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Genetic progress of 18 years of a soybean breeding program for the Brazilian Central-West[1]

Progresso genético de 18 anos de um programa de melhoramento de soja para Centro-Oeste brasileiro

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ABSTRACT - In a breeding program, the estimation of genetic progress over the years provides a broad view of the program as well as grounds for optimal decision-making. In this respect, the present study proposes to estimate the genetic progress of 54 soybean cultivars released to the Brazilian Midwest between the years 2000 and 2017. Two experiments were conducted during the 2017/18 crop year. Grain yield (GY), maturity group (MG), 100-seed weight (100SW), number of pods per plant (NPP), number of seeds per pod (NSP) and plant height (PH) were evaluated. Genetic progress was estimated by the direct methodology and by linear regression. According to the direct method, the average annual genetic progress was positive for GY (1.92%), 100SW (2.69%), NPP (2.31%), NSP (1.10%) and PH (0.32%), but negative for MG (-0.44%). The results obtained using both methodologies agree on the obtained increases for GY and 100SW and the decreases for MG.

Key words: Genetic gain. *Glycine max.* production components.

RESUMO - Em um programa de melhoramento genético, a estimativa do progresso genético ao longo dos anos fornece uma visão ampla do programa, bem como bases para uma ótima tomada de decisão. Nesse sentido, o presente estudo se propõe a estimar o progresso genético de 54 cultivares de soja lançadas para o Centro-Oeste brasileiro entre os anos de 2000 e 2017. Dois experimentos foram conduzidos na safra 2017/18. Foram avaliados o rendimento de grãos (RG), grupo de maturidade (GM), peso de 100 sementes (P100), número de vagens por planta (NVP), número de sementes por vagem (NSP) e altura de planta (AP). O progresso genético foi estimado pela metodologia direta e por regressão linear. De acordo com o método direto, o progresso genético anual médio foi positivo para GR (1,92%), P100 (2,69%), NVP (2,31%), NSP (1,10%) e AP (0,32%), mas negativo para GM (- 0,44%). Os resultados obtidos por ambas as metodologias concordam com os aumentos obtidos para RG e P100 e decréscimos para GM.

Palavras-chave: Ganho genético. *Glycine max.* componentes de produção.

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INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) is an autogamous species originating in Asia. At present, Brazil stands out as the world's first largest producer of soybean, with growing yields obtained in recent years (SCHWALBERT *et al*., 2020; SILVA JUNIOR *et al*., 2018, 2020). In the 2020-21 harvest, Brazil produced 133 million tons of soybean from a planted area of 38 million hectares, representing an average yield of 3,517 kg ha^{-1} (COMPANHIA NACIONAL DE ABASTECIMENTO, 2021). Of this total, the Center-West was the most representative region (52 million tons), with the largest cultivated area (16.1 million hectares) (COMPANHIA NACIONAL DE ABASTECIMENTO, 2021).

Given the notoriety of soybean in Brazil, breeding companies have invested in the development of new cultivars with traits desired by the market (LIU *et al*., 2017; LU *et al*., 2015; TODESCHINI *et al*., 2019), such as high yield; shorter cycle; adaptability to mechanization; resistance to lodging, diseases, pests and nematodes; among others. However, determining the effectiveness of a breeding program over the years requires estimating the genetic progress achieved. This estimate can provide a broad view of the program as well as grounds for decision-making regarding any change in selection methods (FALCONER; MACKAY, 1996).

Studies have demonstrated genetic gains in grain yield (GY), in the soybean crop (RINCKER *et al*., 2014; TOLEDO *et al*., 1990). These gains may be due to several factors, e.g. increased number of seeds per plant and per pod (RINCKER *et al*., 2014), greater resistance to lodging (MORRISON; VOLDENG; COBER, 2000), shorter vegetative period (FELIPE; GERDE; ROTUNDO, 2016), higher photosynthetic rate (LIU *et al*., 2012) and increased nutrient absorption efficiency (MCFARLENE; O'CONNOR, 2014).

Several methodologies have been developed to estimate genetic progress, such as the direct method; Vencovsky method, Fernandes, Morais and Abbud method and Breseghello method; the regression method with original data; the method employing control treatment as a correction factor; the regression method with standardized data; and the method of Fonseca Júnior. The advantage of the direct method lies in that it allows the evaluation of genotypes released in different years, in different environments, during the same crop year. In the linear regression method, the genetic gain is obtained directly by estimating the slope of the equation of the line (TODESCHINI *et al*., 2019). On the other hand, it requires viable seeds from old cultivars for multiplication in sufficient quantity for the execution of the experiment (ATROCH; NUNES, 2000).

In view of the above-described scenario, the present study was developed to estimate genetic progress—using the direct and regression methods—for production components, phenotypic traits and yield in cultivars released to the Brazilian Midwest between the years 2000 and 2017 by a soybean breeding program for the Center-West region of Brazil.

MATERIAL AND METHODS

The experiments were carried out during the 2017/18 crop year at the Coodetec research station (17º45'57" S, 51º01'44" W, average altitude 844 m) and at Instituto Federal Goiano, Rio Verde Campus (17º48'26" S, 50º54'08" W, average altitude 739 m). Both sites are located in the municipality of Rio Verde, state of Goiás, Brazil. Rio Verde is situated in soybean macro-region 3 and micro-region 301, according to the third approach to agricultural zoning, proposed by Santos *et al*. (2018).

This study examined 54 soybean cultivars released by a breeding program to the Brazilian Midwest between 2000 and 2017 (number of cultivars released each year: 2000 - one; 2003 - two; 2005 - one; 2007 - three; 2008 - one; 2009 - nine; 2010 - three; 2011 - eight; 2012 - four; 2013 - nine; 2014 - six; 2015 - two; 2016 - two; and 2017 - three). In the months from July to October 2017, all cultivars were multiplied to standardize vigor and germination for the establishment of the experiments. Sowing took place on 10/17/2017 and 11/02/2017, respectively, at the research station of Coodetec and at IF Goiano.

The experiment was laid out in a randomized block design with three replicates. Plots consisted of four 4-m rows spaced 0.50 m apart, with a final plant stand of 300,000 plants. The two central rows were considered the usable area for the evaluations. All cultivation treatments were carried out in accordance with Embrapa (2013).

The following traits were evaluated: grain yield (GY), obtained by weighing the grains of each plot, adjusting the result for 13% moisture and extrapolating it to kg.ha^{-1}; maturity group (MG), estimated as proposed by Zdziarski *et al*. (2018); 100-seed weight (100SW), obtained by averaging a random take of 100 grains three times in each plot and weighing on a digital scale; number of pods per plant (NPP), determined by counting the number of pods from six plants sampled randomly within each plot and averaging; number of seeds per pod (NSP), obtained by dividing the total number of seeds by the total number of pods; and plant height (PH, in cm), determined by measuring the main stem of six random plants within each plot at the physiological maturity stage.

Data were subjected to individual analysis of variance (Equation 1). After checking for homogeneity of the residual mean squares for all the experiments involved in the analysis by the method of the ratio of the largest and smallest least squares of the residue (REGAZZI *et al.*, 1999), a joint analysis was carried out for all the traits under study (Equation 2).

Individual Analysis of Variance

$$\gamma_{ij} = \mu + G_i + B_j + \varepsilon_{ij} \quad (1)$$

Where: γij is the observed value of genotype i in block j; μ is the overall average of the character; Gi is the effect of genotype i; Bj is the effect of block i; and εij is the random error associated with genotype i in block j.

Joint Analysis of Variance

$$\gamma_{ijk} = \mu + G_i + A_j + GA_{ij} + \varepsilon_{ijk} \quad (2)$$

Where: γ_{ijk} is the observed value of genotype i in environment j in block k; μ is the overall average of the character; G_i is the effect of genotype i; A_j is the effect of environment j; and ε_{ijk} is the experimental error associated with plot *ijk*.

To estimate the combined genetic progress, the mean of each genotype in both environments and of the cultivars released each year, for each trait, was obtained and the direct method was applied. The method consists of estimating the $\bar{y}_{i'} - \bar{y}_i$ difference, termed “total difference”, observed in a given year *i*', relative to the previous year *i*. For the purpose of estimating genetic progress, year *i* is the year of registration of the cultivar.

Genetic difference Δ*G* is defined as follows: $\Delta G_{i'i} = (\bar{y}_{i'} - \bar{y}_i)$.

Therefore, $\Delta G_{i'i}$ can be taken as an estimator of changes in the mean occurring between years *i* and *i*', which is attributed to genotypic changes or an increase in the average productive potential of the treatments.

These estimates ($\Delta Gi'i$, $\Delta Gi''i'$,..., ΔGn, n^{-1}) can be obtained for each biennium. The sum of these quantities represents the cumulative genetic progress; average increase per year is the ratio of cumulative progress to the number of years of evaluation; and relative progress can be estimated as the ratio of estimated progress to the average of the initial cycle.

To estimate genetic progress, simple linear regression analysis was performed between the release years (independent variable) and the means of the agronomic variables (GY, 100SW, NPP, NSP, PH and MG) per year. To check for possible associations, Pearson’s correlation analysis was carried out and the t test was applied. The analysis of variance was performed using the Genes software (CRUZ, 2016) and the regression analyzes using the basic package of the R software.

RESULTS AND DISCUSSION

The sources of variation of *genotype* and *genotype × environment interaction* (G×E) were significant by the F test for all evaluated traits ($p < 0.05$). To estimate genetic progress, the means of the environments were used. Coefficients of variation (CV%) ranged between 8.54 and 19.47%, for PH and NSP, respectively, indicating good experimental precision (data not shown).

There was an increase in GY over the 18 years of breeding, considering the annual genetic progress (Δ*G*) of 1.92% obtained for this trait, which corresponds to 20.80 kg ha^{-1} per year (Table 1). A similar result is illustrated in Figure 1A, which shows that the coefficient of the regression line was 27.61 kg ha^{-1} per year and significant at 5% by the t test ($p < 0.05$). Similar results were obtained by Koester *et al*. (2014) (26.45 kg ha^{-1} per year, in the USA) and by Todeschini *et al*. (2019) (40.06 kg ha^{-1} per year, in the south of Brazil). Toledo *et al*. (1990) evaluated the efficiency of the soybean breeding program in the state of Paraná between 1981 and 1986 and observed gains of 1.8% and 1.3% for the early- and semi-early-maturing genotypes, respectively.

It should be noted that the GY of the cultivar released in 2000 (the only cultivar of that year and the oldest in the data history) exceeded 4600 kg ha^{-1}, indicating high yielding potential. This cultivar obtained similar GY means to those produced by the cultivars released in the years 2008, 2014 and 2017. For this reason, cumulative genetic progress may have been limited, mainly, by linear regression analysis.

The GY means for the cultivars released in 2015 and 2016 (Table 1) were lower than those of the cultivars released in the previous years. This was due to the introgression of wild cultivars in the breeding program, which was aimed at increasing tolerance to nematodes, a trait desired by the market that may have restricted genetic progress for GY.

Maturity group decreased on average by 0.44 per year (Table 1), and, by the regression line, by -0.270 per year, which was significant at 1% by the t test ($p < 0.01$) (Figure 1B). These are expected results, given that in the Brazilian Center-West conditions, where a second harvest is performed (February to May), soybean cultivars with a shorter cycle are desirable for the market. A reduction in the cycle of cultivars over the years of breeding was also observed by Liu *et al*. (2012) and Wu *et al*. (2015). Todeschini *et al*. (2019) evaluated the genetic progress of agronomic and physiological traits in 29 soybean cultivars available for cultivation in the southern region of Brazil between the years 1965 and 2011 and observed an average decrease in total plant cycle of 0.29 days per year.

Table 1 - Genetic progress (ΔG) for grain yield (GY) (kg ha^{-1}) and maturity group (MG) over 18 years of the soybean breeding program

CRY^2	GY	$(\bar{y}_{i'} - \bar{y}_i)^1$	ΔG(%)	MG	$(\bar{y}_{i'} - \bar{y}_i)^1$	ΔG(%)
2000	4619.9	-	-	82.0	-	-
2003	3613.6	-1006.3	-21.78	80.5	-1.50	-1.83
2005	2931.4	-682.1	-18.88	78.0	-2.50	-3.11
2007	3232.4	300.9	10.27	77.6	-0.40	-0.51
2008	4698.5	1466.1	45.36	76.0	-1.60	-2.06
2009	3927.6	-770.8	-16.41	79.4	3.40	4.47
2010	4142.6	215.0	5.47	75.3	-4.10	-5.16
2011	3591.4	-551.2	-13.31	78.0	2.70	3.59
2012	4012.5	421.1	11.73	76.0	-2.00	-2.56
2013	4321.0	308.5	7.69	79.0	3.00	3.95
2014	4542.9	221.8	5.13	78.25	-0.75	-0.95
2015	3973.7	-569.1	-12.53	76.0	-2.25	-2.88
2016	3441.9	-531.8	-13.38	77.0	1.00	1.32
2017	4994.3	1552.4	45.10	75.3	-1.70	-2.21
Sum	-	374.4	34.47	-	-6.70	-7.95
Year	-	20.80	1.92	-	-0.37	-0.44
OM^3	4003.1	-	-	77.7	-	-

[1] Cultivar release year; [2] Difference between the mean observed in a given year and the mean of the year immediately after , expressed in kg ha^{-1}. [3] Overall mean of the released genotypes

Hundred-seed weight (100SW), number of pods per plant (NPP) and number of seeds per plant (NSP) are among the main components of grain production in soybean. Genetic progress for 100SW was 0.16 g, which represents 2.69% per year; for NPP, 0.11 and 2.31% per year (Table 2); and, for NSP, -0.45 and 1.10% per year (Table 3). A different result was obtained by the slope of the regression line, which showed a gain of 0.102 g in 100SW ($p < 0.05$) per year and a decrease of 0.609 (ns) and 1.449 ($p < 0.05$) for NPP and NSP, respectively (Figure 1C, D and E). It is important to note that the different adopted methods and the means of the cultivars released in 2005 for NPP and NSP (108.31 and 190.86, respectively) may have influenced the regression coefficients.

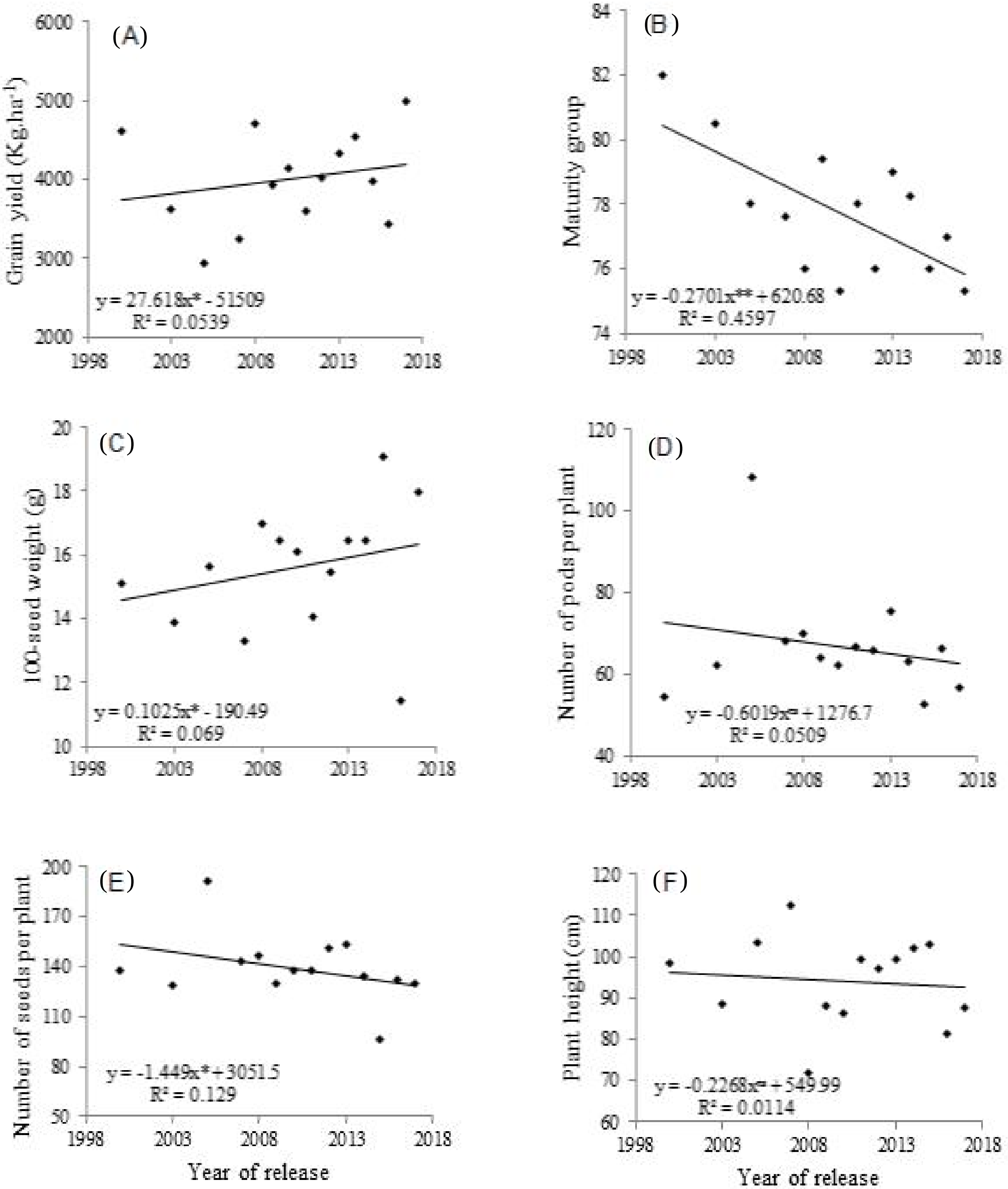
Divergent results are commonly found for these traits. Todeschini *et al*. (2019) evaluated genetic progress in soybean by linear regression and reported positive gains for NPP and non-significant gains for 100SW and NSP. These authors concluded that gains in productivity are associated with NPP, similarly to the results reported by Kahlon and Board (2012) and Suhre *et al*. (2014). However, Wang *et al*. (2016) investigated genetic progress through regression in 25 soybean cultivars released from 1929 to 2004 in China and described that modern cultivars have lower NPP and NSP and higher 100SW, which is associated with higher grain yield, corroborating the results found by Cui and Yu (2005) and Wu *et al*. (2015).

Genetic progress for PH was -0.59 cm and 0.32% per year (Table 3), with the regression showing a slope of -0.22 and no significance detected by the t test (Figure 1F). Decreasing PH was observed in other studies of genetic progress in soybean (RAMTEKE *et al*., 2011; ROGERS *et al*., 2015; TODESCHINI *et al*., 2019). Decreases in PH may be directly related to greater resistance to lodging (TODESCHINI *et al*., 2019). According to Silva *et al*. (2017), tall plants (above 100 cm) generally do not show great resistance to lodging, which can cause grain losses during mechanized harvesting.

Grain yield was positively and significantly correlated with 100SW ($p < 0.01$) and negatively with MG ($p < 0.05$). These results indicate that, in this soybean breeding program, genetic progress in GY is associated with an increase in 100SW (as shown in Figure 2C, D and E), corroborating the findings of Wang *et al*. (2016).

Among the productivity traits, there was an estimated negative correlation for 100SW with NPP ($p < 0.05$), MG ($p < 0.01$) and NSP ($p < 0.05$) and a positive correlation between NPP and NSP ($p < 0.001$). Maturity group was negatively and significantly correlated with GY ($p < 0.05$) and MHS ($p < 0.005$) and positively with NPP ($p < 0.05$) and NSP ($p < 0.05$). According to Resende (2015), indirect selection can be practiced based on correlation estimates to obtain genetic gains for a main trait. Breeding strategies that prioritize indirect selection of the highest means for 100SW and the lowest means for MG can increase genetic progress in the next cultivars released.

Figure 1 - Simple linear regression between release year and grain yield



(A), maturity group (B), 100-seed weight (C), number of pods per plant (D), number of seeds per plant (E) and plant height (F). *, **, ^{ns} significance at $p < 0.05$, $p < 0.01$ and not significant for the slope of the line by the t test

Table 2 - Genetic progress (ΔG) for 100-seed weight (100SW) and number of pods per plant (NPP) over 18 years of the soybean breeding program

CRY^2	100SW	$(\bar{y}_{i'} - \bar{y}_i)^1$	ΔG(%)	NPP	$(\bar{y}_{i'} - \bar{y}_i)^1$	ΔG(%)
2000	15.09	-	-	54.61	-	-
2003	13.86	-1.24	-8.18	62.04	7.43	13.60
2005	15.61	1.75	12.60	108.31	46.27	74.58
2007	13.31	-2.29	-14.68	68.05	-40.26	-37.17
2008	16.96	3.65	27.39	70.14	2.09	3.07
2009	16.45	-0.51	-3.00	63.81	-6.33	-9.02
2010	16.10	-0.35	-2.15	61.97	-1.84	-2.88
2011	14.09	-2.01	-12.49	66.62	4.65	7.50
2012	15.47	1.38	9.82	65.91	-0.71	-1.06
2013	16.46	0.99	6.37	75.30	9.39	14.25
2014	16.46	0.00	0.03	63.26	-12.04	-15.99
2015	19.06	2.60	15.77	52.42	-10.85	-17.14
2016	11.44	-7.62	-39.99	66.16	13.75	26.23
2017	17.97	6.53	57.09	56.61	-9.55	-14.44
Sum	-	2.87	48.58	-	2.00	41.51
Year	-	0.16	2.69	-	0.11	2.31
OM^3	15.59	-	-	66.80	-	-

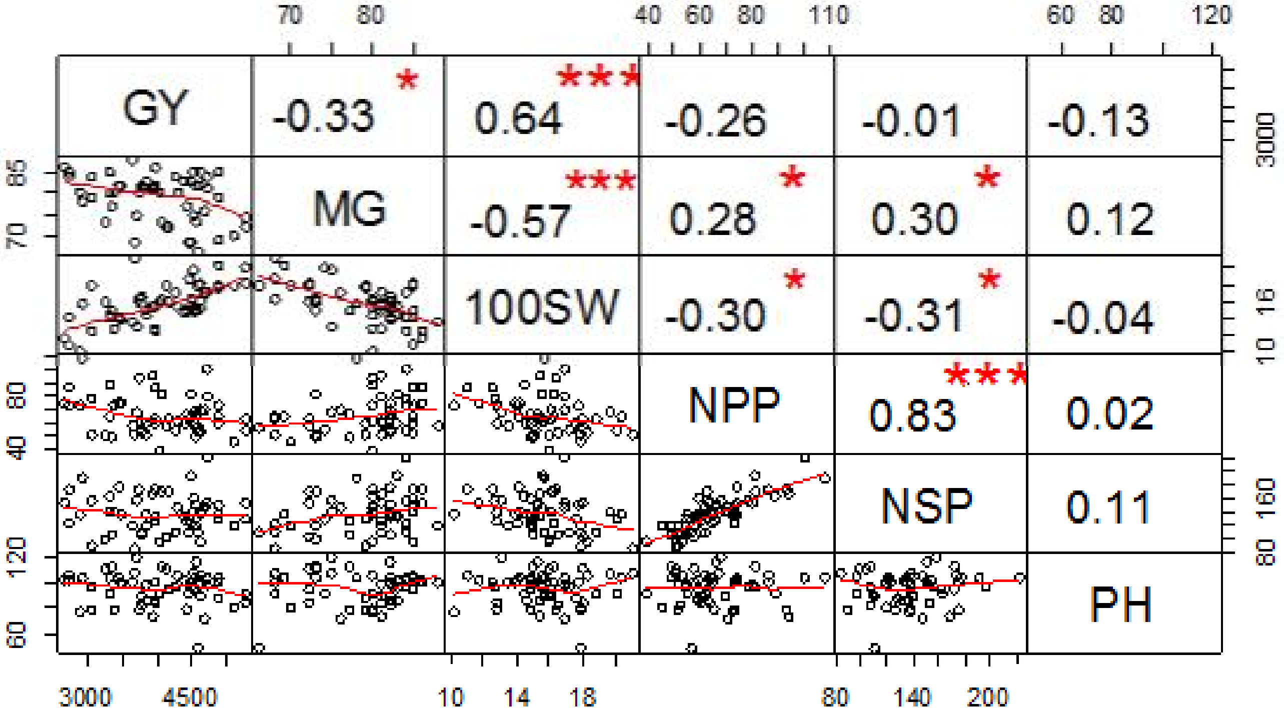
[1] Cultivar release year; [2] Difference between the mean observed in a given year and the mean of the year immediately after , expressed in kg ha^{-1}. [3] Overall mean of the released genotypes

Table 3 - Genetic progress (ΔG) for number of seeds per pod (NSP) and plant height (PH) over 18 years of the soybean breeding program

CRY^2	NSP	$(\bar{y}_{i'} - \bar{y}_i)^1$	ΔG(%)	PH	$(\bar{y}_{i'} - \bar{y}_i)^1$	ΔG(%)
2000	137.95	-	-	98.33	-	-
2003	128.96	-8.99	-6.51	88.75	-9.58	-9.75
2005	190.86	61.90	48.00	103.33	14.58	16.43
2007	142.99	-47.87	-25.08	112.50	9.17	8.87
2008	146.44	3.45	2.41	71.67	-40.83	-36.30
2009	129.48	-16.96	-11.58	87.96	16.30	22.74
2010	137.70	8.22	6.35	86.11	-1.85	-2.11
2011	137.41	-0.29	-0.21	99.27	13.16	15.28
2012	150.65	13.24	9.63	96.88	-2.40	-2.41
2013	153.44	2.78	1.85	99.26	2.38	2.46
2014	133.76	-19.68	-12.82	102.08	2.82	2.85
2015	95.71	-38.05	-28.45	102.92	0.83	0.82
2016	131.84	36.13	37.75	81.25	-21.67	-21.05
2017	129.85	-1.99	-1.51	87.78	6.53	8.03
Sum	-	-8.10	19.83	-	-10.56	5.87
Year	-	-0.45	1.10	-	-0.59	0.32
OM^3	139.07	-	-	94.15	-	-

[1] Cultivar release year; [2] Difference between the mean observed in a given year and the mean of the year immediately after , expressed in kg ha^{-1}. [3] Overall mean of the released genotypes

Figure 2 - Simple linear correlation between all variables



GY = grain yield; MG = maturity group; 100SW = 100-seed weight; NPP = number of pods per plant; NSP = number of seeds per pod and PH = plant height. Significance of the t-test= ***, p < 0,005 **, p < 0,01, *, p < 0,05

CONCLUSION

The breeding program has been efficient to obtain the most productive cultivars and with the least maturity group. The direct and regression methods showed positive genetic gain for grain yield and 100-seed weight and negative for maturity group. In this soybean breeding program, genetic progress in grain yield is associated with an increase in 100-seed weight.

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