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GENETIC POTENTIAL OF SOYBEAN POPULATIONS FOR GRAIN YIELD AND FULL MATURITY

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ABSTRACT

Grain yield is one of the main traits of interest in developing new cultivars. In soybean, significant advancements have been made through optimized crop management, the application of appropriate inputs, effective agronomic practices, and the development of improved cultivars. Without the progress achieved through plant breeding over the last century, the cultivars available today would only support a population of a few million people, making it unlikely for the global population to have reached its current 8 billion (Borém et al., 2021).

INTRODUCTION

The success of a breeding program for self-pollinating plants is intrinsically linked to the meticulous selection of segregating populations for advancement within the program. To achieve this, it is essential to gather accurate information on the mean and variance of these populations. In this context, the methodologies proposed by Jinks and Pooni (1976), as well as the estimation of mean components such as $m+a'$ (representing the contribution of homozygous loci) and d (representing the contribution of heterozygous loci), along with variance components, can serve as effective tools for identifying and advancing superior progenies (Vencovsky, 1987).

The estimation of $m+a'$ offers several advantages over variance components, including the ability to identify the hybrid or population with the highest probability of producing superior lines in the F_∞ generation. Additionally, this estimate has a lower associated error compared to variance components, as it is derived from the mean (Ramalho, 2012). Studies have demonstrated the application of this estimate mainly in crops such as corn and beans (Carneiro et al., 2002; Bison, 2003; Rocha et al., 2015). No reports, however, have been found regarding the use of $m+a'$ estimates at the plot level for soybeans. Nevertheless, incorporating these components into breeding programs holds great promise, as this information can contribute to reducing both the time and costs associated with soybean breeding programs.

The objective was to predict the genetic potential of segregating soybean populations for grain yield and full maturity traits and to select segregating populations associated with high grain yield and fewer days to full maturity.

MATERIAL AND METHODS

Description, localization, and conduction of experiments

The experiments were conducted in the 2018/19 crop season in the state of Minas Gerais, in the municipalities of Ijaci (21° 9' 24" S and 44° 55' 34" W, and an altitude of 833 meters) and Lavras (21° 14' 43" S and 44° 59' 59" W, and an altitude of 919 meters). According to the Köppen classification, the climate of the region is classified as Cwa, a temperate rainy climate (mesothermal), with a dry winter and a rainy summer, subtropical (Dantas *et al*., 2007).

Twenty soybean segregating populations from two generations, F_3 and F_4, obtained from the hybridization of 10 parents were used (Table 1).

Table 1**:** Hybridizations performed and populations obtained.

Populations	**Genealogy**	**Treatment**	**Genealogy**
1	BMXForçaRR x BMXPotênciaRR	11	FMT1 x BRSMG780RR
2	BMXForçaRR x BRSMG780RR	12	FMT3 x BRSMG780RR
3	BMXPotênciaRR x TMG123RR	13	VmaxRR x CD250RR
4	FMT1 x FMT2	14	VmaxRR x BRSMG780RR
5	BMXPotênciaRR x CD250RR	15	TMG123RR xTMGAnta82RR
6	FMT1 x TMG123RR	16	VmaxRR x CD250RR
7	BMXForçaRR x FMT1	17	TMGAnta82RR x BMXForçaRR

8	FMT1 x CD250RR	18	BMXPotênciaRR x FMT2
9	TMGAnta82RR x BMXPotênciaRR	19	BMXForçaRR x BRSMG780RR
10	CD250RR x BRSMG780RR	20	TMGAnta82RR x BMXPotênciaRR

The crosses were performed in a greenhouse during the 2014 crop season. The F_1 seeds were advanced to the 2015/16 crop, also in a greenhouse. Starting from the 2016/17 crop, the populations were grown in the field, sown at a density of 15 plants/m, in plots consisting of four rows, each five meters in length, spaced 0.50 meters apart. In 2016/17 crop, the F_2 seeds were sown, giving rise to the F_3 generation.

In the 2017/18, the F_3 seeds of each population were cultivated, and the populations were subsequently sown in the field, giving rise to the F_4 seeds. The bulk method was performed in all generations. The F_3 and F_4 generations were sown simultaneously in the 2018/19 crop season. A strip-plot design with three replications was employed, with the generation factor (F_3 and F_4) within plots and the 20 segregating populations in the subplots.

A no-tillage system with sowing furrows spaced 0.50 m apart was adopted at the two evaluated sites. In-furrow inoculation with the bacteria *Bradyrhizobium japonicum* was performed immediately before sowing at a dose of 18 mL of concentrated product kg^{-1} of seed (strains SEMIA 5079 and 5080, inoculant Nitragin Cell Tech HC® ($3x10^{9}$ CFU mL^{-1}). A seeder was used to create furrows, and an XR 11002 four-spray nozzle system positioned between fertilizer disks was used to apply a spray volume equivalent to 150 L ha^{-1}. Sowing was performed manually in October 2018 in Lavras and in November 2018 in Ijaci.

The seeds were harvested in the field at the R9 stage (95% of pods mature). After mechanical tracing, the seeds were separated from the impurities with sieves and placed in paper bags. Seeds with high moisture were exposed to the sun until reaching 13% moisture, which is suitable for storage.

Analysis of the data

The data were evaluated through an exploratory data analysis, with a particular focus on detecting outliers. The identification of outliers was carried out through the use Q-Q plot graphs. Homogeneity of variance was calculated according to the maximum F test (Hartley, 1950). The data indicate the absence of outliers, the residuals adhere to a normal distribution ($p > 0.05$) (Shapiro and Wilk, 1965) and the homogeneous variances.

Statistical analysis of the phenotypic data was conducted in three stages. Firstly, individual analysis was performed by site and generation, adopting model (1):

$$y_{ik} = \mu + \beta_k + \theta_i + \varepsilon_{ik} \qquad (1)$$

where: y_{ik}: Observed value for the trait analyzed in genotype i in block k; μ: constant associated with all observations, assumed to be fixed; β_k: effect of block k, assumed to be fixed; θ_i: effect of genotype i, assumed to be fixed; ε_{ij}: effect of the error associated with the observation of genotype i in block j, assumed to be random ($\varepsilon_{ij} \sim N(0, \sigma_e^2)$).

Only those trials with a homogeneity of residual variance were used for the following analyses, without the need of structuring the residual covariance matrix. Using the adjusted means, a joint analysis by location was performed according to the model:

$$y_{ijk} = \mu + \theta_i + \gamma_j + \theta\gamma_{ij} + \beta/\gamma_{kj} + \varepsilon_{ijk} \qquad (2)$$

where: y_{ijk}: Observed value for the trait analyzed in genotype i in block k for location j; μ: constant associated with all observations, assumed to be fixed; θ_i: effect of genotype i, assumed to be fixed; γ: effect of environment j, assumed to be fixed; $\theta\gamma_{ij}$: effect of the interaction between genotype i at site j, assumed to be fixed; β/γ_{kj}: effect of block k within environment j, assumed to be fixed; ε_{ij}: effect of the error associated with the observation of genotype i in block j, assumed to be random (($\varepsilon_{ij} \sim N(0, \sigma_{ej}^2)$).

The following traits were measured: full maturity, comprising the number of days from planting to the point of harvest (represented by 95% of plants with mature pods) and grain yield (kg ha^{-1}), obtained from the individual harvest of each plot after weighing and correcting for 13% moisture. Subsequently, the contribution of the homozygous loci (m+a') by population and by replication was estimated for the grain yield and full maturity traits by the estimator (3):

$$m + a' = 2 \times F_4 - F_3 \qquad (3)$$

where $m + a'$ is the contribution of homozygous loci to grain yield and full maturity traits; F_4 is the grain yield or full maturity of the plot in the F_4 generation; and F_3 is the grain yield or full maturity of the plot in the F_3 generation.

Grain yield, full maturity, $m+a'$ grain yield and $m+a'$ full maturity data were subjected to analysis of variance using R Core Team R environment (2017), and the means were compared by a Scott and Knott (1974) test at 5% probability. The experimental precision was analyzed by coefficient of variation (CV) (Pimentel, 2009) and by accuracy estimation (Resende and Duarte, 2007).

In the third stage, a general joint analysis was conducted, containing the two evaluation sites ang generation according to the model (4):

$$yijkl = \mu + g_i + b_{k(l)} + l_l + (gl)_{il} + (glb)_{(il)k} + p_j + (pl)_{jl} + plb_{(jl)k} + (gp)_{ij} + (gpl)_{ijl} + e_{(ijl)k}$$

(4)

where y_{ijk} is the observed value; μ is a constant associated with all observations; g_i is the effect of generation $_i$; b_k is the effect of block $_k$; $(gb)_{ik}$ is the error associated with generation $_i$ in block k; l_i is the effect of site $_i$; $(gl)_{il}$ is the effect of generation × local interaction; $(glb)_{(il)\,k}$ is the effect of the interaction of generation $_i$ at site $_l$ in block $_k$; p_j is the effect of population $_j$; $(pl)_{jl}$ is the effect of interaction × populations × sites; $plb_{(jl)k}$ is the effect of population interaction $_j$ at site $_l$ in block $_k$; $(gp)_{ij}$ is the effect of the interaction generations × populations; $(\mathrm{gpl})_{\mathrm{ijl}}$ is the effect of the interaction generations × populations × sites; and $_{(\mathrm{ijl})\mathrm{k}}$ is the effect of the generation × population interaction at site $_l$ in block $_k$.

The CV and accuracy were obtained using the following estimators (5):

$$CV\% = \sqrt{\frac{QM_{residual}}{\mu}} \times 100 \qquad r(\%) = \sqrt{1-\frac{1}{Fc}} \times 100 \tag{5}$$

where $CV\%$ is the CV (%); $QM_{residual}$ is the mean square of the residual of the analysis of variance; μ is the overall mean; $r(\%)$ is the accuracy (%); and Fc is the F value calculated from the populations.
Correlations were performed between the trait-based grain yield and $+a'$ grain yield and full maturity and $m+a'$ full maturity. Pearson's linear correlation analyzes were performed using R Core Team environment. Significance was assessed using a Mantel test. This test calculates the correlation between two matrices (Pearson correlation), performing numerous permutations on the values of the two matrices and computing the correlation value (R) for each permutation of matrices. Subsequently, it compares the actual correlation value (R) from the data with all R values obtained from the numerous permutations through a statistical test. This aims to determine whether the correlation value truly exists or if it could be simply a result of chance.

RESULTS

For the grain yield trait, all the sources of variation were significant ($p \leq 0.05$), except for the triple interaction (G*P*L) (Table 2). For full maturity, only the triple interaction and the individual sources of variation were significant. For m+a' grain yield and m+a' full maturity, all the sources of variation were significant. However, it is important to note that although the interactions were significant, the focus of the results is the findings of the overall mean.

Table 2: Summary of joint analysis of variance for grain yield (Yield), full maturity (FM), m+a' grain yield (m+a' Prod) and m+a' full maturity (m+a' FM). The analysis involved 20 segregating soybean populations and two generations (F3 and F4) at two sites (Ijaci and Lavras), MG, during the 2018/19 crop.

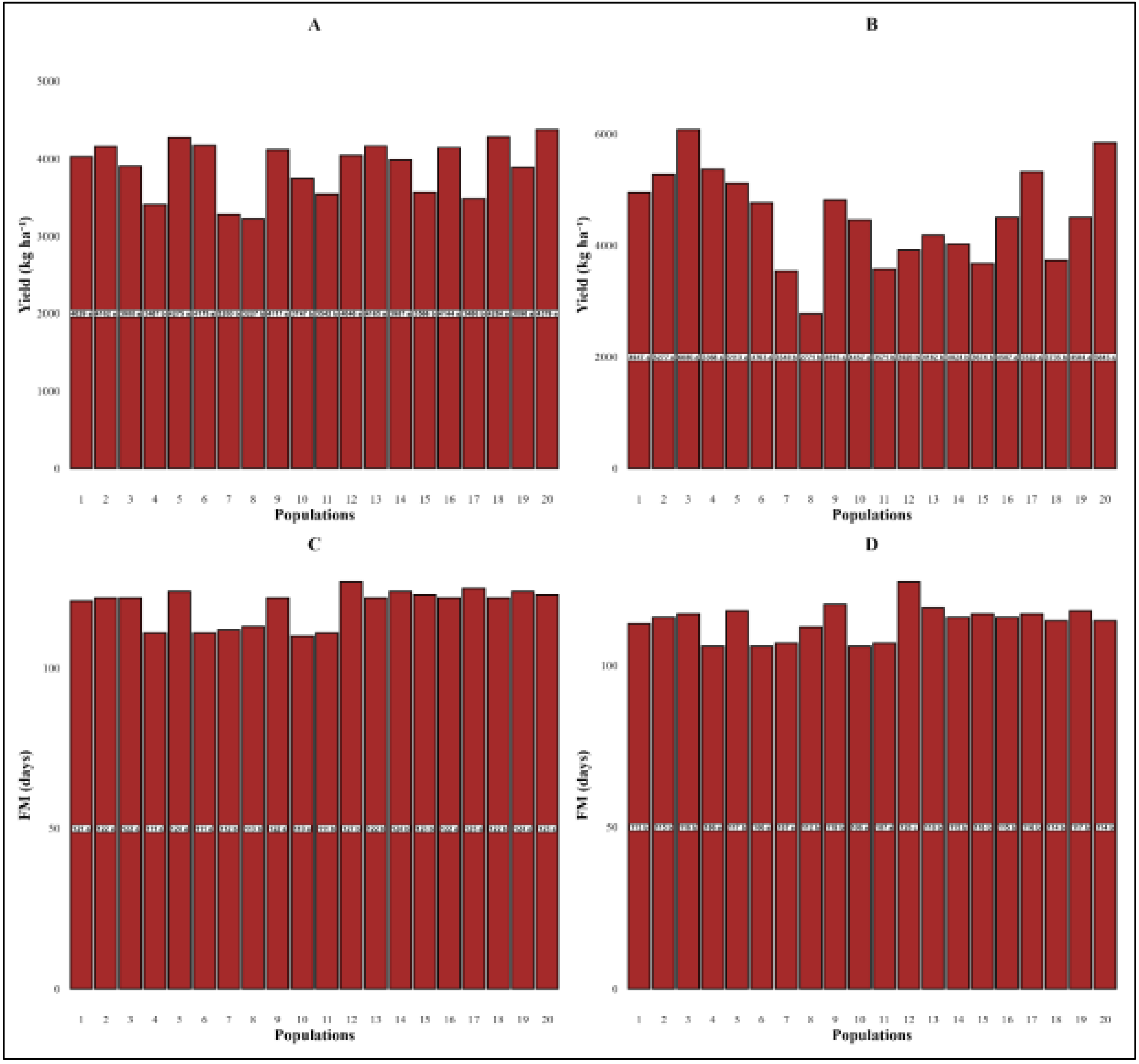
		p-value			
SV	**DF**	**Yield (kg ha^{-1})**	***m+a'* Yield**	**FM (day)**	***m+a'* FM**
Sites (S)	1	0,0002*	0,0005*	0,0009*	0,0000*
Generations (G)	1	0,0006*	-	0,0014*	-
G*S	1	0,0443*	-	0,0909	-
Populations (P)	19	0,0000*	0,0031*	0,0000*	0,0000*
P*S	19	0,0000*	0,0171*	0,5868	0,0000*
G*P	19	0,0040*	-	0,2322	-
G*P*S	19	0,0719	-	0,0000*	-
CV (%)	-	-	29,5	-	3,57
CV 1 (%)	-	8,4	-	3,2	-
CV 2 (%)	-	15,8	-	2,2	-
CV 3 (%)	-	14,9	-	2,0	-
Accuracy	-	75,19	59,18	98,25	90,07
General Average	-	3890,85	4520,71	119,48	114

Significant at a 5% probability level.
$^{CV\ 1}$ Subplot Coefficient of Variation
$^{CV\ 2}$ Parcel Coefficient of Variation
$^{CV\ 3}$ Error Coefficient of Variation

In this study, the estimates for the full maturity trait were of low magnitude (0.7% to 4.5%) and therefore considered optimal. The accuracy ranged from 59.18% to 98.25% and was considered moderate to high. There was an average of 17 days of variation in the overall mean time to full maturity among the populations, with population 12 being the slowest (127 days) and population 10 the fastest (110 days), while populations 4, 6 and 11 each took 111 days.

The averages of the 20 segregating soybean populations for grain yield, full maturity, m+a' yield and m+a' full maturity are shown in Figure 1. Grain yield ranged from 3227 kg ha^{-1} to 4379 kg ha$^{-1.}$ Segregating populations 1, 2, 3, 5, 6, 9, 12, 13, 14, 16, 18, 19 and 20 had the highest phenotypic means. The estimates of this value ranged from 2771 to 6080, and populations 1, 2, 3, 4, 5, 6, 9, 10, 16, 17, 19 and 20 had higher values than the other populations (Figure 1). The estimates of m+a' full maturity ranged from 106 to 126 and were divided into three groups, with the lowest values in populations 4, 6, 7, 10 and 11.

Figure 1: Joint phenotypic means for the grain yield (Yield) (A), *m+a'* grain yield (B), full maturity (FM) (C), *m+a'* full maturity (*m+a'* FM) (D) for 20 segregating soybean populations.



DISCUSSION

To proceed with the evaluation of generations within the same population, the effect of genotype x environment interaction must be attenuated, justifying the adoption of strip-plot design in this experiment, making generations from the same population contiguous. The success in selecting superior genotypes is intrinsically related to experimental precision. In the present study, two estimates were used to assess experimental precision: the coefficient of experimental variation (*CV*), classified according to Pimentel (2009), and accuracy, classified according to Resende and Duarte (2007). In this experiment, the *CV* estimates were considered excellent to good, indicating that there were no major implications of the experimental design; only for the estimation of grain yield m+a', the *CV* was considered fair to poor (Pimentel, 2009; Soares, 2020).

Productivity is a quantitative trait, i.e., polygenic, and therefore, strongly influenced by the environment, which justifies the low magnitude of the CV in the m+a' estimation for grain yield. These estimates fall within the values commonly reported for soybean cultivation. On the other hand, the number of days to maturity is a highly heritable trait, thus minimally influenced by the environment (Amaral *et al*., 2019), resulting in lower CVs (Pereira *et al*., 2017; Zambiazzi *et al*., 2017; Gesteira *et al*., 2018). In this study, high accuracy values were found for days to maturity (0.9825) and consequently, for the m+a' estimation (0.9007), in accordance with the conclusion based on the *CV*.

In general, the main differences observed in the experiment are due to the utilized segregating populations, demonstrating the individual performance of each population and the variability obtained through hybridizations. The segregating populations obtained showed promising attributes, with most of them showing grain yields above the national average of 3527 kg ha^{-1} (Conab, 2025), and there is variability among the populations for this trait. Although the segregating soybean populations belong to the same breeding program, there are differences in their genetic background (cultivars from different companies), ensuring the existence of variability. Carneiro *et al*. (2019) evaluated lineages from a soybean breeding program and found differences among the tested lines due to contrasting genetic origins.

Increasing productivity and reducing days to maturity are among the principal objectives in soybean breeding programs (Carneiro *et al*., 2019); population 6 in this experiment is attributed to this aspect. However, a significant portion of populations exhibit high productive potential but with an extended cycle. It's worth noting that as full maturity decreases, there's also a reduction in grain yield, as evidenced in the data of this experiment, where among the four segregating populations with the lowest full maturity (populations 4, 6, 10, and 11), only one falls among the most productive populations. Gesteira *et al*. (2018) found significant and high-magnitude phenotypic correlations (0.7417) between grain yield and full maturity for soybeans, demonstrating that later maturing genotypes were more productive, although genotypes with lower full maturity and good grain yield can be identified.

The m+a' grain yield estimation represents the contribution of homozygous loci to the grain yield trait, and the higher this value, the greater the contribution of these loci to the trait in question. The m+a' full maturity trait should be interpreted inversely; in other words, lower values indicate a higher contribution of homozygous loci to the lower full maturity of the populations. Ideally, a segregating population should have high values of m + a' and d, as this population should produce lines with high average yields and substantial variation, an important goal for plant breeders (Abreu, 2002).

Comparisons of m+a' estimates among different populations allow them to be classified in terms of the average frequency of favorable homozygous alleles. Among the parents of the three segregating populations, 4, 6, and 10, stand out the cultivars CD250RR, TMG123RR, and BRSMG780RR, as well as the FMT1 line; Gesteira *et al*. (2015) identified earlier maturing genotypes in the southern region of Minas Gerais, among which the CD250RR cultivar and FMT1 line stood out due to their lower full maturity. CD250RR belongs to maturity group 5.5 and is considered super early. BRSMG780RR has exceptionally high yield potential and greater production stability in the presence of diseases, and the TMG123RR cultivar, besides having good production potential, also exhibits tolerance to diseases.

The lower full maturity and m+a' full maturity estimation observed in Ijaci may have occurred due to the sowing period. Sowing in Lavras and Ijaci was done on 21/10/2018 and 28/11/2018, respectively, resulting in a 38-day difference. Silva *et al*., (2019), assessing productive performance and vegetative traits of six soybean cultivars in four different times and two distinct environments, observed that delaying the sowing time led to a reduction in the number of days to flowering and vegetative cycle of the cultivars, causing a reduction in grain productivity, behavior similar to that found in this study. This reduction in the crop cycle is due to the photoperiod; as soybean is a short-day plant, its flowering occurs when the photoperiod is shorter than a critical maximum. Thus, flowering induction happens if the day duration is equal to or less than the critical value characterizing that genotype (Sediyama *et al*., 2015).

Pearson's linear correlation estimates for the segregating populations were obtained to correlate grain yield with m+a' grain yield and full maturity with m+a' full maturity. Both values were significant, with 0.66 for the correlation between grain yield values and 0.90 for the correlation between full maturity values (data not shown). Phenotypic and genetic correlations between traits are also of great importance, as they measure the interaction between two traits or the joint variation in two variables (Ramalho *et al*., 2012).

Correlation measures the intensity of association between two variables, which can be positive (e.g., when both variables increase) or negative (e.g., when one variable increases and the other decreases). In this study, the correlation between the grain yield and full maturity traits with their respective m+a' values had high magnitude (Carvalho *et al*., 2004), reinforcing the importance of this strategy for selecting the best segregating populations.

Estimates of m + a’ for the traits grain yield and full maturity show differences in the contributions of the homozygous loci of the evaluated segregating populations, enabling the selection of superior groups. The FMT1 x TMG123RR deriving population stands out for being the only one to associate high grain yield and m + a’ grain yield, full maturity and m + a’ full maturation.

ACKNOWLEDGEMENTS

The authors acknowledge support from the Conselho Nacional de Desenvolvimento Científico e Tecnológico—CNPq (National Council for Scientific and Technological Development), the Fundação de Amparo à Pesquisa do Estado de Minas Gerais—FAPEMIG (Minas Gerais State Agency for Research and Development), and the Coordenação de Aperfeiçoamento de Pessoal de Nível Superior—CAPES (Brazilian Federal Agency for Support and Evaluation of Graduate Education). The authors also acknowledge support from a CNPq research productivity scholarship.

The authors acknowledge the support of the internationalization project funded by FAPEMIG and developed at Universidade Federal de Lavras.

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