MAIKON FIGUEREDO LEMOS

ADAPTABILITY, STABILITY AND ESTIMATION OF GENETIC PARAMETERS IN SOYBEAN AND SORGHUM.

Thesis submitted to the Genetics and Breeding Graduate Program of the Universidade Federal de Viçosa in partial fulfillment of the requirements for the degree of *Doctor Scientiae*.

Adviser: Aluízio Borém de Oliveira

Co-advisers: Maicon Nardino

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Adviser

I dedicate this thesis to God, whose guidance and strength have been my foundation throughout this journey. Without His blessings, this work would not have been possible.

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To God.

My Wife

To my parents.

My Friends.

My Advisor.

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ABSTRACT

LEMOS, Maikon Figueredo, D.Sc., Universidade Federal de Viçosa, May, 2024. **Use of r packages based on quantitative genetics in the optimization of breeding programs.** Advisor: Aluízio Borém de Oliveira. Co-advisor: Maicon Nardino.

Optimizing breeding programs is currently essential for competitiveness in the seed market share. Ther goal is to develop improved cultivars that are stable, high-yielding, and suitable for a variety of environments. This work aimed to analyze the use of R packages in optimizing breeding programs exploring their applications, benefits, and limitations for sorghum and soybean data analysis. I) select commercial grain sorghum hybrids with greater adaptability and yield stability in three regions of California using R packages; II) analyze the genetic parameters of the different soybean groups to identify the best lines based on MGIDI. This thesis is divided into two chapters. Is important to identify good commercial grain sorghum hybrids with greater adaptability and yield stability in that state. Twelve commercial cultivars were evaluated at three sites in California. Six agronomic traits were evaluated: emergence (EMER), days to flowering (DTF), plants per hectare (PPH), grain yield (KG/HA), panicle length (PANICLE), 1,000-grain weight (TGW) in each plot, data were analyzed with R software v.4.2.3, and the Metan package was used for all BLUP and AMMI analyses. We obtained high precision in the analyzed data, except for the EMER variable. The AMMI analysis had significant environmental effects for the variables DTF, KG/HA, and PANIC. There were genetic effects for PHA and emergence, as well as GxE effects for TWG. For stability and adaptability, we analyzed using BLUP. Cultivars 2, 7, and 9 were more stable for most traits except TWG. For the WASSB analyses, cultivars 3, 4, and 9 were plotted in the fourth quadrant, showing themselves more high-yielding and stable. Environmental interactions in sorghum cultivars directly affect their responses, in addition, the variation components act differently for each variable, therefore cultivar 2 and cultivar 7 stood out as stable and adapted in the studied environments, and BLUP and AMMI showed adequate precision for sorghum selection. The second article analyzed the genetic parameters of different soybean groups to identify the best lines based on MGIDI. Soybean cultivars from Embrapa's genetic breeding program were used, and the experiment was divided according to maturity groups (early, medium, and late) and different technologies: RR® (glyphosate-resistant) and Bt® (lepidopteran resistant). Three agronomic traits were selected: plant height (cm), yield (kg/ha) and ideotype. The ideotype was visually evaluated in the field based on the plant's vigor and lodging, with scores ranging from 1 to 5, 1 being the best and 5 being the worst. Lines in groups 5 and 6 have low heritability for yield, and maturity groups directly interfere with genetic factors. Based on MGIDI and BLUPS, lines LRRE 7 and 9 of Group 1, LIPROE 7 and BRS 590 of Group 2, LRRM 7 and 9 of Group 3, LIPROM 3 and 9 of Group 4, LRRL 4 and Monsoy 9144 of group 5 and HO Cristalina and BMX Extreme.

Keywords: heritability, panicle, environmental, cultivars, soybean, yield

RESUMO

LEMOS, Maikon Figueredo, D.Sc., Universidade Federal de Viçosa, Maio de 2024. **Utilização de pacotes R baseados em genética quantitativa na otimização de programas de melhoramento genético.** Orientador: Aluízio Borém de Oliveira. Coorientador: Maicon Nardino.

A otimização dos programas de melhoramento é essencial para ser competitivo no mercado de sementes hoje em dia. O objetivo é desenvolver cultivares melhorados que sejam duráveis, de alto rendimento e adequadas a uma variedade de ambientes. O objetivo foi analisar a utilização de pacotes R na otimização de programas de melhoramento, explorando suas aplicações, benefícios e limitações para análise de dados de sorgo e soja; I) selecionar híbridos comerciais de sorgo granífero com maior adaptabilidade e estabilidade de produção em três regiões da Califórnia usando pacotes R; II) analisar os parâmetros genéticos dos diferentes grupos de soja para identificar as melhores linhagens com base no MGIDI. Esta tese está dividida em dois capítulos. A Califórnia possui o maior rebanho leiteiro dos Estados Unidos e por isso é importante identificar bons híbridos comerciais de sorgo granífero com maior adaptabilidade e estabilidade de produção no estado. Foram avaliadas seis características agronômicas, emergência (EMER), dias para florescimento (DTF), plantas por hectare (PPH), produtividade de grãos (KG/HA), comprimento da panícula (PANICLE), peso de 1.000 grãos (TGW), em cada parcela, os dados foram analisados com o software R, e o pacote Metan foi utilizado para todas as análises BLUP e AMMI. Houve efeitos ambientais significativos na análise AMMI para as variáveis DTF, KG/HA e PÂNICA, houve efeitos genéticos para PHA e emergência e efeito GxE para TWG. Para análises de estabilidade e adaptabilidade utilizando BLUP, as cultivares 2, 7 e 9 foram mais estáveis para a maioria das características, exceto TWG. Para as análises WASSB, as cultivares 3, 4 e 9 foram plotadas no quarto quadrante, mostrando-se mais produtivas e estáveis, em geral. As interações ambientais nas cultivares de sorgo afetam diretamente suas respostas, além disso, os componentes de variação atuam de forma diferente para cada variável, portanto a cultivar 2 e a cultivar 7 se destacaram como estáveis e adaptadas nos ambientes avaliados, e o BLUP e AMMI apresentaram precisão adequada para a seleção de sorgo. O segundo capítulo tem como objetivo analisar os parâmetros genéticos dos diferentes grupos de soja para identificar as melhores linhagens com base no MGIDI. Foram utilizadas cultivares de soja do programa de melhoramento genético da Embrapa, e o experimento foi dividido de acordo com grupos de maturidade (precoce, média e tardia) e diferentes tecnologias: RR® (tolerante ao glifosato) e Bt® (resistente a lagartas). Três características agronômicas foram selecionadas: altura de planta (cm), produtividade (kg/ha) e ideótipo. O ideótipo é avaliado visualmente em campo com base no vigor e acamamento da planta, com notas que variam de 1 a 5, sendo 1 o pior e 5 o melhor. As linhagens dos grupos 5 e 6 apresentam baixa herdabilidade e os grupos de maturidade interferem nos fatores genéticos. Baseado em MGIDI e BLUPS, linhas LRRE 7 e 9 do Grupo 1, LIPROE 7 e BRS 590 do Grupo 2, LRRM 7 e 9 do Grupo 3, LIPROM 3 e 9 do Grupo 4, LRRL 4 e Monsoy 9144 do grupo 5 e HO Cristalina e BMX Extrema.

Palavras-chave: herdabilidade, panícula, ambiental, cultivares, soja, produtividade

SUMMARY

CHAPTER I

1.0 GENERAL INTRODUCTION

Optimizing breeding programs is essential for modern agriculture to produce improved crop types that are durable, high-yielding, and suitable for various environments (Chris Gaynor et al., 2021). Even if they work well, traditional plant breeding techniques often face problems with time management, resource allocation, and the complexity of genetic data. The use of computational tools and statistical approaches to improve the efficiency and effectiveness of yield has undergone a radical change due to rapid progress in these (Kinghorn et al., 2022; Hassanpour et al., 2023).

The R programming language has emerged as a leading platform in this computing revolution, with a vast collection of specialized packages designed to assist in various areas of program improvement optimization (Chris Gaynor et al., 2021; Caamal-Pat et al., 2021). These R packages provide breeders with robust data analysis, visualization, simulation, and decision-making tools, extracting valuable information from complex breeding data and making sound selection and mating decisions (Olivoto and Lúcio, 2020).

Integrating R packages into breeding programs can revolutionize traditional breeding strategies by facilitating improved selection, optimizing breeding projects, and accelerating genetic gain (Caamal-Pat et al., 2021; Klein et al., 2023).

Multivariate analysis, which combines a series of traits with significant computational modeling, is a valid and reliable statistical analysis that can be used to achieve excellent genetic stability results, discriminating and interpreting the GEI effect in multi-environmental genotype assays (Huang et al., 2016; Olivoto et al., 2019) Therefore, to establish accurate selection criteria for use in breeding programs, plant breeders must investigate the links between traits that affect yield. Earlier authors often looked to interaction models, sometimes challenged by stability analyses, including joint regression (Yates and Cochran, 1938).

Understanding the complex link between genotype and phenotype is crucial to crop improvement and sustainable agricultural methods; the process of genetic improvement is essential to world agriculture, soybean, corn, rice, and now sorghum, leading this effort to maximize each increasing the process (Danilevicz et al., 2022; Hossain et al., 2022). The use of computational tools, especially the R programming language, has become essential to understanding the complex composition of genetic responses that underpin the traits of these cultures (Chris Gaynor et al., 2021).

Increasingly, digital tools are used to determine existing environmental relationships affecting plants' quantitative and quantitative traits. The authors (Olivoto et al., 2019; Chris Gaynor et al., 2021) have increasingly demonstrated that as much as R packages to analyze different factors of various types of crops ranging from creeping plants to trees, the lack of hand of work, the urgency of obtaining faster results, optimizing and increasingly accelerating the use of these tools.

This thesis aims to analyze the use of R packages in optimizing breeding programs exploring their applications, benefits, and limitations in analyzing sorghum and soybean data.

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CHAPTER II

2.0 ADAPTABILITY AND STABILITY OF COMMERCIAL GRAIN SORGHUM CULTIVARS IN CALIFORNIA

ABSTRACT

Sorghum bicolor (*L.*) is the fifth most important cereal regarding global yield and harvested area. The use of sorghum cultivars requires an understanding of the performance of potential genotypes in different environmental conditions, and, with this, the study of adaptability and stability of behavior is essential to optimize planting. This research aimed to select commercial grain sorghum hybrids with greater adaptability and yield stability in California, USA. Twelve commercial cultivars were evaluated in three locations in California. Six agronomic traits, emergence (EMER), days to flowering (DTF), plants per hectare (PPH), grain yield (KG/HA), panicle (PANICLE), 1000-grain weight (TGW) were evaluated in each plot. The data were analyzed with R v.4.2.3 software, and the Metan package was used for all BLUP and AMMI analyses. We obtained high accuracy in the data analyzed, except for the EMER variable. There were significant environmental effects in the AMMI analysis for the DTF, KG/HA, and PANICLE variables, as well as genetic effects for PHA and emergence and a GxE effect for TWG. For stability and adaptability analyses using BLUP, cultivars 2, 7, and 9 proved more stable for most traits except TWG. For WASSB analyses, cultivars 3, 4, and 9 were plotted in the fourth quadrant, proving more productive and stable. In the IPCA analysis, in general, cultivars 2, 3, and 9 were more stable and adaptable in all environments, and in the Anova analysis based on AMMI, there were significant environmental effects for DTF, KG/HA, and PANICLE, as well as substantial genetic effects for PHA and emergence and genotype-environment interaction (GxE) in the TWG variable. Environmental interactions in sorghum cultivars directly affect their responses, in addition, components of variation act in different ways for each variable, so cultivar 2 and cultivar 7 stood out as stable and adapted in the environments evaluated, and BLUP and AMMI analysis showed adequate accuracy for sorghum cultivation.

Keywords: *Sorghum bicolor (L),* GXE Interaction, WAASB, heritability, panicle

2.1 Introduction

The world's growing population, coupled with the increasingly pressing challenges of climate change, poses an unprecedented threat to global food security (FAOSTAT, 2022). Our agricultural systems' resilience is being tested as we face the consequences of changing weather patterns, prolonged and severe droughts, and increasing water scarcity (Mansour et al., 2021). In this context, cultivating drought-tolerant crops is becoming a priority, and one such crop that remains resilient in the face of these challenges is the sorghum, *Sorghum bicolor* (L.).

Sorghum bicolor (L.) is the fifth most important cereal regarding global yield and harvested area (FAOSTAT, 2022). The United States (US) is the leading global producer, accounting for 17% of total yield over the last five years (FAOSTAT, 2022). In the US, sorghum is mainly used as a fodder crop and is rapidly emerging as a biofuel option (Carcedo and Ciampitti, 2023). Compared to other cereals, sorghum is more tolerant of high temperatures and drought (Reynolds et al., 2016).

Sorghum is a carbohydrate-rich species from the Gramineae family that originated in Africa (Hossain et al., 2022), (Reddy and Reddy, 2019). It is a species that tolerates low input levels, making it indispensable for areas with little rainfall (Stamenković et al., 2020). Such intriguing details make it an ideal species for exploring evolutionary connections with other grass species and conducting research from different perspectives on climate change to ensure food security (Mickelbart et al., 2015; Hossain et al., 2022). The use of sorghum cultivars requires an understanding of the performance of potential genotypes in different environmental conditions. Genotype-by-environment interactions make recommending cultivars for different environments difficult, making adaptability and stability analyses necessary (Fillipe De Souza et al., 2013). The study of adaptability and stability allows the identification of genotypes with predictable behavior in specific or general environments and genotypes sensitive to favorable environmental variations (Cruz et al. 2004).

There are various methods for analyzing the adaptability and stability of genotypes when grown in different environments. The use of a particular method for analyzing experimental data depends mainly on the number of environments available, the precision required, and the type of information desired (Schmildt et al., 2011).

Researchers deal with multi-environment data (between sites, years, management practices, or combinations of these factors) in an attempt to find out how a trait varies between environments (Balestre et al., 2009), an alternative to mitigate the effects of the G × E interaction is to identify and select genotypes with greater adaptability and productive stability. Numerous methods have been reported in the literature for studying adaptability and stability in multi-environment trials (De Moraes et al., 2020). The proposed methods can be based on variance analysis components, the regression method, non-parametric methods, multivariate methods, mixed models, and new methods such as factorial analytical models (De Moraes et al., 2020; Anuradha et al., 2022).

This study aimed to select commercial grain sorghum hybrids with greater adaptability and yield stability in three regions of California.

2.2 Materials and Methods

The experiment was carried out at three sites: Kearney Agricultural Research and Extension Center (KARE), West Side Research and Extension Center (WSREC), and UC DAVIS (Figure 1), which have different soil and climate traits. Data on planting date, previous crops planted, and type of irrigation used are shown in Table 1. Twelve commercial grain sorghum hybrids were used, which were coded from 1 to 12 (Table 2) and planted in a randomized complete block design with three replications with four rows of plants per plot and 20 plants per row. Irrigation was carried out to meet the crop's demand based on its evapotranspiration.

Table 1. Summary of the locations where trials were located.

Trial Location	Soil Type	Irrigation	Planting Date	Rainfall (jan-set 2022)	Previous Crop
Kare	Hanford sandy loam	Furrow irrigation	June 1, 2022	129.54 mm	Winter forage (Oats)
WSREC	Panoche clay loam	Furrow irrigation	June 6, 2022	79.51 mm	Sorghum
DAVIS	Yolo loam	Furrow irrigation	June 6, 2022	125.72 mm	Fallow

2.2.1 Traits evaluated

Six main agronomic traits were selected for statistical analysis of stability and adaptability: emergence (EMER), days to flowering (DTF), plants per hectare (PPH), grain yield (KG/HA), panicle (PANICLE), 1000-grain weight (TGW). In addition to these variables, panicle length (PLH) and plant height (HEIGHT) were added to analyze variance components.

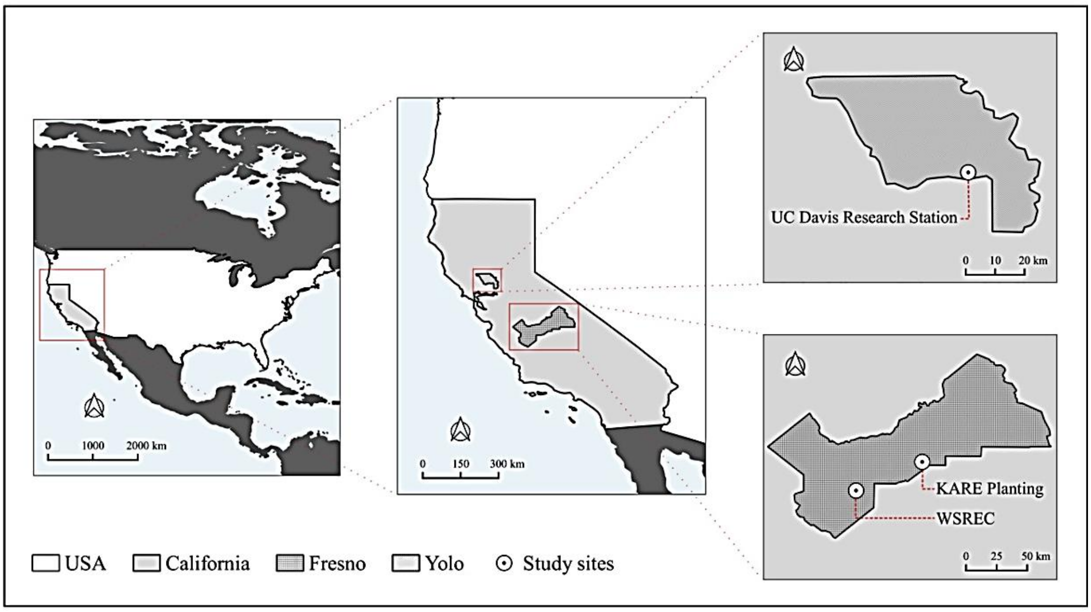

Figure 1. Location map of experimental sites.

2.2.2 Statistical analysis

The data was analyzed using the software R v.4.2.3(R Core team, 2023) using the package metan (Olivoto and Lúcio, 2020). For each set of data, cross-validation (CV) analyses were carried out for the BLUP and AMMI family models using the "cv_BLUP" and "cv_AMMIf" functions from the "metan" package. The analyses of variance data were evaluated based on the AMMI equation with significant results ($P>0.05$), the variance components and the significance level of the effects of genotype, environment, and E x G interaction were determined, and the best linear unbiased prediction (BLUP) for the genotypes tested in each environment or combined across all environments was calculated. In addition, the coefficients of variation (CV%), broad-sense heritability (H^2), coefficient of variation (CVg), accuracy, residual coefficient of variation (CVr), and the overall mean for each trait were calculated implemented in R according to the methodology of (Olivoto and Lúcio, 2020).

The sum of squares for the G x E interaction was divided into n singular axes or interaction principal components (IPCA), which describe the standard portion (ANOVA), with each axis corresponding to an AMMI model. Generally, when G x E interactions are significant, AMMI models with one or two main axes (AMMI-1 and AMMI-2 models, respectively) are the most commonly used due to their simplicity in biplot graph representations.

Table 2. Hybrid information and inputs used in the statistical data.

Entry	Company	Hybrid
1	Dyna-Gro	M59GN94
2	Dyna-Gro	M60GB31
3	Dyna-Gro	M63GB78
4	Dyna-Gro	M67GB87
5	Dyna-Gro	M71GR91
6	Dyna-Gro	M72GB71
7	S&W Seed	SP7715
8	S&W Seed	SP72M42
9	S&W Seed	SP78M42
10	S&W Seed	NK8828
11	S&W Seed	SPSD455
12	S&W Seed	Filler NK8828

2.3 Results

In the analysis of variance components (Table 3), the heritability showed a low relationship between the parameters evaluated, demonstrating high environmental interference and, consequently, low genotypic action. However, the plant per hectare (PPE) variable had higher values for both H^2 and coefficient of variation. Most variables were analyzed with high accuracy, but we obtained lower accuracy for yield (Kg/ha) and emergence (EMER). In the relative yield coefficient, we obtained high heats where, according to (Pimentel et al., 2014), values above 1.0 are considered favorable, and according to (Marcos Deon Vilela de Resende, 2007) and a good accuracy of the data, being similar to the accuracy data (Table 3).

Table 3. Heritability, accuracy, genotype-environment correlation (GEIr2), coefficient genotypic (CVg), coefficient residual (CVr), and CV ratio.

Parameters	**EMER**	**PLH**	**DTF**	**PPH**	**HEIGHT**	**PANICLE**	**TWG**	**KGHA**
Heritability	0.0280376	0.24923	0.21728	0.45129	0.28406	0.024983	0	0.02253
GEIr2	0.5952931	0.19143	0.38374	0.08095	0	4.42E-18	0.308	0.14781
Accuracy	0.3232540	0.81503	0.74687	0.92255	0.883869	0.432891	0	0.37067
CVg	2.9872773	3.08604	2.91959	11.6246	4.220386	2.074149	0	3.07013
CVr	10.94925	4.62307	3.95614	11.8346	6.700161	12.95754	6.348	18.6294
CV ratio	0.2728293	0.66753	0.73798	0.98225	0.629893	0.160073	0	0.1648

Emergence (EMER), panicle length (PLH), days of flower (DTF), plant per acre (PPH), panicle exertion, grain weight in thousand (TWG), Yield (KG/HA).

According to the AMMI analysis (Table 4), there were significant effects ($p \leq 0.005$) for the environment in the variables DTF, KG/HA, and PANICLE were significant for the genotype effect the variables PHA and emergence were significant corresponding to 43.9% and 8.97% respectively of the variation, for the genotype x environment interaction (G x E) the variable thousand-grain weight (TWG) had a significant effect corresponding to 42.8 of the variation.

Table 4. Table de analyzes AMMI for variable Days to flowering (DTF), Planta per hectare (PPH), Yield (KG/HA), panicle exertion, emergence e peso de grain (TGW).

		DTF		PPH		KH/HA		PANICLE		EMERGENCE		TGW	
		MSS	Var (%)	MSS	Var (%)	MSS	Var (%)	MSS	Var (%)	MSS	Var (%)	MSS	Var (%)
ENV	2	278912.9*	100	2798409.42	-	25101461.1*	100	78.02*	100	14237.84	-	277.51*	42.8
REP	6	27.18	-	27972567.2	-	18690987	-	10.01	-	143.8704	-	1.61	-
GEN	11	202.31	-	167400238*	43.9	34732041	-	17.94	-	473.4234*	8.97	6.31	-
GEN: ENV	22	89.45	-	24926654.6*	-	59921541	-	11.49	-	424.0749	-	9.58*	16.3
PC1	12	153.39	-	45698050	13.7	34141581	-	21.07	-	636.1048*	13.14	12.47*	11.5
PC2	10	12.74	-	0	-	25779960	-	-	-	169.6391	-	6.12	-
Residuals	66	23.02	-	16407932.6	-	117147558	-	15.61	-	73.86027	-	3.63	-
Total	129	4385.04	-	32515869.4	-	541428280	-	15.11	-	450.2375	-	10.04	-

MSS = Mean sum of squares; df = Degrees of freedom; PC = Principal Component;
*=Significant at 5 % level.

To identify potential hybrids from multi-environment trials (METs), breeders often use various statistical tools, such as AMMI, GGE biplot, BLUP, or their combinations.

For the DTF variable, cultivars 4, 7, 9, 2, and 12 obtained the highest values (Figure 2), where most cultivars had cross-interactions between environments, as shown by the AMMI yield (Figure 3). It can be seen that cultivars 7 and 2 had an attenuating decrease with the change of environment, according to the WAASB analysis per plot. According to the WAASB analysis, cultivar 9 is in quadrant IV (Figure 4), thus performing above average and with better stability. Cultivar 12 was plotted in quadrant II, its value being above average, as were cultivars 7 and 2. However, these last two cultivars are distant from the WAASB line, making them less stable, corroborating with (Figure 2). Finally, cultivar 9 was the cultivar that showed the best performance and stability for the DTF variable.

For the PPH variable, analysis with BLUP indicated that cultivars 2, 3, 5, and 11 obtained the highest classification, and variable 9 obtained the lowest performance (Figure 2). Some genotypes obtained cross-interactions; however, genotype 2 remained stable in this IPCA analysis (Figure 3). According to WAASB data (Figure 4), genotypes 2, 5, 7, and 11 obtained the best average yield and stability, as shown in quadrant IV. Genotype 5 is more stable as it is closer to the WAASB line.

For the variable KG/HA in the BLUP, cultivars 9.5, 1, and 4 obtained the highest values, and cultivar 8 was plotted with the lowest value (Figure 2). Cultivars 2 and 11 had the highest average yield values and good stability according to the IPCA analysis (Figure 3). According to the WAASB analysis, cultivars 4, 9, 5, and 1 are in quadrant II (Figure 4), so they are the most stable and have the highest yields, with cultivar 1 standing out the most as it is close to the WAASB line.

For the PANICLE variable, the BLUP analysis (Figure 2) identified that cultivars 6, 2, 8, and 12 had the best performance; in the IPCA1 analysis (Figure 3), cultivars 6 and 4 were more stable and had average yields; in the WAASB analysis (Figure 4), cultivar 2 had the best yield performance and excellent stability.

As for emergence according to BLUP (Figure 2), cultivars 7, 2, 3, and 5 obtained the best values, while for the IPCA1 analysis, cultivar 7 proved to be more stable and had more satisfactory average values. Cultivars 2 and 10 obtained crossed results showing high instability (Figure 3), and in the WAASB analysis (Figure 4), cultivars 3 and 2 obtained higher average values, showing better performance and optimum stability.

For the weight of 1000 grains (TGW), the BLUP analysis did not identify any difference between the cultivars (Figure 2). According to the WAASB, cultivar 1 was the only cultivar that showed in the graph (Figure 4) that it had high yields and good stability, being in quadrant IV and close to the central WASSB line.

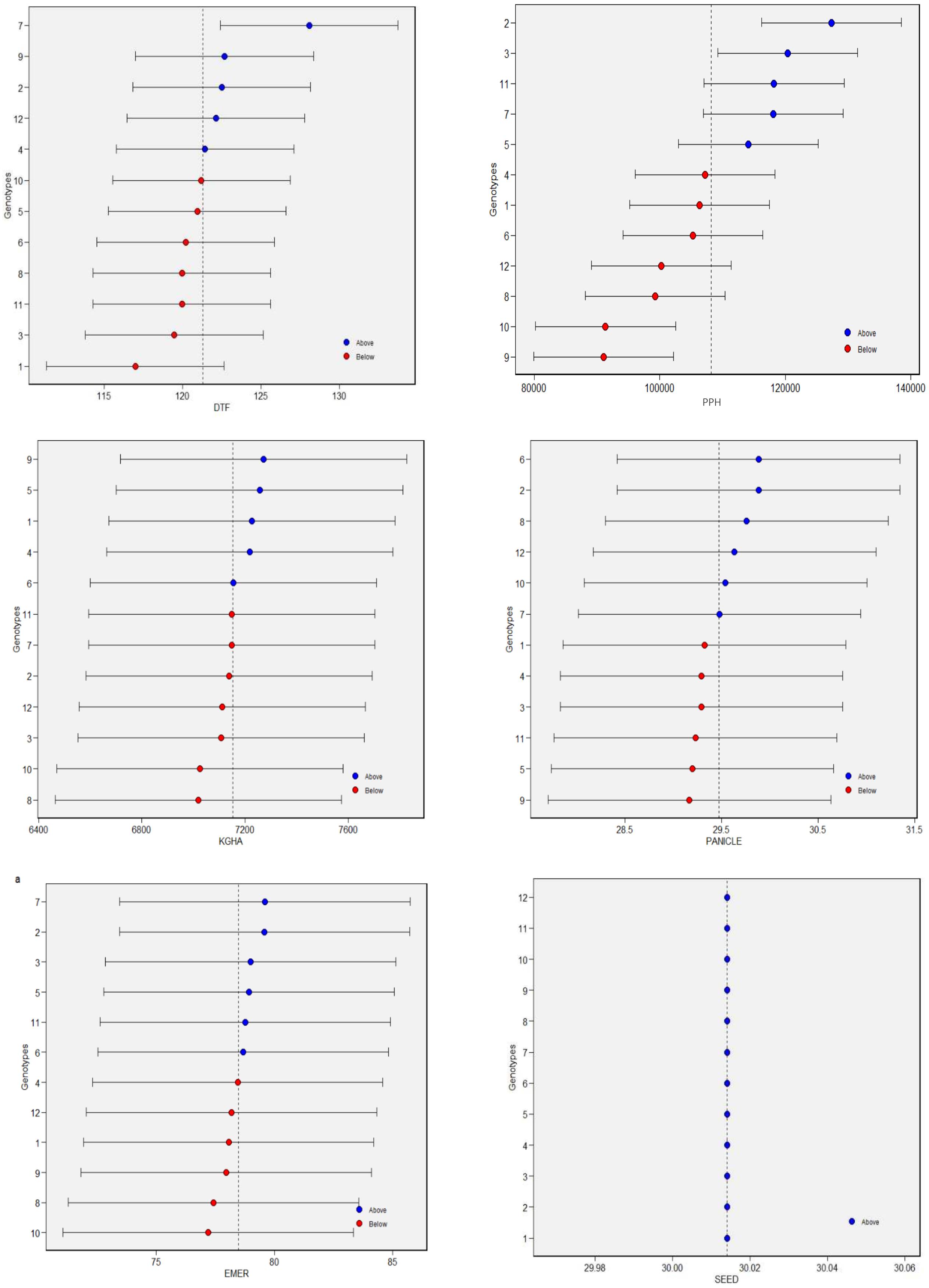

Figure 2. Best linear unbiased prediction (BLUP) of sorghum cultivars.

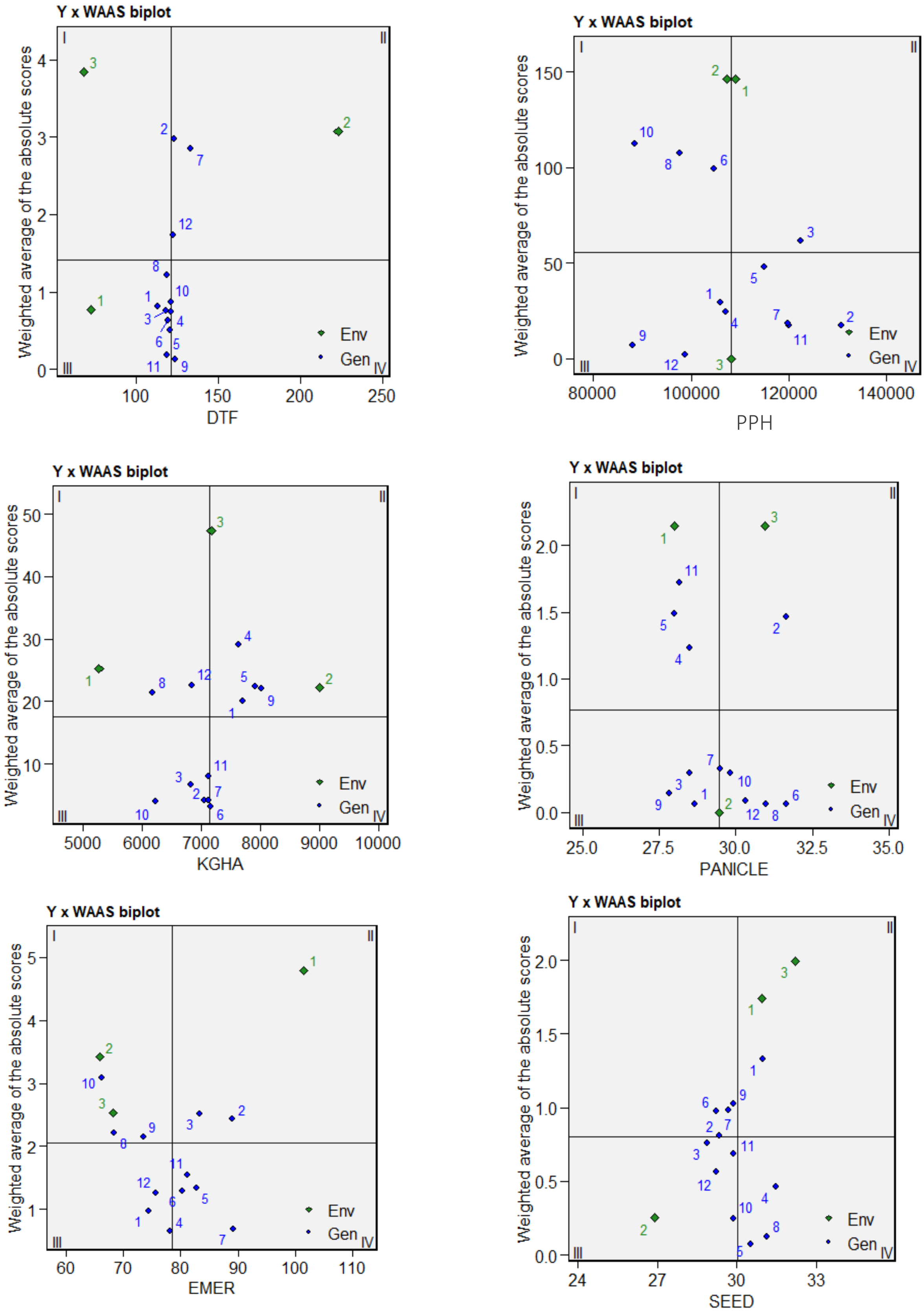

Figure 3. WAASB by yield plot presents genotypes' overall performance and stability, environmental yield, and discriminative ability.

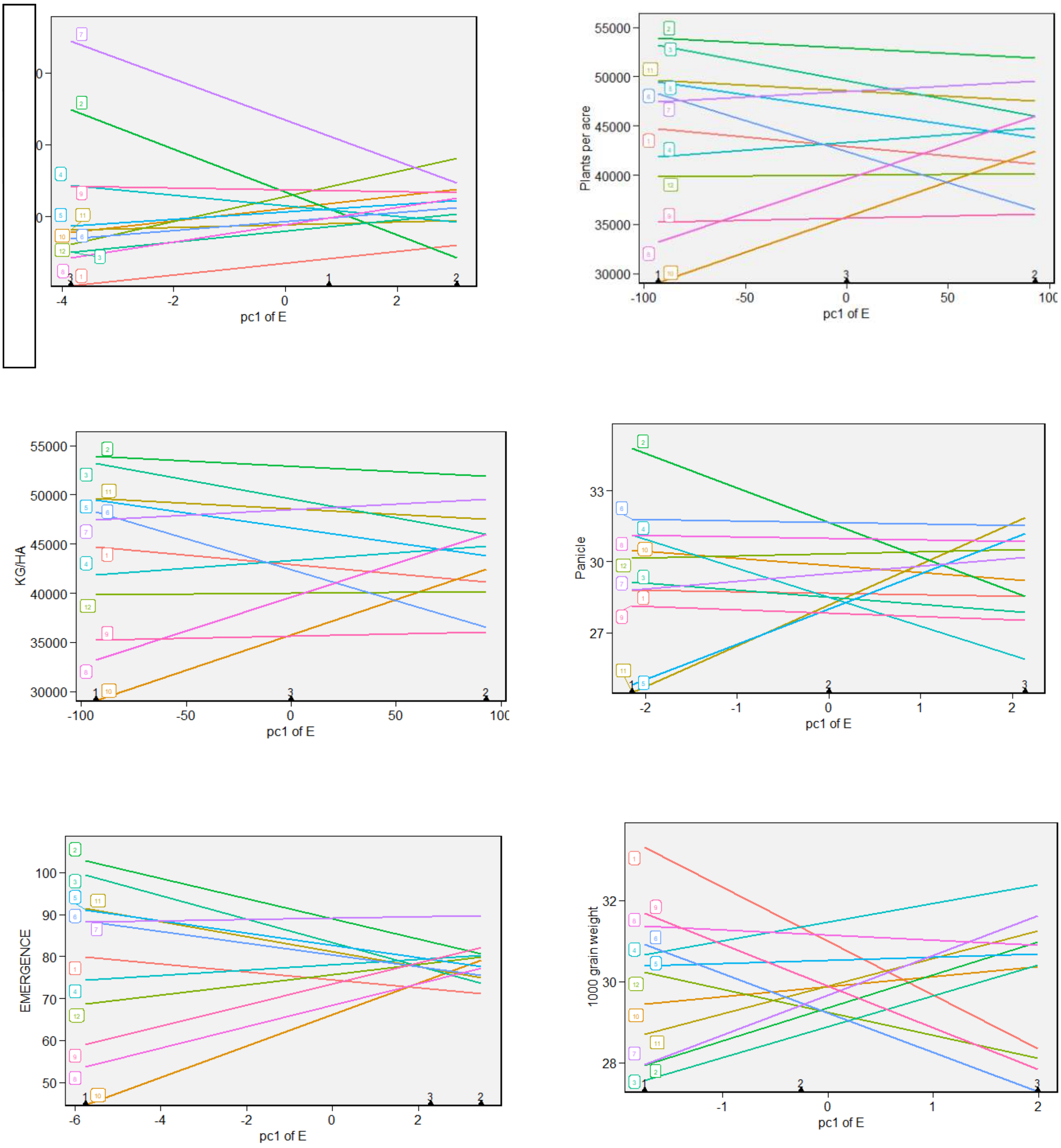

Figure 4. Performance of genotypes across the environments in the six datasets presented in AMMI's yield by environmental IPCA1.

2.4 Discussion

When working with sorghum cultivars in different environments, in general, there are G x E interactions, thus altering the behavior of varying crop traits in some way. Some traits are more affected by the environment, such as yield (Yield) (Ndiaye et al., 2019), which tends to have a positive or negative correlation depending on the conditions of the environment tested. Some traits are linked to more genes; therefore, genetic factors have a more significant influence on their results, interacting directly with the weight per thousand grains (TGW). Similar to this study's results were also observed in the literature (Almeida Filho et al., 2014; Ndiaye et al., 2019). We can see that the components of variation act differently on each variable, and (Olivoto et al., 2019) when evaluated independently, the percentage of variability is dissipated in the components.

Although some variables did not have significant G x E interactions, AMMI and WASBY analysis was carried out because there were a lot of cross-interactions (Figure 4). It can also be seen that some genotypes behave differently when the environment changes (Chapman et al., 2000). The behavior of genotypes for some variables when the environment is modified can vary without significant static E x G interactions.

Significant G x E interactions indicate the differential response of genotypes between environments (Adjebeng-Danquah et al., 2017). Looking at the climatic traits of each environment (Table 3), they differed in altitude, latitude, longitude, and climate, including rainfall and temperature. A significant G x E interaction can also be attributed to predictable factors such as soil management, pests and diseases, irrigation, and fertilization, and unpredictable factors such as precipitation, temperature, relative humidity, and solar radiation (de Albuquerque et al., 2023). These authors also reported that climatic parameters and soil types are two main factors determining genotypic performance in different locations.

BLUP represents the genotypic value of the genotypes and is preferable for predicting the overall performance of the genotypes (Taleghani et al., 2023). In addition to BLUP, AMMI, and GGE biplot analyses can be used to reveal yield performance and stability in all environments, allowing selection for broad or specific adaptability based on the objectives of the breeding program (Olivoto et al., 2019b).

According to (Olivoto et al., 2019), when analyzing genetic predictions with BLUB and AMMI, among others, it is necessary to analyze broadly and, if possible, together, in this study, we noticed that some genotypes (Figure 2), (Figure 3) and (Figure 4) in the BLUP analysis when analyzed alone might not answer how the cultivars behave in multiple environments (Yan et al., 2007; Worede et al., 2020) in addition, in Figure 3 we can see cross movements in the yield and adaptability of the cultivars. When the environment influences variables, they can fluctuate directly, thus modifying their stability and yield in different environments (Saltz et al., 2018). In this study, we noticed many environmental variations, both in the climatic sense (rainfall, temperature) and agronomic sense, such as soil type. Despite this, some cultivars, such as 2, 7, and 9, stood out. This can be seen in (Table 3) where, according to (Dario Delgado et al., 2019), when there are low heritability values, the genetic effects are low, and there is a greater tendency for the environmental effect.

2.5 Conclusion

In this study, cultivars 2 (M60GB31) from Dyna-Agro® and 7 (SP7715) and 9 (SP78M42) from S&W Seeds® proved to be more stable and adaptable in the environments tested.

There was no significant genetic effect for the variables evaluated, most of which were environmental.

Data analysis with AMMI and BLUP showed good accuracy for sorghum cultivation.

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CHAPTER III

3.0 GENETIC PARAMETERS OF DIFFERENT MATURITY GROUPS AND MIGIDI ANALYSIS FOR SOYBEAN LINES

ABSTRACT

Soybean (*Glycine max*) is an oilseed crop with various commercial cultivars adapted for cultivation in different latitudes worldwide. Relative maturity is a classification designed to consider all the factors that affect the harvest date: the number of days from planting to physiological maturity. Accordingly, our goal was to analyze the genetic parameters of the different soybean groups to identify the best lines based on MGIDI. This work was conducted in the experimental field of the Fundação Bahia, located in the municipality of Luís Eduardo Magalhães -BA. Soybean cultivars from Embrapa's genetic breeding program were used, and the experiment was divided according to maturity groups (early, medium, and late) and different technologies: RR® (glyphosate-resistant) and Bt® (*Bacillus thuringiensis*). Three agronomic traits were selected: plant height (cm), yield (kg/ha) and ideotype. Based on plant vigor and lodging, the ideotype is assessed visually in the field, with scores ranging from 1 to 5, where 1 is the lowest and 5 is the highest. Data manipulation and index calculation were carried out in the R software using the "gamem" function for the genetic parameters and the "MGIDI" function for the ideotype analyses, both of which are in the 'metan' package. In the analysis of genetic parameters for yield, there was high heritability only for the cultivars in group 1, with values above 0.5. For plant height, the heritability values were considered high for all the groups except group 2, while the heritability values for cultivars in groups 5 and 6 (late group) were average. In the BLUP analysis between the groups, group 6 stood out with the best performance in yield and plant height, all the groups were above the ideal average, thus demonstrating excellent values regardless of the group. As for the ideotype, only group 5 was less than ideal when working with the genetic parameters of autogamous species. There is a considerable variation in the results and low heritability values for yield are considered normal due to environmental factors, which have a strong influence. Lineages from groups 5 and 6 have low heritability and maturity groups directly interfere with genetic factors. Based on MGIDI and BLUPS, the lines LRRE 7 and 9 from Group 1, LIPROE 7 and BRS 590 from Group 2, LRRM 7 and 9 from Group 3, LIPROM 3 and 9 from Group 4, LRRL 4 and Monsoy 9144 from group 5 and HO Cristalina and BMX Extrema.

Keywords: Environmental, cultivars, soybean, yield.

3.1 Introduction

Soybean (*Glycine max*) is an oilseed crop with various commercial cultivars adapted for cultivation in different latitudes worldwide (Zanon et al., 2015). This crop has been gaining more space globally, being a fundamental commodity for Brazil's Gross Domestic Product growth and ranking among the nation´s top exported items (Rocha et al., 2018; Caldas et al., 2023).

It is also one of the most important crops globally, playing a crucial role in food security and the agricultural economy (Nair et al., 2023). The high market potential, coupled with the excellent crop adaptability across all Brazilian territories, has led to its increasingly widespread cultivation in every country region, significantly contributing to the national economy (Vollmann and Škrabišová, 2023). Its adaptability to different climatic conditions makes it a highly valued crop in various agricultural systems.

One of the most influential traits in soybean yield is its maturity group, which is critical in determining the plant's growth period and its adaptability to different regions (Alliprandini et al., 2009). Researchers are working to develop cycle varieties that meet the needs and demands of the market (Rodrigues et al., 2001), and these aspects are justified because they reduce yield costs and reduce exposure to biotic and abiotic stresses, as well as contribute to the off-season crop cultivation (Ceccon et al., 2013).

Relative maturity is a classification designed to consider all the factors that affect the harvest date: the number of days from planting to physiological maturity (Alliprandini et al., 2009). Relative maturity groups are divided into tenths to obtain a relative value. The method used to determine this is the observation of 95% of brown fruit, according to Spehar (2010), where a variety with a relative maturity rating of 3.5 can reach the stage of 95% brown (mature) pods five days later than a variety with a rating of 3.0 (Zhang et al., 2007). The classic approach to describing relative maturity in Brazil uses early, intermediate, and late cultivars (EMBRAPA, 1998; Spehar, 1994). This method can describe relative maturity locally but has not been successful in describing relative maturity in the wide range of environments and latitudes throughout Brazilian soybeans.

From that, it is crucial to understand how maturity groups interfere in the breeding process, where at the field level, they directly interfere in decision-making within the breeding process (Alliprandini et al., 2009), and understanding how each maturity group behaves in a given environment is important for selection advances (Liu et al., 2020).

Genetic parameters play a fundamental role in soybean cultivation, influencing various essential traits, from adaptation to different environments to grain quality (Rodrigues et al., 2001). Along with the importance of choosing the right maturity group (SEDIYAMA, T.; SILVA, F.; BORÉM, 2015), there is an important variation to be studied within each group, which can move the decision-making process faster for breeders. Accordingly, our goal was to analyze the genetic parameters of the different soybean groups to identify the best lines based on MGIDI.

3.2 Material and methods

3.2.1 Field trial location

This work was conducted in the experimental field of the Fundação Bahia, located in the municipality of Luís Eduardo Magalhães -BA, with geographical coordinates of 12°05'47.4"South 45°42'35.9"West and an altitude of 720m. The area used is in a field irrigated by a central pivot, measuring 16,056 m².

3.2.2 Experimental design, crop management, and assessed traits

Soybean cultivars from Embrapa's genetic breeding program were used, and the experiment was divided according to maturity groups (early, medium, and late) and different technologies: RR® (glyphosate-resistant) and Bt® (*Bacillus thuringiensis*) (Table 1). The experimental design was randomized blocks in each trial. The groups consisted of 16 treatments with four replications, totaling 64 plots. Each treatment had four commercial cultivars as a control, with known traits, and 12 lines in VCU. Sowing was carried out mechanically using an Embrapa plot planter. Four applications of herbicide were made. The experiment was conducted in a rainfed system, with some applications of water to maintain the experiment through the center pivot.

Table 1. Maturity groups, technologies, and growth types of soybean lines and cultivars.

Group	Maturity groups*	Technology	Type of growth
1	Early	RR	Determined/indeterminate
2	Early	IPRO	Determined/indeterminate
3	Medium	RR	Determined/indeterminate
4	Medium	IPRO	Determined/indeterminate
5	Late	RR	All
6	Late	IPRO	All

*RR- Roundup; IPRO- intacta RR2 PRO®

Three agronomic traits were selected: plant height (cm), yield (kg/ha) and ideotype. Based on plant vigor and lodging, the ideotype is assessed visually in the field, with scores ranging from 1 to 5, where 1 is the lowest and 5 is the highest.

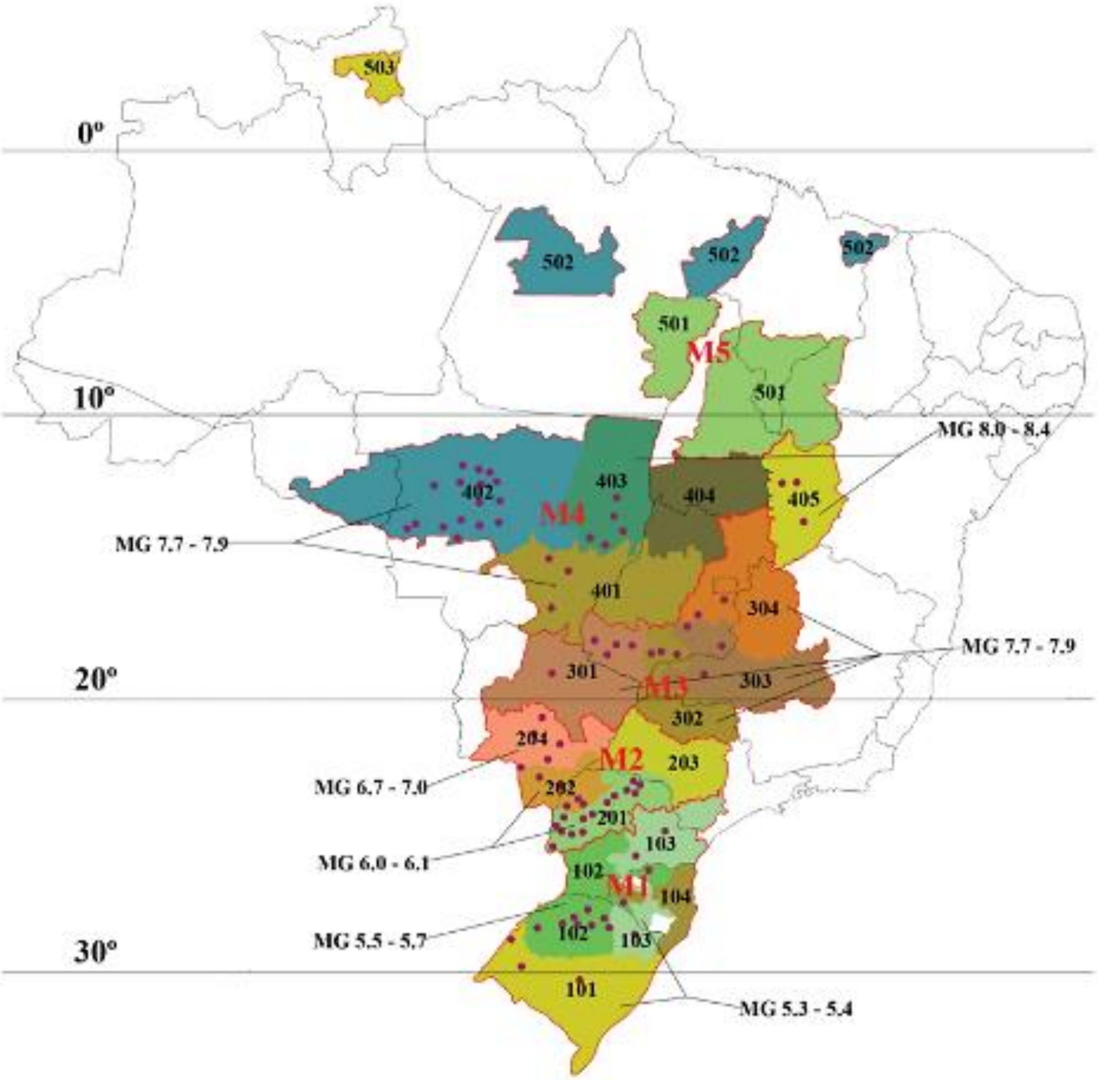

Figure 1. Soybean maturity groups according to latitude in Brazil.

3.2.3 Statistical analysis

The Restricted Maximum Likelihood (REML) method was used to estimate the variance components and genetic parameters according to the following statistical model: $Y_{ij} = m + g_i + r_j + e_{ij}$, where Y_{ij} is the response variable of the i-th genotype and in the j-th block; m is the overall mean (fixed); g_i is the effect of the i-th genotype (considered random); r_j is the effect of the j-th replication (considered fixed); and e_{ij} is the random error. This approach made it possible to estimate phenotypic variance (σ^2P), broad-sense heritability (H^2), genotypic correlation between performance genotypes x environments (RGE), genotypic coefficient of variation (CVg), residual coefficient of variation (CVr) and coefficient of variation of the ratio between genotypic and residual coefficient of variation (CVratio).

The multi-characteristic genotype-ideotype distance index, MGIDI, was calculated (Olivoto e Nardino, 2020) and used to select genotypes in plant breeding programs based on multiple traits using the following equation:

$$MGIDI_i = \Sigma^{f}_{j=1}[(F_{ij}-F_j)^2]^{0.5}$$

Where $MGIDI_i$ is the multicharacteristic genotype-ideotype distance index for the i-th genotype; F_{ij} is the score of the i-th genotype on the j-th factor (i = 1, 2, ..., g; j = 1, 2, ..., f), where g and f are the number of genotypes and factors, respectively, and F_j is the j-th ideotype score. The genotype with the lowest MGIDI is closest to the ideotype and should have the desired values for all the analyzed traits.

Data manipulation and index calculation were carried out in the R software using the "gamem" function for the genetic parameters and the "MGIDI" function for the ideotype analyses, both of which are in the 'metan' package.

3.3 Results

In the analysis of genetic parameters for yield (Figure 2), there was high heritability only for the cultivars in group 1, with values above 0.5. For plant height, the heritability values were considered high for all the groups except group 2, while the heritability values for cultivars in groups 5 and 6 (late group) were average. For the coefficient of genotypic variation for the yield variable, maturity group 3 had the lowest value and group 1 the highest, with 23.8%. For plant height, the lowest value was in group

3, and the highest was in group 5, with 19.7%. In the ideotype variable, the highest values were observed in groups 5 and 6, which are late cultivars. In the CV ratio for yield, only the cultivars in group 1 had values above 1.0, while for plant height, only maturity group 2 had a value below 1.0. For the ideotype, the cultivars in late groups 5 and 6 had lower values, but only group 5 had values below 1.0, which is considered ideal for the selection procedure (Cruz, 2013). The accuracy of the data was high on average, with group 1 standing out in terms of yield with a value above 90%. Only group 2 stood out for plant height, and in the ideotype, all the values were above 90%, which is considered an excellent threshold for data accuracy.

In the BLUP analysis between the groups (Figure 3), group 6 had the best yield and plant height performance. All the groups were above the ideal average, thus demonstrating excellent values regardless of the group. As for the ideotype, only group 5 was less than ideal. The BLUPS of the lines for each maturity group were also evaluated (Figure 3), where group 1 cultivars and lines 1, 2, 10, 11, and 12 were distinct with their performance in all variables. Only BMX Potencia had above-average plant height and ideotype values among the commercial cultivars. As for group 2, the commercial genotypes and strain 7 performed poorly for yield and plant height. For the ideotype, the cultivars BRS 5980, M Soy 7110, and alignment 7 were the least satisfactory.

For group 3, lines 7 and 11 were the best performers in the traits evaluated. In group 4, plant height and ideotype in cultivar M Soy 7739 and lineage 8 performed below the ideal. Regarding yield, the commercial cultivars BMX Power IPRO and HO Macarai IPRO and lines 2, 3, and 4 stood out. In group 5, there was a high degree of variation in yield, where the commercial cultivars BRS 8781, BRS 9280, M SOY 9144, and lines 1, 6, and 11 performed best. Lines 2, 4, 6, 7, 8, and the commercial lines had the best values for plant height. BRS Sambaiba, M Soy 9144, and lines 1 and 4 performed best for ideotype. For group 6, in the ideotype and yield traits, the BRS 9180 cultivar and lines 9 had the best performance, while for plant height, lines 3 and 9 did not perform satisfactorily.

When we consider the selection pressure of 25% (Figure 5), two cultivars or lines were selected from each maturity group. Lineages 7 and 9 were selected for Group 1, lineages 8 and 10 for Group 2, lineages 7 and 9 for Group 4, lineages 3 and 9 for Group 5, lineage 4 and the commercial cultivar M Soy 9144, and cultivars BMX Extrema IPRO and HO Cristalina IPRO for group 6. The selection of lines/cultivars indicates that they have the potential to give rise to new cultivars, presenting the desired traits and differentiating themselves from cultivars already on the market.

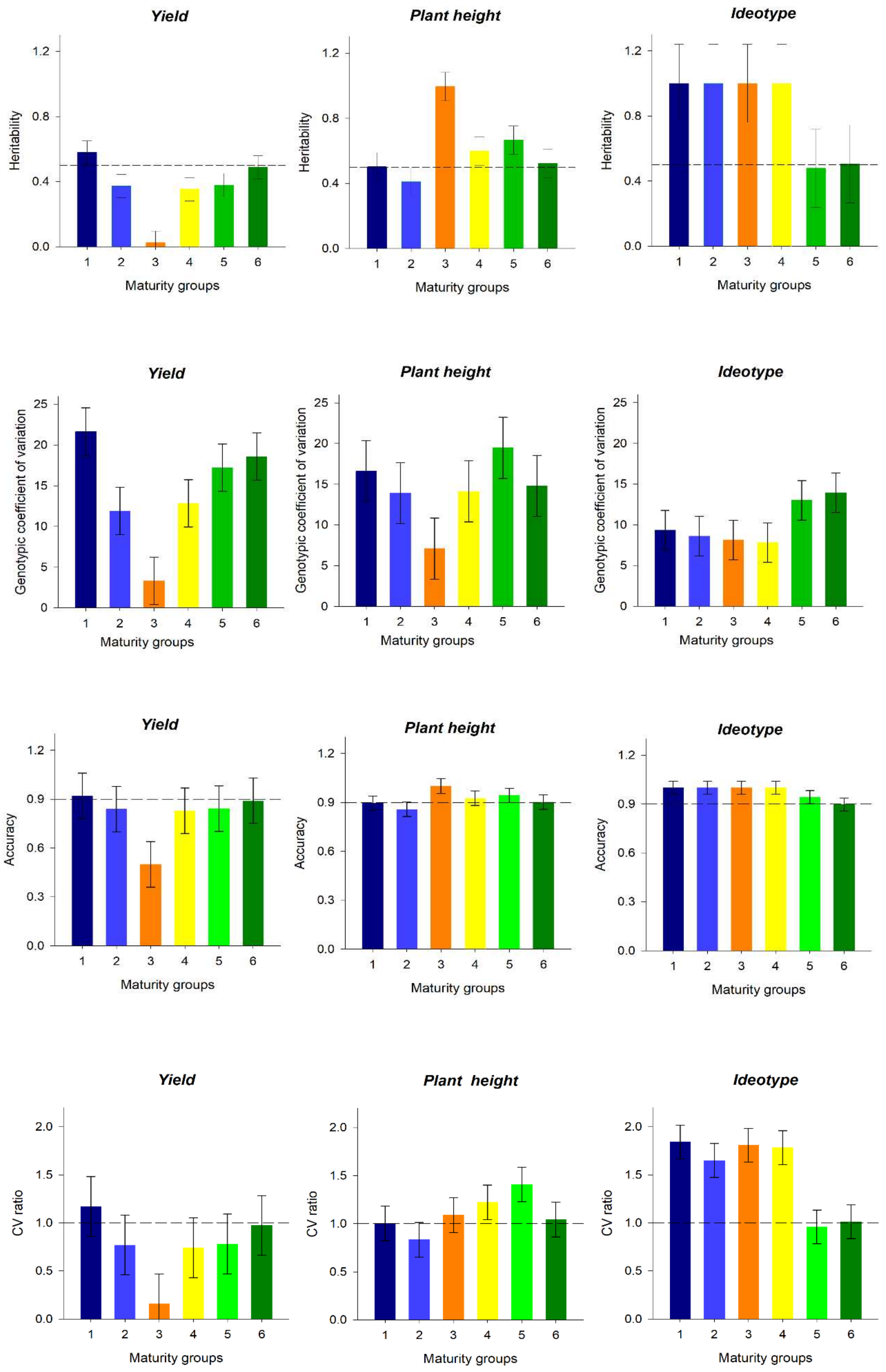

Figure 2. Heritability, accuracy, and CV ratio of maturity groups based on the yield, plant height, and ideotype variables.

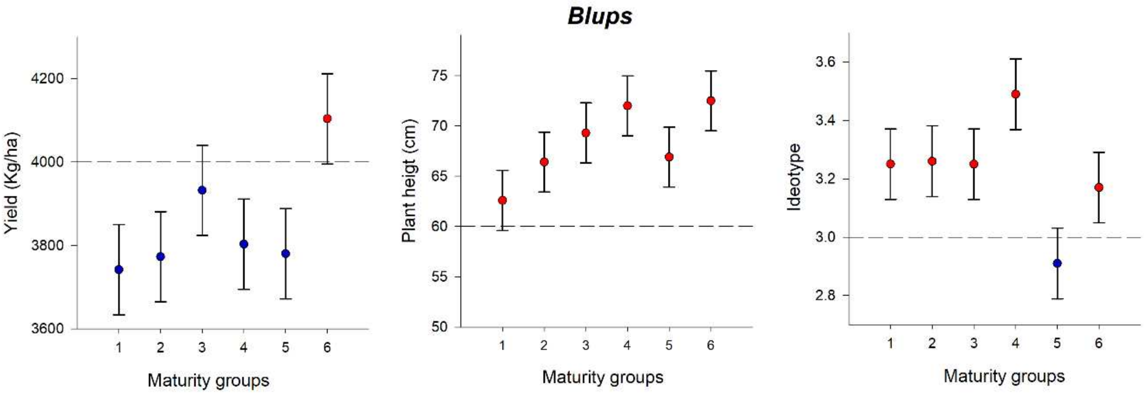

Figure 3. BLUPS of yield, plant height, and ideotype of the different soybean maturity groups.

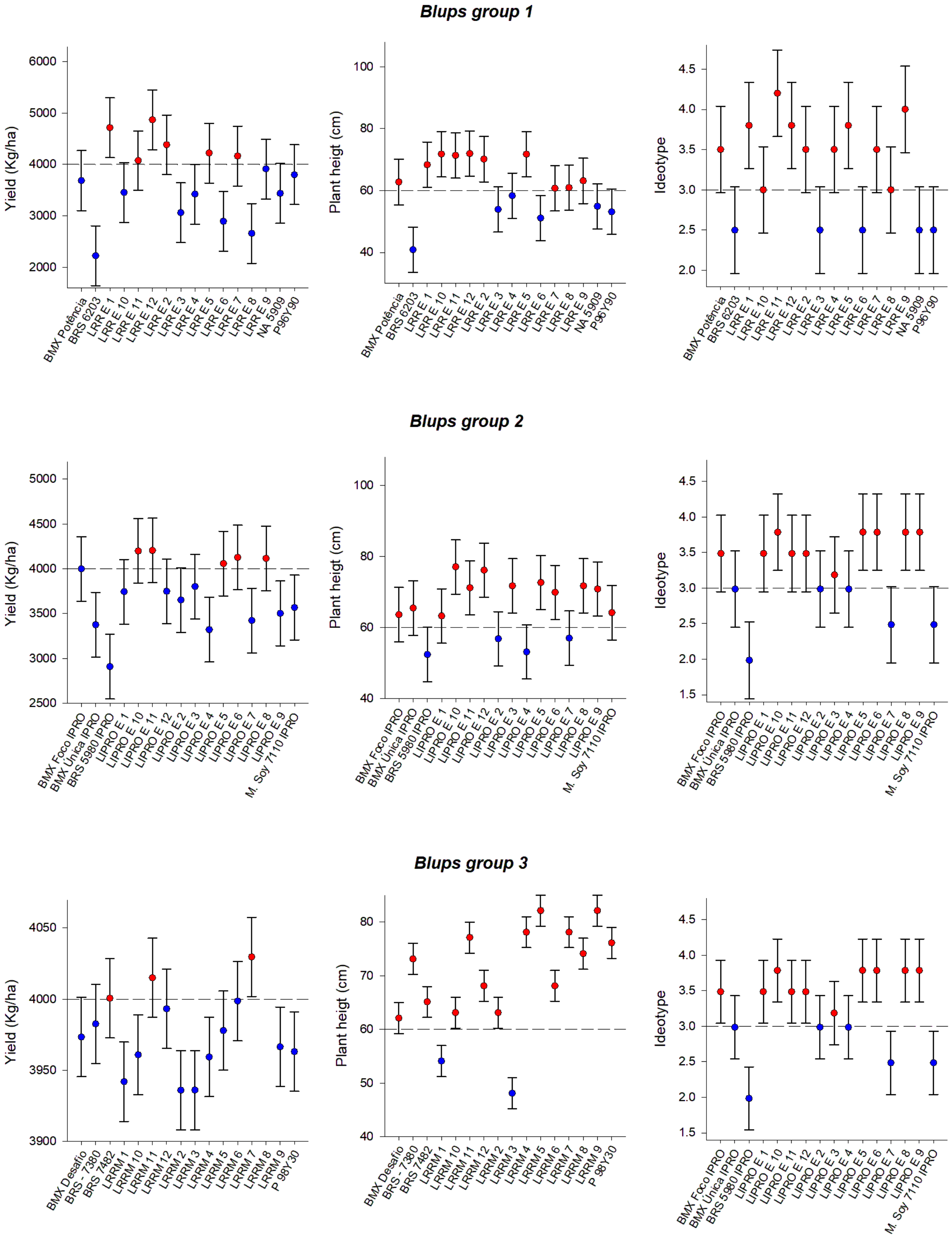

Figure 4. BLUP of yield, plant height, and ideotype of soybean genotypes for different maturity groups.

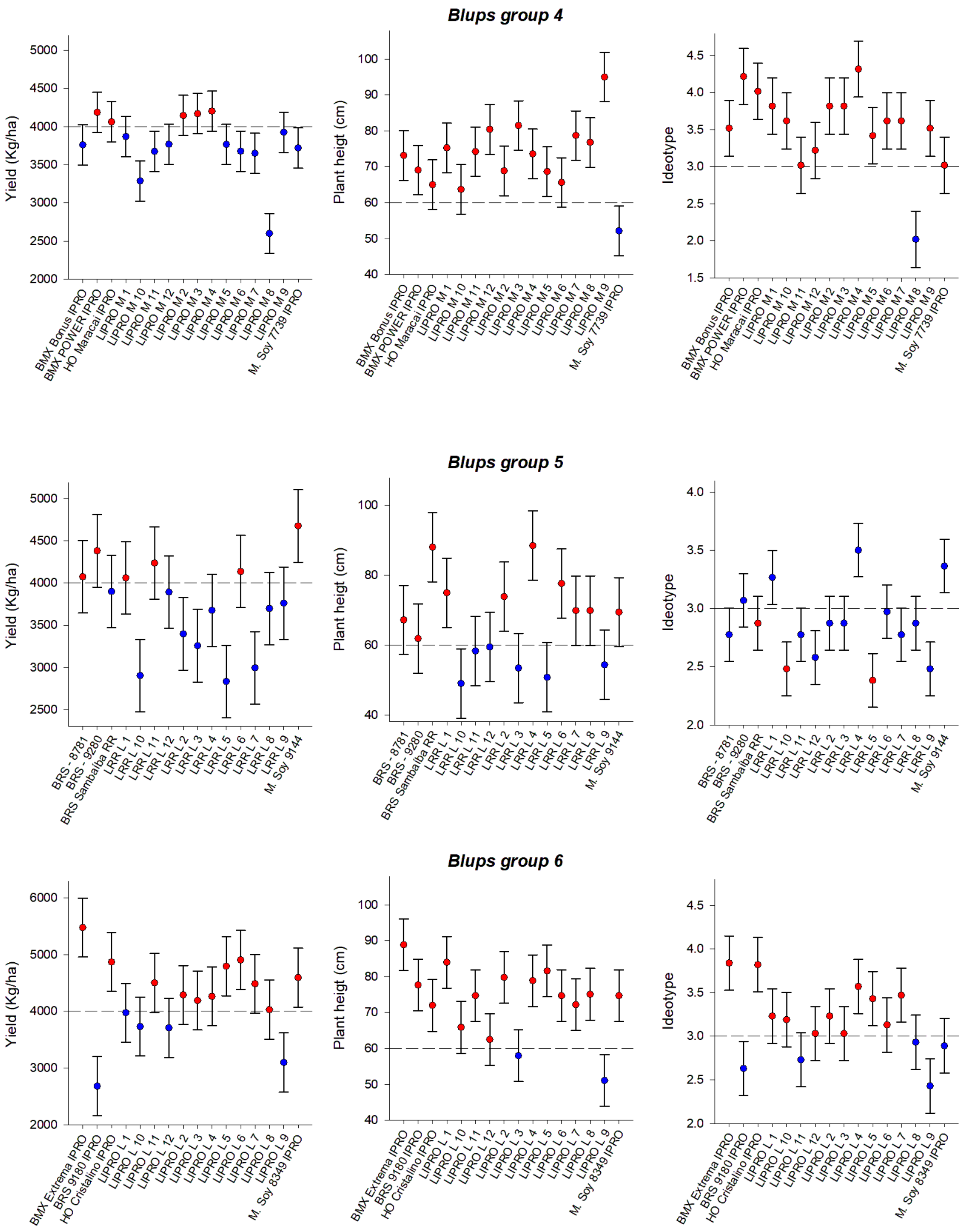

Figure 5. BLUPS of yield, plant height, and ideotype of soybean genotypes for different maturity groups.

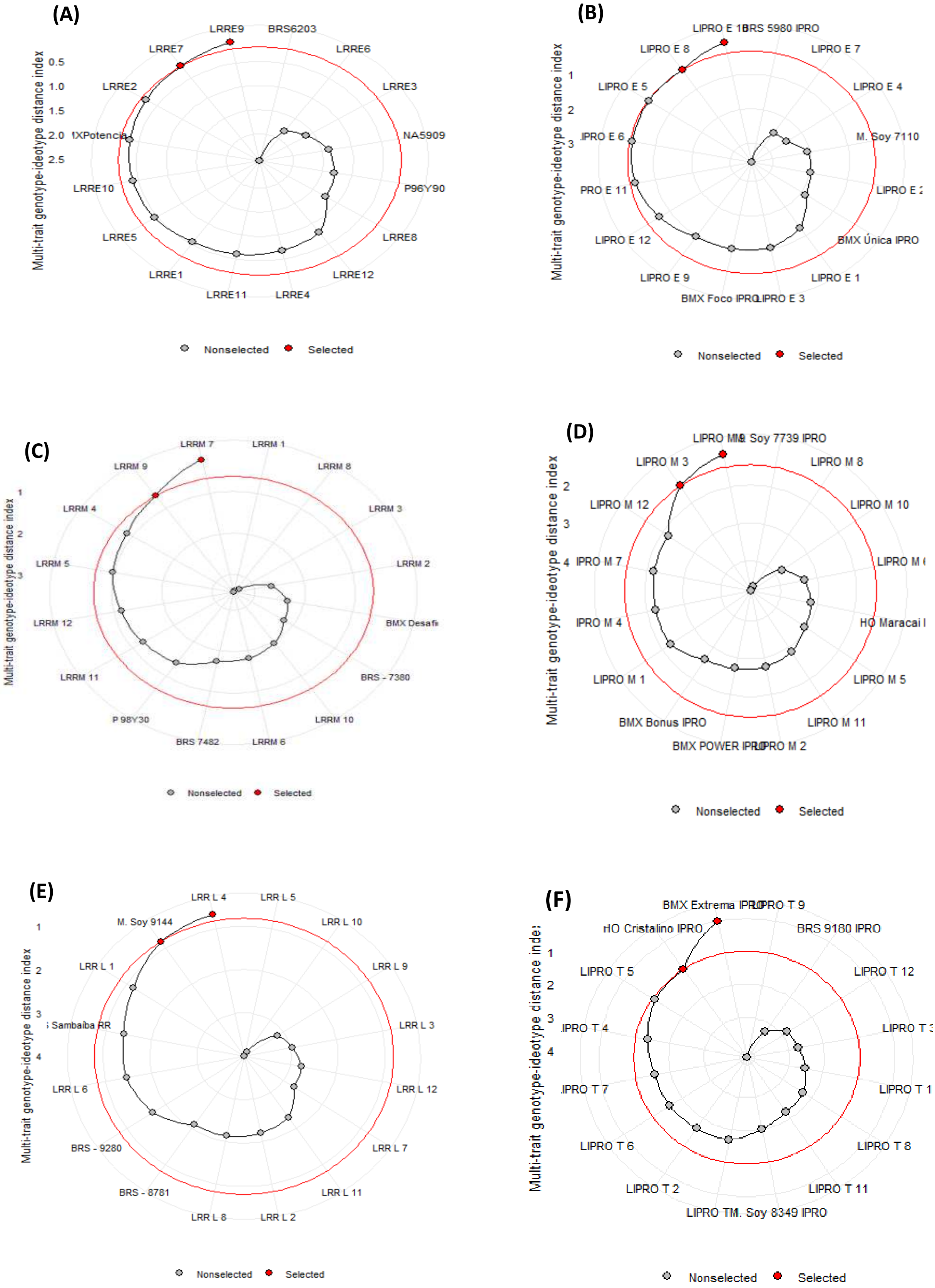

Figure 6. Ranking of genotypes based on the Multi-Trait Genotype-Ideotype Distance Index (MGIDI) for each maturity group 1 (A), group 2 (B), group 3 (C), group 4 (D),

group 5 (E) and group 6 (F). The red line refers to the selection intensity of 25%, accounting for the selection of 2 genotypes.

3.4 Discussion

When working with genetic parameters of autogamous species, there is a considerable variation in the results (SEDIYAMA, T.; SILVA, F.; BORÉM, 2015), and low heritability values for yield are considered normal due to the environmental factor, which has a strong influence. When analyzing genotypes with different maturity groups, the yield was directly linked to the environmental coefficient (Gauch e Zobel, 1988). Another factor that can interfere with heritability is temperature, where climatic conditions can significantly affect medium and late-cycle cultivars (Fernandes, M. A., Oliveira, M. A., Silva, M. F., & Machado, 2017). Similarly, plant height highly depends on the environment and maturity group, with early cultivars tending to have higher heritabilities (Costa et al., 2008). Results of coefficients of variation from other studies found similar values for both early and late cultivars (Hossain et al., 2023). The coefficient of genetic variation values (Fig. 2) reflects a favorable situation for selecting these traits studied, with possibilities for gains using simple selection methods (Romais Schmildt et al., 2011). The work by Hamawaki et al., (2012) showed similar results for CVratio and accuracy, and the low accuracy values for the cultivars in group 3 can be explained by the layout of the experiment in the field, where the pivot curve may have caused mechanical damage to the data collection.

According to (Resende et al, 2017) BLUP can be used in different ways and at different breeding stages, providing a broader view of the results. In late planting, the performance of cultivars in ideal conditions can increase the seed and, consequently, their yield (Follmann et al., 2018). For the soybean crop, plant height has a positive cause-and-effect relationship (da Cruz et al., 2010). According to (Follmann et al., 2019), it can be inferred that cultivars with an estimated BLUP greater than or equal to 55 cm have an additive genetic effect, which is beneficial for selection. As for the ideotype, the longer the soybean is in the field, the more likely it is to be affected by diseases and other extended cycle problems (Azevedo et al., 2007).

Regarding individual analysis, genetic variations can influence each line in a specific way (Volpato et al., 2018). Each cultivar can perform in a particular way (de Albuquerque et al., 2023), which was observed in this study (Fig. 4). There are reports from other research that corroborate our work (Teng et al., 2017; Follmann et al., 2018), where the performance of each cultivar was influenced by the G x E interaction and also by the genetic traits of each group (Hu et al., 2014). In each group, MGIDI detected the best lines and some commercial cultivars (Fig. 5), showing how genetic and environmental variation can affect these traits. This index helps in the selection process and contributes to the advancement of lines (Olivoto, TiagoOlivoto, T, Nardino, M, Meira, 2021). (Klein et al., 2023), working with black oats proved that MGIDI can indicate the best genotypes. The potential of MGIDI for selecting soybean cultivars has already been demonstrated, and there is also a similarity between the best genotypes with BLUP values and with MGIDI (Jean Vitor.R. Carvalho, C. Pradebon, 2023).

3.5 Conclusion

Lineages from groups 5 and 6 have low heritability and maturity groups directly interfere with genetic factors. Group 6 had better BLUPS values and environmental factors that interfere with ideotypes.

Based on MGIDI and BLUPS, the lines LRRE 7 and 9 from Group 1, LIPROE 7 and BRS 590 from Group 2, LRRM 7 and 9 from Group 3, LIPROM 3 and 9 from Group 4, LRRL 4 and Monsoy 9144 from group 5 and HO Cristalina and BMX Extrema from group 6 stood out from the others within each group.

4.0 General conclusions

The use of the R package proved to be quite effective in analyzing genetic parameters of soybean and sorghum crops.

In this study, the Metan package proved to be highly efficient in assisting decision-making in analyzing the crops studied.

The insights obtained from this analysis can inform breeders and agronomists in the selection of traits associated with adaptability and stability.

Studies can expand this analysis by incorporating additional environmental variables and more robust data sets.

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