant. Corroborating our data, Garcia and Juliatti (2012) and Martins et al. (2018) also considered the genotype EMGOPA 316 and MG/BR 46 (Conquista) as resistant and MR, respectively, when compared to other commercial cultivars.

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 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).

VS	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).

	Trait					Trait			
Genotype	NDF	NDM	HSW	GY	Genotype	NDF	NDM	HSW	GY
UFUA113P2	42	98	15.62	16.98	UFUA94P1	45	104	18.82	52.50
UFUA96P1	47	108	21.91	24.82	UFUA79P1	45	100	9.69	13.86
UFUA86P1	44	98	17.23	25.84	UFUA38P2	47	103	7.53	12.34
UFUA105P2	43	116	15.47	17.94	UFUA140P1	42	105	31.72	34.23
UFUA48P1	44	108	26.01	28.42	UFUA136P3	38	97	9.16	9.35
UFUA138P3	39	100	10.28	15.36	UFUA145P2	44	107	10.52	12.62
UFUA134P3	40	109	14.79	21.44	UFUA91P1	42	105	17.15	42.36
UFUA34P3	41	100	13.85	15.39	UFUA28P1	42	105	13.94	25.65
UFUA58P1	44	110	19.64	36.93	UFUA27P2	42	105	20.85	36.91
UFUA84P2	39	106	7.23	8.89	UFUA93P2	39	101	5.51	13.44
UFUA14P1	44	111	14.54	32.42	UFUA25P1	40	112	18.19	33.84
UFUA46P1	43	100	20.16	22.16	UFUA86P3	40	109	16.59	32.35
UFUA83P1	44	108	16.33	35.11	UFUA82P1	40	108	15.18	20.80
UFUA106P1	41	109	13.91	20.59	UFUA36P1	48	112	14.97	31.74
UFUA12P2	43	96	11.01	11.97	UFUA81P1	42	109	14.79	51.92
UFUA20P1	43	106	8.81	17.28	UFUA96P2	40	106	25.27	28.71
UFUA143P1	41	104	8.64	16.61	UFUA85P2	40	105	16.13	16.46
UFUA144P2	41	106	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, F_1 and F_2 in soybean grown in greenhouse in 2018 harvested in Uberlândia, Minas Gerais State, Brazil.

Trait	P2		F_1		F_2	
	$\bar{X}$	σ^2	$\bar{X}$	σ^2	$\bar{X}$	σ^2
NDF	41.37	3.27	40.50	6.26	38.68	16.53
NDM	109.05	100.25	109.29	14.38	107.03	32.35
PHF	83.07	95.45	81.00	128.09	83.26	161.86
PHM	115.00	92.51	123.25	287.93	123.37	380.63
NNF	10.00	1.33	11.21	2.34	9.24	4.10
NNM	15.27	1.53	17.83	9.79	15.63	8.63
NP1G	2.40	5.42	11.66	80.23	5.12	33.33
NP2G	18.00	63.69	37.33	291.36	22.44	208.38
NP3G	36.02	345.66	31.75	274.71	23.18	311.09
TNP	56.42	568.66	80.75	986.98	50.74	1000.41
NSP	2.62	0.11	2.25	0.05	2.36	0.04
HSW	16.13	6.69	17.72	10.38	16.49	26.62
GY	26.14	97.53	33.07	236.68	20.62	138.99

P2 = MG/BR 46 (Conquista); F_1 = P1 × P2; F_2 = self-pollination of F_1 plants; NDF = number of days to flowering; NDM = number of days to maturity; PHF = plant height at flowering (cm); PHM = plant height at maturity (cm); NNF = number of nodes on the main stem at flowering; NNM = number of nodes on the main stem at maturity; NP1G = number of pods with 1 grain; NP2G = number of pods with 2 grains; NP3G = number of pods with 3 grains; TNP = total number of pods; NSP = number of seeds per pod; HSW = one hundred seed weight (grams); GY = grain yield (grams); $\bar{X}$ = average; σ^2 = variance.

The maturity time was analyzed by means of NDF (number of days to flowering) and NDM (number of days to maturity) of P2, F_1 and F_2. These agronomic traits are quite relevant to the choice of the cultivar, as they allow for better planning of planting and harvesting activities. Our results demonstrated that P2 reported an NDF of 41.37 days and NDM of 109.05 days. F_1 (NDF = 40.50 days; NDM = 109.29 days) and F_2 (NDF = 38.68 days and NDM = 107.03 days) showed similar results in comparison to P2 (Table 5), thus revealing that the genotypes can be classified as an early cycle cultivar. The maturity time of a cultivar is a factor that interferes with the final severity of the WM disease. According to Yang et al. (1999), early cycle cultivars are more resistant to *S. sclerotiorum* due to the shorter flowering period, which lowers predisposition to infection by ascospores. According to our data, Arantes (1996) described a similar maturity time to MG/BR 46 (Conquista) (NDF = 48 to 54 days and NDM = 109 to 140 days).

Other agronomic traits evaluated were PHF (plant height at flowering) and PHM (plant height at maturity), which are important factors that avoid lodging in the plants. The averages of PHM in P2 (115.00 cm), F_1 (123.25 cm) and F_2 (123.37 cm) generations were close to the recommended values (Table 5). According to Andrade et al. (2018), another important point to consider is whether plants are at an ideal height, without the occurrence of lodging, thereby allowing good air circulation and quicker drying within the crop canopy. It is worth noting that these factors can significantly reduce the intensity of WM (Andrade et al., 2018).

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), F_1 (NNF = 11.21 nodes and NNM = 17.83 nodes), and F_2 (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 F_1, and 50.74 pods and 2.36 seeds for F_2 (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, 18.0 and 36.02 pods, respectively. These results were slightly better than those found in F_1 (NP1G = 11.66; NP2G = 37.33 and NP3G = 31.37) and F_2 (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), F_1 (17.72 grams), and F_2 (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), F_1 (33.07 grams), and F_2 (20.62 grams) generations. The highest GY value observed for the F_1 generation can be attributed to the heterosis or hybrid vigor phenomenon, since heterosis is defined as the superiority of individuals from the F_1 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 conduction 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.

Table 6 – Estimation of phenotypic variance, genotype variance, environmental variance, broad–sense heritability, average degree of dominance and number of genes of agronomic traits obtained in the generations P2, F_1 and F_2 in soybean grown in greenhouse in 2018 harvested in Uberlândia,in the state of Minas Gerais, Brazil.

Trait Parameters	Parameters					
	σ^2_P	σ^2_G	σ^2_E	h^2 (%)	*Km*	n
NDF	16.53	13.26	3.26	80.24	–0.56	5.89
NDM	32	–	100	–	–1.12	–
PHF	161.86	66.40	95.45	41.03	–0.54	7.95
PHM	380.63	288.12	92.51	75.69	–2.49	5.15
NNF	4.10	2.773	1.33	67.53	66.66	5.45
NNM	8.63	7.09	1.54	82.18	–54.06	4.51
PN1G	33.33	27.90	5.42	83.72	1.05	10.75
PN2G	208.38	144.69	63.69	69.43	0.85	7.311
PN3G	311.09	–	345.66	–	–0.40	–
TNP	1000.41	431.75	568.66	43.15	2.14	8.67
NSP	0.04	0.03	0.01	71.60	0.63	6.96
HSW	26.62	19.92	6.69	74.84	–7.71	6.71
GY	138.99	41.46	97.53	29.82	–9.77	15.74

NDF = number of days to flowering; NDM = number of days to maturity; PHF = plant height at flowering (cm); PHM = plant height at maturity (cm); NNF = number of nodes on the main stem at flowering; NNM = number of nodes on the main stem at maturity; PN1G = number of pods with 1 grain; PN2G = number of pods with 2 grains; PN3G = number of pods with 3 grains; TNP = total number of pods; NSP = number of seeds per pod; HSW = one hundred seed weight (grams); GY = grain yield (grams); σ^2_P = phenotypic variance; σ^2_G = genotype variance; σ^2_E = environmental variance; h^2 = broad–sense heritability (%); *Km* = average degree of dominance; n = number of genes in determining trait.

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 and 69 individuals were chosen (Tables 7 and 8).

The selection gain for NDM returned one of the lowest individual gains (14 %), and the variation was between 92 and 97 days, with an average of 95.59 days (Table 7). This result demonstrates that the individuals selected have an earlier cycle when compared to the P2 parent, which attracts the interest of the current market. The traits with higher selection gains were PN1G (114 %) and PN2G (71 %), followed by TNP (44 %) (Table 8).

A number of MR transgressive genotypes were selected as superior individuals in this base population (Tables 7 and 8). The MR genotypes that stood out in terms of agronomic traits were: UFUA113P2, UFUA96P1, UFUA48P1, UFUA138P3, UFUA58P1, UFUA84P2, UFUA14P1, UFUA46P1, UFUA106P1, UFUA12P2, UFUA143P1, UFUA94P1, UFU38P2, UFUA140P1, UFUA136P3, UFUA145P2, UFUA28P1, UFUA27P2, UFUA36P1, UFUA81P1, UFUA96P2, UFUA85P2. Most of the MR transgressive genotypes presented an earlier cycle and good HSW and GY, which corroborated our data in Table 4. These findings highlight the great potential of these genotypes to become cultivars that will satisfy the requirements of the market.

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, UFUA20P2, 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 F_2 soybean population from the cross EMGOPA 316 × MG/BR46 (Conquista), average of selected individuals ($\bar{X}_S$) and selection gain (*GS*%) of agronomic characters.

SI	NDM	SI	PHF	SI	PHM	SI	NNF	SI	NNM
UFUA1P1	92	UFUA7P1	100	UFUA2P1	155	UFUA2P1	12	UFUA2P1	19
UFUA5P2	93	UFUA11P3	74	UFUA2P2	144	UFUA14P1	11	UFUA2P2	18
UFUA8P3	97	UFUA29P2	84	UFUA7P1	145	UFUA19P1	13	UFUA7P1	18
UFUA9P1	97	UFUA31P1	104	UFUA13P1	180	UFUA20P1	11	UFUA10P1	21
UFUA9P2	97	UFUA33P1	95	UFUA33P1	158	UFUA21P1	11	UFUA11P3	25
UFUA9P3	97	UFUA36P1	106	UFUA34P1	141	UFUA22P1	12	UFUA22P1	21
UFUA11P2	92	UFUA38P1	98	UFUA36P1	143	UFUA25P1	12	UFUA23P1	19
UFUA12P1	96	UFUA38P2	102	UFUA36P2	174	UFUA29P1	11	UFUA25P1	18
UFUA12P2	96	UFUA42P1	118	UFUA38P1	151	UFUA29P2	11	UFUA28P1	18
UFUA13P1	97	UFUA42P2	116	UFUA42P1	162	UFUA31P1	12	UFUA29P1	21
UFUA16P2	97	UFUA46P2	104	UFUA42P2	152	UFUA32P1	11	UFUA29P2	18
UFUA20P2	97	UFUA46P3	98	UFUA43P1	152	UFUA33P1	11	UFUA31P1	22
UFUA21P2	97	UFUA47P2	94	UFUA44P1	147	UFUA34P1	12	UFUA33P1	23
UFUA22P2	96	UFUA48P1	107	UFUA44P2	165	UFUA34P2	11	UFUA34P1	20
UFUA24P2	97	UFUA49P1	98	UFUA45P1	141	UFUA36P1	13	UFUA36P1	18
UFUA34P2	97	UFUA49P2	103	UFUA46P1	157	UFUA38P1	12	UFUA38P1	22
UFUA40P2	93	UFUA51P1	101	UFUA47P2	140	UFUA40P1	11	UFUA40P1	22
UFUA43P3	97	UFUA53P1	97	UFUA48P1	151	UFUA40P2	15	UFUA42P1	20
UFUA44P3	93	UFUA58P1	111	UFUA49P2	150	UFUA41P1	13	UFUA42P2	21
UFUA46P2	93	UFUA58P2	106	UFUA51P1	140	UFUA42P1	12	UFUA43P1	19
UFUA52P3	99	UFUA62P2	100	UFUA51P2	153	UFUA42P2	13	UFUA45P1	20
UFUA53P2	92	UFUA64P2	96	UFUA52P1	162	UFUA45P1	15	UFUA48P1	19
UFUA55P1	97	UFUA66P1	97	UFUA53P1	146	UFUA48P1	11	UFUA52P1	19
UFUA55P2	97	UFUA66P2	105	UFUA54P2	162	UFUA57P1	14	UFUA58P2	20
UFUA63P1	96	UFUA68P1	100	UFUA58P1	142	UFUA58P1	13	UFUA73P1	22
UFUA64P1	97	UFUA68P2	106	UFUA58P2	157	UFUA58P2	12	UFUA75P1	21
UFUA64P2	97	UFUA69P2	106	UFUA61P2	151	UFUA60P1	12	UFUA78P1	21
UFUA65P1	97	UFUA70P2	98	UFUA64P1	156	UFUA69P1	12	UFUA80P1	19
UFUA65P2	97	UFUA70P3	104	UFUA66P2	153	UFUA73P1	11	UFUA80P2	19
UFUA65P3	97	UFUA72P2	108	UFUA66P4	150	UFUA75P1	13	UFUA82P1	21
UFUA67P2	97	UFUA74P1	94	UFUA68P1	147	UFUA76P1	14	UFUA84P1	19
UFUA69P2	97	UFUA76P1	95	UFUA69P1	144	UFUA77P1	11	UFUA85P1	19
UFUA70P3	95	UFUA78P2	95	UFUA70P1	143	UFUA78P1	12	UFUA85P2	19
UFUA72P2	93	UFUA85P1	112	UFUA70P2	150	UFUA78P2	12	UFUA87P1	19
UFUA74P1	93	UFUA91P1	102	UFUA73P1	150	UFUA80P1	11	UFUA87P2	19
UFUA79P2	97	UFUA93P1	97	UFUA80P2	162	UFUA82P1	14	UFUA89P1	20
UFUA79P3	97	UFUA95P1	94	UFUA85P1	141	UFUA85P1	12	UFUA90P1	19
UFUA86P2	97	UFUA98P1	94	UFUA104P3	162	UFUA85P2	12	UFUA91P1	19
UFUA102P2	97	UFUA99P1	104.5	UFUA105P1	166	UFUA91P1	12	UFUA92P1	21
UFUA103P2	97	UFUA103P2	94	UFUA107P2	156	UFUA92P1	14	UFUA95P1	19
UFUA104P1	97	UFUA107P2	115	UFUA110P1	145	UFUA93P1	12	UFUA96P1	21
UFUA104P2	97	UFUA110P1	110	UFUA112P2	145	UFUA94P1	12	UFUA98P1	19
UFUA110P2	93	UFUA111P1	105.5	UFUA112P3	161	UFUA96P1	12	UFUA99P1	20
UFUA111P2	97	UFUA114P2	96	UFUA113P2	145	UFUA96P3	12	UFUA101P2	19
UFUA114P2	95	UFUA116P1	104	UFUA113P3	169	UFUA98P1	13	UFUA105P1	20
UFUA116P1	97	UFUA116P2	98	UFUA115P1	153	UFUA99P1	12	UFUA106P1	21
UFUA117P1	92	UFUA120P2	96	UFUA116P2	148	UFUA101P1	12	UFUA107P2	20
UFUA120P2	93	UFUA121P3	105	UFUA117P1	141	UFUA106P1	13	UFUA109P2	20
UFUA120P3	93	UFUA122P1	95	UFUA123P1	141	UFUA109P2	12	UFUA110P1	20
UFUA121P2	97	UFUA122P2	101	UFUA124P1	143	UFUA110P1	13	UFUA113P1	20
UFUA126P2	93	UFUA124P1	103	UFUA129P2	143	UFUA111P1	14	UFUA115P1	23
UFUA128P1	97	UFUA124P3	108	UFUA134P1	165	UFUA117P1	12	UFUA117P1	23
UFUA128P2	97	UFUA131P1	100	UFUA135P1	141	UFUA123P1	13	UFUA125P1	22
UFUA128P3	96	UFUA135P1	103	UFUA135P2	142	UFUA125P1	13	UFUA134P1	21

Continue...

Table 7 – Continuation.

UFUA130P1	97	UFUA135P3	105	UFUA136P1	142	UFUA127P2	12	UFUA137P1	20
UFUA130P2	97	UFUA136P2	100	UFUA139P2	158	UFUA130P1	12	UFUA139P2	19
UFUA130P3	94	UFUA137P3	97	UFUA140P2	151	UFUA131P1	13	UFUA140P1	22
UFUA132P2	97	UFUA138P1	96	UFUA148P2	153	UFUA138P3	12	UFUA140P2	20
UFUA135P3	96	UFUA138P3	101	UFUA149P1	172	UFUA141P1	12	UFUA141P2	21
UFUA136P3	97	UFUA139P2	114	UFUA152P2	142	UFUA141P2	13	UFUA142P1	20
UFUA137P2	97	UFUA140P2	95	UFUA153P3	181	UFUA144P1	12	UFUA143P1	19
UFUA137P3	95	UFUA143P1	103	UFUA154P3	141	UFUA145P2	12	UFUA144P1	21
UFUA138P2	97	UFUA155P1	94	UFUA155P3	144	UFUA156P2	12	UFUA146P1	21
UFUA142P3	95	UFUA155P2	98	UFUA156P3	151	UFUA157P1	12	UFUA148P2	19
UFUA145P3	93	UFUA156P1	97	UFUA157P1	154	UFUA158P1	13	UFUA149P1	23
UFUA146P3	93	UFUA157P1	111	UFUA157P2	146	UFUA159P1	12	UFUA152P2	23
UFUA147P3	96	UFUA157P2	104	UFUA157P3	151	UFUA160P1	12	UFUA153P3	21
UFUA155P2	96	UFUA162P3	95	UFUA163P2	149	UFUA161P1	12	UFUA156P3	19
UFUA157P3	95	UFUA163P2	104	UFUA163P3	142	UFUA162P3	12	UFUA158P1	19
$\bar{X}_S$	95.59	$\bar{X}_S$	101.62	$\bar{X}_S$	151.59	$\bar{X}_S$	12.25	$\bar{X}_S$	20.19
GS%	14.68	*GS%*	9.04	*GS%*	17.32	*GS%*	21.90	*GS%*	23.93

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; *GS%* = 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.

SI	PN1G	SI	PN2G	SI	TNP	SI	SNP	SI	HSW	SI	GY
UFUA2P1	8	UFUA10P1	94	UFUA2P1	85	UFUA1P2	2.71	UFUA5P1	22.30	UFUA2P1	35.58
UFUA2P2	12	UFUA14P1	52	UFUA10P1	133	UFUA5P1	2.66	UFUA5P2	22.34	UFUA5P1	29.66
UFUA6P3	8	UFUA18P1	36	UFUA14P1	95	UFUA7P2	2.67	UFUA7P1	20.54	UFUA6P3	31.24
UFUA10P1	10	UFUA19P1	47	UFUA17P1	76	UFUA9P2	2.67	UFUA9P3	23.39	UFUA14P1	32.42
UFUA16P2	11	UFUA20P1	53	UFUA18P1	84	UFUA10P1	2.78	UFUA11P1	31.40	UFUA16P3	30.44
UFUA19P1	11	UFUA21P1	52	UFUA19P1	114	UFUA12P1	2.09	UFUA16P3	22.39	UFUA18P1	39.19
UFUA20P1	24	UFUA22P1	58	UFUA20P1	89	UFUA15P1	2.65	UFUA21P1	21.28	UFUA19P1	49.50
UFUA21P1	8	UFUA24P1	44	UFUA21P1	111	UFUA17P1	2.62	UFUA24P2	29.70	UFUA22P2	53.57
UFUA22P1	9	UFUA24P3	39	UFUA22P1	150	UFUA23P1	2.63	UFUA24P3	22.78	UFUA23P1	39.67
UFUA24P1	9	UFUA27P2	34	UFUA23P1	86	UFUA25P2	2.76	UFUA27P2	20.85	UFUA24P3	59.22
UFUA25P1	10	UFUA28P1	37	UFUA24P1	84	UFUA26P1	2.67	UFUA33P1	21.05	UFUA25P1	33.84
UFUA28P1	11	UFUA29P1	32	UFUA24P3	103	UFUA27P1	2.65	UFUA38P1	27.17	UFUA26P1	36.06
UFUA29P1	11	UFUA29P2	42	UFUA25P1	79	UFUA35P1	2.67	UFUA42P1	23.48	UFUA27P2	36.91
UFUA31P1	36	UFUA31P1	38	UFUA26P1	94	UFUA36P1	2.55	UFUA45P1	19.81	UFUA29P2	44.15
UFUA32P1	24	UFUA32P1	48	UFUA28P1	81	UFUA38P2	2.54	UFUA46P1	20.16	UFUA33P1	52.41
UFUA33P1	18	UFUA33P1	65	UFUA29P2	99	UFUA39P2	2.54	UFUA47P1	26.48	UFUA35P1	35.98
UFUA34P1	16	UFUA34P1	61	UFUA31P1	116	UFUA40P1	2.54	UFUA48P1	26.01	UFUA36P1	31.74
UFUA38P1	21	UFUA36P2	42	UFUA32P1	106	UFUA41P3	2.72	UFUA49P2	27.59	UFUA36P2	45.12
UFUA31P1	8	UFUA38P1	46	UFUA33P1	142	UFUA44P2	2.57	UFUA51P2	23.49	UFUA40P1	34.95
UFUA41P3	9	UFUA41P1	37	UFUA34P1	114	UFUA49P3	2.63	UFUA54P2	23.06	UFUA41P3	33.92
UFUA44P1	10	UFUA41P3	33	UFUA36P1	89	UFUA51P3	2.62	UFUA56P3	22.30	UFUA47P3	54.64
UFUA47P3	8	UFUA44P1	35	UFUA36P2	75	UFUA53P2	2.62	UFUA58P1	19.64	UFUA55P3	30.46
UFUA48P1	49	UFUA45P1	47	UFUA38P1	128	UFUA55P2	2.55	UFUA61P1	20.31	UFUA58P1	36.93
UFUA49P2	12	UFUA48P1	45	UFUA40P2	83	UFUA58P1	2.54	UFUA63P2	30.50	UFUA60P1	31.83
UFUA53P2	9	UFUA58P1	32	UFUA42P1	77	UFUA58P2	2.72	UFUA64P2	32.66	UFUA60P2	43.28
UFUA60P1	10	UFUA60P2	51	UFUA45P1	106	UFUA61P1	2.68	UFUA66P4	19.57	UFUA70P3	34.79
UFUA60P2	24	UFUA63P2	37	UFUA48P1	173	UFUA62P3	2.67	UFUA69P1	21.29	UFUA74P1	33.71
UFUA61P1	8	UFUA69P2	33	UFUA58P2	74	UFUA64P3	2.60	UFUA72P2	29.75	UFUA75P1	51.83
UFUA62P3	9	UFUA73P1	33	UFUA60P2	109	UFUA65P1	2.57	UFUA73P1	19.27	UFUA76P1	49.57
UFUA70P1	8	UFUA75P1	48	UFUA69P2	86	UFUA65P2	2.71	UFUA75P1	21.42	UFUA77P1	31.37
UFUA73P1	13	UFUA77P1	72	UFUA73P1	110	UFUA66P2	2.62	UFUA78P1	19.62	UFUA81P1	51.92
UFUA75P1	18	UFUA78P1	33	UFUA75P1	96	UFUA77P1	2.64	UFUA78P3	20.30	UFUA82P2	46.14

Continue...

Table 8 – Continuation.

UFUA77P1	26	UFUA80P1	44	UFUA77P1	144	UFUA82P2	2.57	UFUA80P2	20.05	UFUA83P2	35.11
UFUA80P2	9	UFUA82P1	76	UFUA82P1	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	UFUA121P2	26.06	UFUA96P3	36.96
UFUA113P3	11	UFUA114P1	50	UFUA105P1	127	UFUA104P1	2.64	UFUA132P2	27.78	UFUA97P3	64.10
UFUA114P1	10	UFUA115P1	39	UFUA107P1	85	UFUA105P1	2.72	UFUA133P1	25.55	UFUA99P1	35.66
UFUA115P1	17	UFUA117P1	35	UFUA110P1	146	UFUA108P2	2.66	UFUA133P2	24.48	UFUA103P2	38.77
UFUA117P1	11	UFUA125P1	47	UFUA114P1	92	UFUA113P2	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	UFUA122P2	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	UFUA15P1	38.45
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	UFUA141P2	40	UFUA137P2	96	UFUA138P1	2.64	UFUA148P1	22.29	UFUA127P2	33.07
UFUA137P2	15	UFUA141P2	40	UFUA139P1	99	UFUA142P1	2.60	UFUA148P2	21.24	UFUA128P4	38.35
UFUA141P1	12	UFUA142P1	59	UFUA140P2	75	UFUA142P3	2.71	UFUA148P3	19.80	UFUA130P1	34.25
UFUA141P2	11	UFUA143P1	35	UFUA141P2	77	UFUA144P1	2.55	UFUA152P2	35.55	UFUA137P1	31.49
UFUA142P1	20	UFUA144P1	35	UFUA142P1	102	UFUA145P2	2.63	UFUA153P3	23.60	UFUA138P1	39.77
UFUA144P1	11	UFUA146P1	30	UFUA143P1	94	UFUA145P3	2.59	UFUA154P1	23.36	UFUA139P1	31.49
UFUA148P2	10	UFUA148P2	54	UFUA145P1	78	UFUA147P2	2.72	UFUA154P3	19.68	UFUA142P3	35.21
UFUA152P2	12	UFUA148P3	31	UFUA146P1	128	UFUA148P1	2.57	UFUA157P1	29.26	UFUA144P1	62.87
UFUA152P3	20	UFUA149P1	40	UFUA149P1	101	UFUA155P4	2.60	UFUA157P2	20.47	UFUA147P1	30.74
UFUA154P3	14	UFUA152P3	54	UFUA152P3	104	UFUA156P4	2.69	UFUA157P3	33.59	UFUA150P1	36.65
UFUA157P3	11	UFUA153P3	41	UFUA153P3	75	UFUA157P3	2.61	UFUA158P1	22.79	UFUA156P2	53.09
UFUA158P1	13	UFUA158P1	53	UFUA158P1	133	UFUA161P1	2.59	UFUA159P1	26.71	UFUA156P3	40.42
UFUA160P2	17	UFUA159P1	58	UFUA159P1	131	UFUA163P1	2.57	UFUA160P1	34.10	UFUA163P1	40.96
UFUA162P3	13	UFUA162P3	47	UFUA162P3	78	UFUA163P3	2.61	UFUA163P2	25.01	UFUA163P2	76.27
$\bar{X}_S$	13.98	$\bar{X}_S$	45.55	$\bar{X}_S$	103.17	$\bar{X}_S$	2.63	$\bar{X}_S$	24.18	$\bar{X}_S$	40.15
GS%	114.80	*GS*%	71.47	*GS*%	44.58	*GS*%	8.08	*GS*%	34.92	*GS*%	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; $\bar{X}_S$ = mean of selected individuals; *GS*%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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