

Morphological characterization and selection of maize genotypes for the semiarid region

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Abstract

Maize has great importance in the semi-arid region of Sergipe. The zoning of the culture in the region is due to the studies directed to the selection and adaptability of genotypes to adverse conditions. In view of this, the objective was to characterize and select corn genotypes for grain production in the semi-arid region of Sergipe. For this, 78 corn genotypes were evaluated in Nossa Senhora da Glória, Sergipe, Brazil. Using the BLUE's estimates for grain yield, 43 genotypes were selected. It was observed that the earliest genotypes corresponded to the highest average in grain yield, therefore, the characteristics related to flowering can be used in the indirect selection of genotypes. The experimental XB7530, DGX20 S03, DGX20 S02, DGX20 S01, LG 6036 PRO3 and EX3561L VIP3 were selected, and these provided 551.15 kg ha⁻¹ of genetic gain in the experimental population. Furthermore, these are indicated for the formation of dialels in a breeding program in the semiarid region of Sergipe.

Introduction

Corn (*Zea mays* L.) is one of the most important cereals in the world, in the 2020 crop alone, 103,235.064 thousand tons were produced in Brazil, with the Northeast region contributing 8,723.8 thousand tons (IBGE 2020). For the 2021/2022 crop, Brazil should have total corn production close to 96,392.1 thousand tons due to wide climatic variation from the previous year (CONAB 2021). In the Northeast, for 2021, there was an increase of 7.8% in the corn planting area, and a reduction in production of 0.5% compared to 2020 is expected (IBGE 2020). Only in the state of Sergipe a decrease in corn production close to 19.5% is already estimated due to long periods of drought (Observatório de Sergipe 2021).

The Northeast, although it has more fertile soils and the area destined for corn cultivation has increased in recent years, grain productivity is lower than other regions. This is due to the range corresponding to the semi-arid climate, characterized by the occurrence of high temperatures, high evapotranspiration rates, poor rainfall distribution, and long periods of drought (Oliveira et al. 2019). The climate in question is present in an area of 969,589 km² of the Brazilian territory, dispersed throughout the northeastern states Ceará, Sergipe, Paraíba, Rio Grande do Norte, Piauí, Pernambuco, Bahia, Alagoas and part of the southeast, in the state of Minas Gerais (Correia et al. 2011).

Corn, as well as beans and soybeans, is not a highly drought-tolerant crop, and because of this, for a long time, the reality of the Brazilian semiarid region was of agriculture limited to subsistence (Lopes et al. 2020). However, the crop has great socioeconomic and cultural importance in the region (Lopes et al. 2019). The feasibility and zoning of the crop for the semiarid region was only possible thanks to the studies carried out with the crop aimed at its adaptability to adverse conditions, mainly regarding the selection and crossing of genotypes in genetic improvement programs (Silva et al. 2021).

Thanks to the work focused on the improvement of cultivars, currently, this same region has stood out in the agricultural market, because, according to information extracted from the Banco do Nordeste, for the year 2020, in the Northeast was estimated harvest of 6,873,918 thousand tons of corn, with an increase of approximately 5.4% when compared to the previous year (Carneiro et al. 2020).

In this context, it is intended to implement a maize breeding program for the development of conventional cultivars, studying the crop in the target environment. Thus, increasing the probability of selecting genotypes that

can express favorable genes for adaptation in the semi-arid region. Thus, promising results are sought with the pioneering work in development of morphological characterization of corn germplasm, conducted by the Study Group on Plant Improvement in the Semiarid (GEMS), linked to the Federal University of Sergipe (UFS).

For the development of this first work, several methodologies are applied, among them the mixed models for variability analysis, the application of genetic divergence to determine divergent groups and the study of correlations between variables to facilitate the selection of variables that are difficult to measure.

Knowing this, the objective was to characterize and select maize genotypes for grain production in the semi-arid region of Sergipe using the REML/BLUP methodology.

Material And Methods

Site Description

The experiment was implemented during the harvest period at the experimental farm of Embrapa - Semiarid, located in the municipality of Nossa Senhora da Glória (10° 12' 50.6" S latitude and 37° 19' 03.2" W longitude and average altitude of 210m), Alto Hinterland in the Sergipe region. Sowing was performed on May 29, 2020, with harvest on November 5 of the same year.

According to Alvarez et al. (2013) the climatic type of the region is As, characterized by having hot and dry summers and precipitation in the winter months and, although the municipality does not have a BSh (semi-arid) climate, it borders cities of semi-arid predominance, such as Porto da Folha - SE and Gararu - SE, i.e., it is a transition area (Alvarez et al. 2013).

During the conduct of the experiment, according to data collected in the experimental unit of Embrapa - Semiarid, it has a weather station belonging to the National Institute of Meteorology (INMET), maximum temperature of 28.88 °C and minimum of 19.20 °C, and precipitation accumulation of 339.60 mm were dated.

Genetic material and evaluation

In the experiment, 78 corn genotypes were evaluated, including 19 experimental and 59 commercial cultivars. To identify the two types of cultivars, a search was performed using the Ministry of Agriculture, Livestock and Supply (MAPA) platform with national registry of cultivars (RNC), where information was obtained from the evaluated commercial and experimental cultivars (CULTIVARWEB 2021).

All genotypes were sown manually, with spacing of 0.2 m x 0.5 m, with a population of 100,000 plants ha⁻¹. In the foundation fertilization, following the fertilizer recommendation for corn culture (Sobral et al. 2007), the formulation 06-24-12 was used, with an application of 500 kg ha⁻¹, and in the covering, when 50% of the experiment reached the V4 to V6 stages, the formulation 46-00-00 was applied, with a dosage of 150 kg ha⁻¹, divided in 50% with an interval of 8 days between each application.

The experimental design was in randomized blocks, with two repetitions. Each plot consisted of two corn rows, each containing 25 plants. The agronomic characteristics evaluated were: PH - plant height (m), EH - ear height (m), SD - stalk diameter (cm), MF - male flowering (days), FF - female flowering (days), ASI - anthesis-silking interval (days), RPE - relative position of the ear (m), NEP - number of ears per plant, NRE - number of kernel row

per ear, NKR - number of kernel per row, EL - ear length (cm), EG - ear girth (cm), 1000GW - 1000 grain weight (g), EWP - ear weight per plant (kg), GWP - grain per plant (kg) and GY - grain yield (kg ha⁻¹).

ASI, RPE and GY were given by the following equations, respectively:

$$ASI = FF - MF \quad Ex (1)$$

Where: FF = female flowering (days after the emergency); MF = male flowering (days after the emergency).

$$RPE = \frac{EH}{PH} \quad Ex (2)$$

Where: EH = Ear height (m); PH = plant height (m).

$$GY = \frac{PGST}{ST} * QP \quad Ex (3)$$

Where: GY = Grain Yield (kg ha⁻¹); PGST = Grain production per plant (kg); ST = Stand; QP = Quantity of plants per hectare.

Grain yield was adjusted to 13% moisture. All collected data were subjected to analysis of variance via mixed models and the contrast between commercial and experimental genotypes, where fixed effect was stated for genotypes, and random for repetition effect, using the lme4 statistical package (Bates et al. 2012). All statistical analyses were performed in R Foundation (2017) software, version 4.1.0.

Characterization I: experimental vs commercial

This step was performed to select the best genotypes that were evaluated, among commercial and experimental ones, following the mixed model's equation (Resende 2002):

$$y = Xb + Za + Wc + e \quad Ex (4)$$

Where: y = vector of data; b = vector of genotype effects (fixed); a = vector of block effects (random); c = vector of plot effects (random); e = vector of errors or residues (random); X, Z and W = incidence matrices for these effects.

Using the ggplot2 package (Wickham et al. 2016), boxplot distribution analysis was performed. In addition, for the purpose of better characterization of the materials and studies of the variables, Pearson's linear correlation was estimated with the corrplot package (Wei and Simko 2021).

Verifying variability for the GY variable, we proceeded with the selection of genotypes using the BLUE estimate extracted from the fixed effect model. The selection of genotypes was based on the BLUE-GY variable, a standardized variable (mean zero and standard deviation 1), created for this purpose. At the time of selection, the dummy variable was established with the denomination "good" and "bad" for genotypes above and below the created BLUE-GY mean, respectively.

Characterization II: genetic divergence

After characterization I, the genotypes denominated as "good", were filtered constituting a single database used in the determination of genetic divergence, for purposes of determining the heterotic clustering. The distance matrix was determined by the Euclidean distance method with the BLUE's of all measured variables. Clustering was performed using the dendrogram by the UPGMA method. It was previously determined the division of five groups by the cutree method and to visualize these results it was used the ape package (Paradis et al. 2004), the groups were separated by colors, namely: black (BLOCK I), purple (BLOCK II), green (BLOCK III), blue (BLOCK IV) and red (BLOCK V).

Characterization III: Variance components

This step was performed to determine the possibility of genetic gains from selecting only experimental materials. For this, it was stated that the genotypes are the random effects, and the fixed effects were given by the blocks, following the mixed model's equation:

$$y = Xb + Za + Wc + e \quad \text{Ex (5)}$$

Where: y = vector of data; b = vector of block effects (fixed); a = vector of population effects of experimental genotypes (random); c = vector of plot effects (random); e = vector of errors or residues (random); X , Z and W = incidence matrices for the referred effects.

Estimates of variance components and genetic parameter were performed using the package metan (Olivoto and Lúcio 2020). The estimated genetic parameters were: σ^2_g (genetic variance), percentage of genetic variance, σ^2_e (environmental variance), percentage of environmental variance, σ^2_p (phenotypic variance), heritability in the broad sense, heritability at the mean level, coefficient of genetic variance (%) and the coefficient of phenotypic variance (%). For the estimation of genetic gain only the economic value variable of GY was used, following the equation:

$$GA = h^2 \times sd \quad \text{Ex (6)}$$

Where: h^2 = the broad-sense heritability; sd = selection differential, obtained by the difference between the overall population mean (experimental genotypes) and the mean of the selected genotypes (experimental genotypes selected in characterization I).

Results And Discussion

According to the analysis of variance (Table 1), the variables plant height (PH), ear height (EH), flowering interval (ASI), male flowering (MF), female flowering (FF), number of rows per ear (NRE), number of grains per row (NKR), spike length (EL), 1000-grain weight (1000GW), grain weight per plant (GWP), relative spike position (RPE) and grain yield (GY) were significant at 1% ($p \leq 0.01$), and that of ear weight per plant (EWP) was significant at 5% ($p \leq 0.05$).

The significant variables contributed to differentiate the 78 corn genotypes, showing that there is genetic variability in the materials evaluated, and, according to Cruz et al. (2014), the differentiation of genotypes is essential in a breeding program, because it favors the selection of genotypes (Tavares et al. 2018).

In the 1000GW and GY variables, the means of the experimental and commercial genotypes showed statistical difference at 5% ($p \leq 0.05$) by contrast analysis (Table 1), which indicates variability between the two types of cultivars for these variables.

The coefficient of variation (CV) ranged between 2 and 22.74% (Table 1), being within the ideal for a corn experiment, which shows homogeneity in data collection (Fritsche Neto et al. 2017). On the other hand, the CV for IF was considered very high (41.5%), probably due to the wide variability of maturity for the genotypes evaluated. These results corroborate with those found by Suthamathi and Nallathambi (2018), who when evaluating maize strains in a semi-arid region, showed CV values equal to 39.73%.

Distinguishing the performance of commercial and experimental genotypes is important in the context of identifying the standards that should or should not be improved in cultivars already available to the producer. This distinction, which can be translated into genetic variability among genotypes, enables the implementation of the breeding program with these materials in the target region (Sheikh et al. 2017). In addition to this, one can better observe secondary traits, i.e., those that influence PG (Sheikh et al. 2017).

In the distribution analysis, using the boxplot, it is possible to observe the trend by means of the median and quartiles of the distribution of the commercial and experimental genotypes, and to demonstrate the variability within each type (Figure 1).

In the FF, MF and ASI traits, relative to the beginning of the reproductive stage, the trend of higher averages was observed for the experimental genotypes (Figure 1e, 1f and 1g). This may be an explanation for the drop in the averages of the experimental ones in grain yield (Figure 1d), since, according to Paterniani et al. (2019) and Rocha et al. (2021), genotypes that present a high ASI and later cycle are more susceptible to abiotic stresses, especially water deficit, which can cause sterility or severely reduce the number of grains per ear.

For the GY variable, the commercial genotypes presented the highest averages, having genotypes with yields above $10,000 \text{ kg ha}^{-1}$, which may be a consequence of the earliness and lower ASI, observed for most commercial genotypes (Figure 1d).

The correlation coefficient is used to identify the interaction between variables, such as the positive or negative influence that one character has on another and can assist the breeder in selecting materials with good performance in variables that are difficult to measure (Miot 2018).

According to Figueiredo Filho and Silva Junior (2009), the closer the correlation coefficient is to 1, the greater the positive correlation between the characters, similarly, the closer to -1, the greater the negative correlation. Thus, six positive and significant correlations were identified between the variables (Figure 2), they are: PH and EH (0.7), FF and MF (0.81), RPE and EH (0.74), GWP and EWP (0.77), and for the economic value variable, GY was positively correlated with GWP and EWP (0.98 and 0.82, respectively). Besides this, there were also negative and significant correlations between GY and FF (-0.60), GY and ASI (-0.41), FF and GWP (-0.50) and FF and EWP (-0.44), which allows us to observe that, the increase in ASI and FF leads to low corn grain yield (Figure 2).

The negative correlations corroborate with those obtained by Melo et al. (2018), who, when evaluating maize genotypes under water stress, found that earlier genotypes with lower ASI present higher grain yields and, consequently, greater adaptability in regions with characteristics like the semiarid.

According to the distribution of means (Figure 1), the population of early genotypes is more productive and, consequently, more adaptable to the conditions of the semi-arid region of Sergipe, a fact proven in the correlation analysis (Figure 2), with a negative correlation between FF and GY (Figure 2). Thus, it is affirmed that the FF and ASI characteristics can be used to help the indirect selection of individuals. Thus, the selection of more precocious genotypes with lower ASI is suggested to obtain more productive materials for the semiarid region of Sergipe (Carvalho et al. 2020).

Regarding, the selection of genitors, in the case of morphological evaluations in the field, is based on their respective phenotypic averages. In the case of maize, selection is mainly done by grain yield (kg ha^{-1}), since this is the economic trait of interest in the crop (Sheikh et al. 2017). Guimarães et al. (2019), when working with selection of maize genotypes, stated that these should present the highest yields and economic gains for the region where the breeding program is being conducted.

The selection using mixed models aims to differentiate, from a production variable, the genotypes by the averages adjusted by BLUP, when considering random effect, or BLUE, when considering fixed effect (Resende and Alves, 2021). Santos et al. (2021) also used the mixed model methodology (REML/BLUP) to select genotypes from the corn grain yield variable.

In Figure 3, the "good" genotypes are those with high grain yield, based on the BLUE's, estimated via mixed models. That said, the commercial BM 930 PRO2 (44) and AS 1868 Pro3 (74) were selected as superior among the others, followed by SHS 5570 (41) and LG 3040 VIP3 (63). Six experimental genotypes were rated as "good", among them DGX 20 S03 (26) that was close to the commercial ones selected in the rank (Figure 3).

In the formation of the crossing blocks, the distribution and genetic divergence could be observed (Figure 4). The first (BLOCK I) and the fifth block (BLOCK V) accounted for the largest number of grouped genotypes (15 and 13 genotypes, respectively) (Figure 4), while the second block (BLOCK II) consisted of only one genotype (Figure 4).

The experimental genotypes were present in two blocks, BLOCK I and V. In BLOCK I were grouped the experimental XB 73530, DGX 20 S02 and DGX 20 S03, and in BLOCK II the DGX 20 S01, EX 3591 L VIP3 and LG 6036 PRO3 (Figure 4).

All the blocks formed grouped genotypes with statistically equal means for GY, FF, NRE and SD, as there was no statistical difference among the selected genotypes for these variables. BLOCK V grouped the genotypes with higher averages for PH, EH, NEP, EWP and GWP, and, also, was the only group to stand out in the lowest ASI. BLOCK I gathered the genotypes with higher averages in EL, BLOCK III with higher ones in EG and 1000GW and BLOCK IV only in 1000GW.

Considering the increased frequency of favorable alleles in the crossing group of experimental genotypes, we indicate as genitors those allocated in blocks III and V, because the crossing of these blocks will allow greater chances of achieving earlier and more productive genotypes in segregating generations (Rotili et al. 2012).

Aiming at the possibility of gains with the selection by the experimental genotypes, the genetic parameters were estimated (Table 2). It was observed that the selective accuracy was between 0.34 and 0.93. According to Resende and Duarte (2007), accuracy below 0.50 is considered low, between 0.5 and 0.7 moderate, high between 0.7 and 0.9, and very high above 0.9. Thus, it can be stated that for the variable GY (0.78) and variables for

indirect selection FF and ASI (0.81 and 0.87, respectively) showed high selective accuracy (Table 2), that is, their genetic values are close to the real one.

The phenotypic variance seen in all variables was higher than the genotypic variance, which shows that the environmental variance interfered significantly in the estimates of this genetic parameter.

The CVg varied between 1.84 and 20.87 among all variables (Table 2). For FF, ASI, and GY, the CVg was 1.84, 20.87 and 13.04%, respectively, and the CVe was 1.83, 28.00 and 14.83%, respectively, showing that the environment had low influence on the estimation of genetic values in the population (Table 2). Close values of CVg and CVe obtained were presented by Tesfaye et al. (2021) when they evaluated the genetic parameters in maize productivity under semiarid conditions.

According to Resende (1995), heritability ≤ 0.5 is considered low, between 0.15 and 0.5 moderate, and above 0.5 high. With the heritability for FF, ASI and GY of 0.5, 0.35 and 0.43, respectively, it is seen that selection of the genotypes within the experimental population can be effective in achieving genetic gains for grain yield.

The heritability at mean level, ranged from 0.12 to 0.86, with 0.67, 0.53 and 0.61 observed in FF, ASI, and GY variable, respectively (Table 2). These high values of heritability point to an indication of reproducibility and phenotypic stability of the characters by the evaluated population (Freitas et al. 2006), which indicates the feasibility of inserting the six experimental genotypes selected in the population in a maize breeding program (Cruz et al. 2020).

The genetic gain obtained in GY by the population of the six experimental genotypes selected earlier was 551.15 kg ha⁻¹ in the average of the improved population (Table 2). With the positive gain of these genotypes, it can be stated that these six experimental genotypes are potential genitors for a plant breeding program in the hinterland of the Sergipe region.

Conclusion

Diallel formation between the experimental genotypes XB 7530, DGX 20 S03, DGX 20 S02, DGX 20 S01, LG 6036 PRO3 and EX 3561 L VIP3 is indicated in plant breeding program in the High hinterland of the Sergipe region.

The commercial genotypes BM 930 PRO2, AS 1868 PRO3, SHS 5570 and LG 3040 VIP3 are indicated for grain production under semi-arid conditions.

The use of the female and male flowering characteristics is indicated in the indirect selection of genotypes with higher grain yields in semi-arid region.

Declarations

Ethics approval and consent to participate

All authors approved and are aware of the ethical values and participation in the manuscript submission.

Consent for publication

All authors are consenting to the submission of the manuscript.

Availability of data and materials

All data and statistical evaluations are available from the authors.

Competing interests

Not applicable.

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Not applicable.

Authors' contributions

Eduarda Silveira and Gustavo Hugo wrote the main manuscript text. The other authors, together with Eduarda, processed the statistical analyzes and conducted the field experiment. All authors reviewed the manuscript.

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Tables

Table 1. Results of the variance analysis via mixed models of the 78 corn genotypes (fixed effects) and the mean contrast between the commercial and experimental ones, evaluated in High hinterland of Sergipe.

Effect	DF	MS							
		PH	EH	SD	MF	FF	ASI	NRE	NKR
Genotype	77	0.03**	0.02**	0.04 ^{ns}	6.04**	5.75**	0.77**	4.27**	13.98 ^{ns}
Error	77	0.01	0.006	0.04	2.06	1.59	0.92	1.03	13.82
Mean (Ex)		2.23 ^{ns}	1.23 ^{ns}	2.18 ^{ns}	63 ^{ns}	64.15 ^{ns}	1.15 ^{ns}	16.57 ^{ns}	31.07 ^{ns}
Mean (Cm)		2.26 ^{ns}	1.26 ^{ns}	2.16 ^{ns}	62.09 ^{ns}	62.91 ^{ns}	0.92 ^{ns}	16.12 ^{ns}	31.58 ^{ns}
CV (%)		5.59	7.12	9.5	2.31	2	41.5	6.27	11.83
Effect	DF	MS							
		EL	EG	1000GW	NEP	EWP	GWP	RPE	GY
Genotype	77	3.5**	0.06 ^{ns}	1,868.2**	0.01 ^{ns}	0.001*	0.0005**	0.002**	4,112,674**
Error	77	1.39	0.04	484.64	0.01	0.0008	0.0003	0.001	1028.17
Mean (Ex)		16.17 ^{ns}	4.57 ^{ns}	267.5*	0.98 ^{ns}	0.12 ^{ns}	0.07 ^{ns}	0.55 ^{ns}	6,879.18*
Mean (Cm)		15.77 ^{ns}	4.58 ^{ns}	270.06*	1.04 ^{ns}	0.13 ^{ns}	0.08 ^{ns}	0.56 ^{ns}	7,865.87*
CV (%)		7.44	4.76	8.14	10.88	22.74	20.4	6.36	22.16

* and **: significance at 1% and 5%, respectively; ns: not significant; AS: average square; CV: coefficient of variance (%); Cm: commercial genotypes; Ex: experimental genotypes; PH: plant height (m); EH: ear height (m); SD: stalk diameter (cm); MF: male flowering (days); FF: female flowering (days); ASI: anthesis-silking interval (days); NRE: number of kernel row per ear; NKR: number pf kernel per row; EL: ear length (cm); EG: ear girth (cm); 1000GW: 1000 grain weight (g); NEP: number of ears per plant; EWP: ear weight per plant (kg); GWP: grain per plant (kg); RPE: relative position of the ear (m) e GY: grain yield (kg ha⁻¹).

Table 2. Estimates of variance components and genetic parameters for the 19 experimental genotypes evaluated in the high hinterland of Sergipe.

Parameters	PH	EH	RPE	FF	MF	ASI	NEP	NRE
σ^2_g	0.01	0.01	0.0007	1.39	2.07	0.15	0.0008	3.006
Por _g	40.92	52.50	31.23	50.26	61.49	35.7	6.14	76.03
σ^2_e	0.01	0.009	0.001	1.38	1.29	0.27	0.01	0.94
Por _e	59.08	47.49	68.76	49.73	38.51	64.29	93.86	23.96
σ^2_p	0.02	0.02	0.002	2.77	3.37	0.42	0.01	3.95
h ²	0.41	0.52	0.31	0.5	0.61	0.35	0.06	0.76
h ² mg	0.58	0.68	0.47	0.67	0.76	0.53	0.12	0.86
Accuracy	0.76	0.83	0.68	0.81	0.87	0.72	0.34	0.93
CV _g	4.57	8.37	4.78	1.84	2.28	20.87	2.78	10.45
CVe	5.49	7.96	7.09	1.83	1.81	28.00	10.88	5.87
CV _g x CVe	0.83	1.05	0.67	1.005	1.26	0.74	0.26	1.78
Parameters	NKR	EL	EG	1000GW	EWP	GWP	SD	GY
σ^2_g	1.49	2.07	0	803.00	0.0003	0.0002	0.009	805,143.00
Por _g	12.04	53.58	0	55.29	28.06	36.08	20.88	43.59
σ^2_e	10.91	1.79	0.04	649.41	0.0008	0.0003	0.04	1,041,671.00
Por _e	87.95	46.41	100.00	44.71	71.94	63.92	79.12	56.40
σ^2_p	12.41	3.87	0.04	1,452.49	0.001	0.0005	0.04	1,846,814.00
h ²	0.12	0.53	0	0.55	0.28	0.36	0.21	0.43
h ² mg	0.21	0.69	0	0.71	0.44	0.53	0.34	0.61
Accuracy	0.46	0.83	0	0.84	0.66	0.73	0.58	0.78
CV _g	3.93	8.91	0	10.59	14.20	15.32	4.46	13.04
CVe	10.63	8.29	4.43	9.52	22.74	20.40	8.69	14.83
CV _g x CVe	0.37	1.07	0	1.11	0.62	0.75	0.51	0.88
Genetic Gain								551.15

σ^2g : genetic variance; Porg: percentage of the genetic variance; σ^2e : environmental variance; Pore: percentage of the environmental variance; σ^2p : phenotypic variance; h^2 : heritability in the broad sense; h^2mg : heritability at the mean level; CVg: coefficient of genetic variance (%); CVe: coefficient of environmental variance (%); PH – plant height (m), EH – Ear height (m), SD – stalk diameter (cm), MF – male flowering (days), FF – female flowering (days), ASI - anthesis-silking interval (days), RPE – relative position of the ear (m), NEP – number of ears per plant, NRE – number of kernel row per ear, NKR – number pf kernel per row, EL – ear length (cm), EG – ear girth (cm), 1000GW – 1000 grain weight (g), EWP – ear weight per plant (kg), GWP – grain per plant (kg) e GY – grain yield (kg ha⁻¹).

Figures

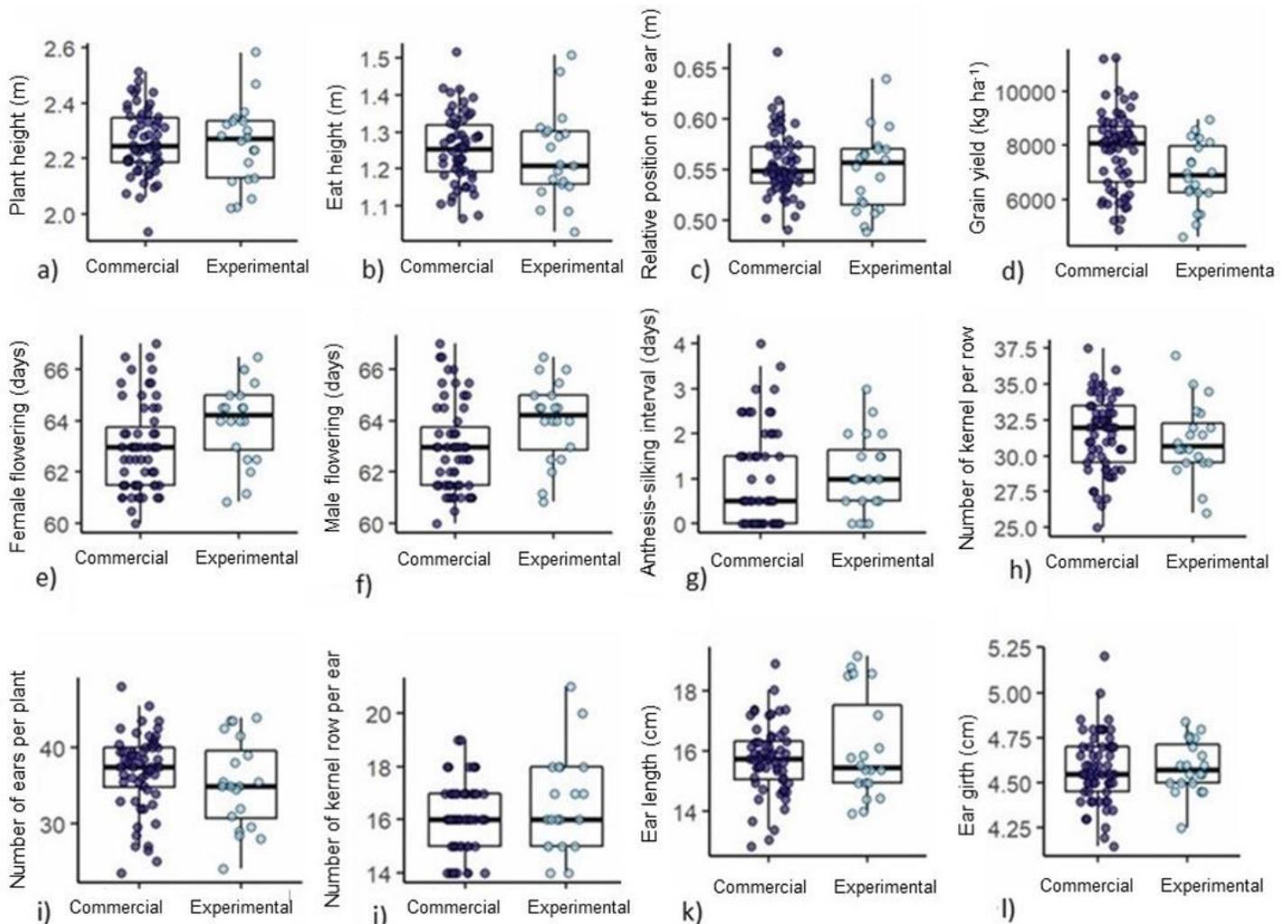


Figure 1

Boxplot distribution analysis of the means of the commercial and experimental genotypes for the variables of plant height (1a), ear height (1b), relative position of the ear (1c), grain yield (1d), female flowering (1e), male flowering (1f), anthesis-silking interval (1g), number of kernel per row (1h), number of ears per plant (1i), number of kernel row per ear (1j), ear length (1k) e ear girth (1l).

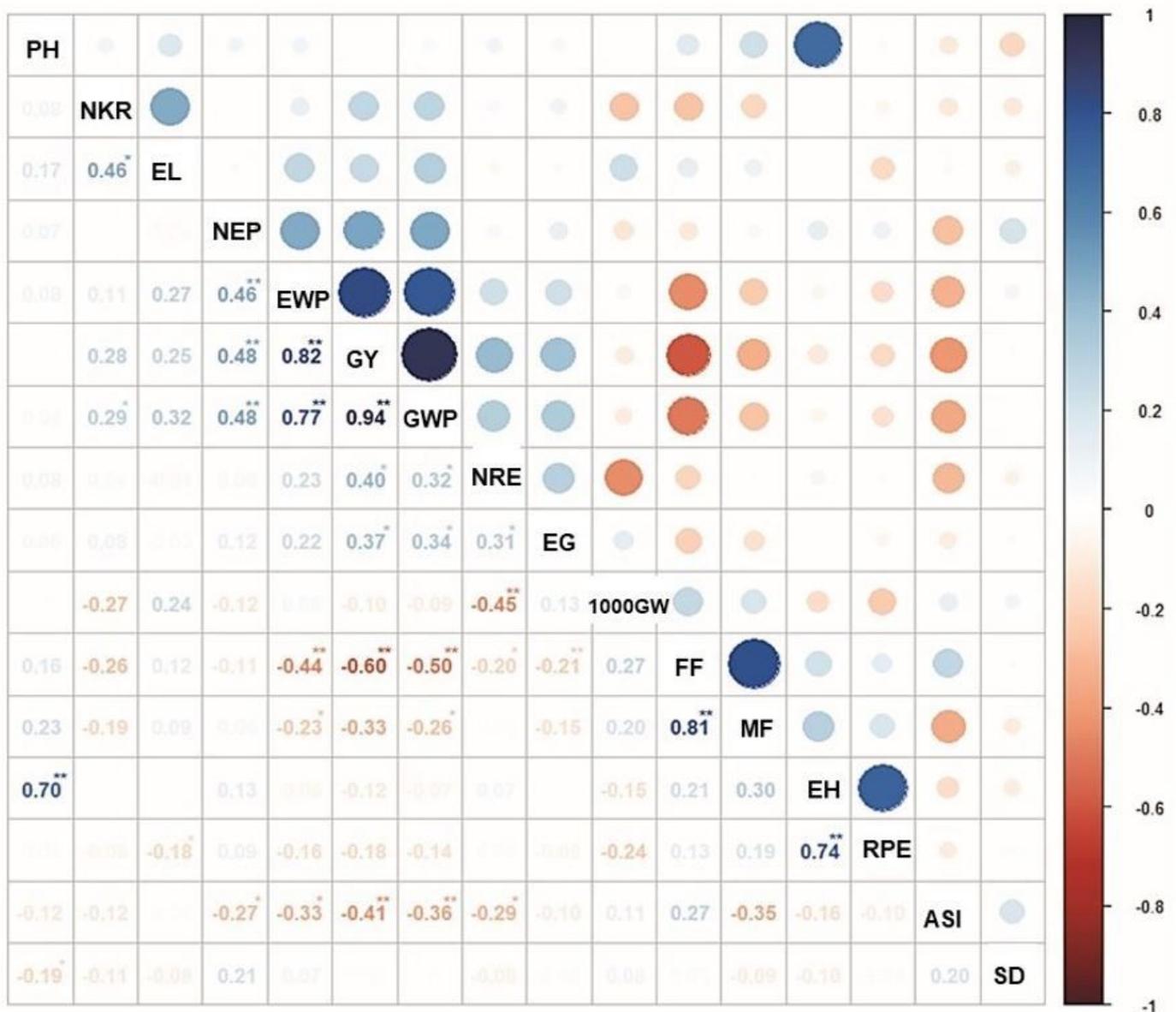


Figure 2

Correlation among the variables evaluated in the 78 genotypes. PH – plant height (m), EH – Ear height (m), SD – stalk diameter (cm), MF – male flowering (days), FF – female flowering (days), ASI - anthesis-silking interval (days), RPE – relative position of the ear (m), NEP – number of ears per plant, NRE – number of kernel row per ear, NKR – number of kernel per row, EL – ear length (cm), EG – ear girth (cm), 1000GW – 1000 grain weight (g), EWP – ear weight per plant (kg), GWP – grain per plant (kg) e GY – grain yield (kg ha⁻¹).

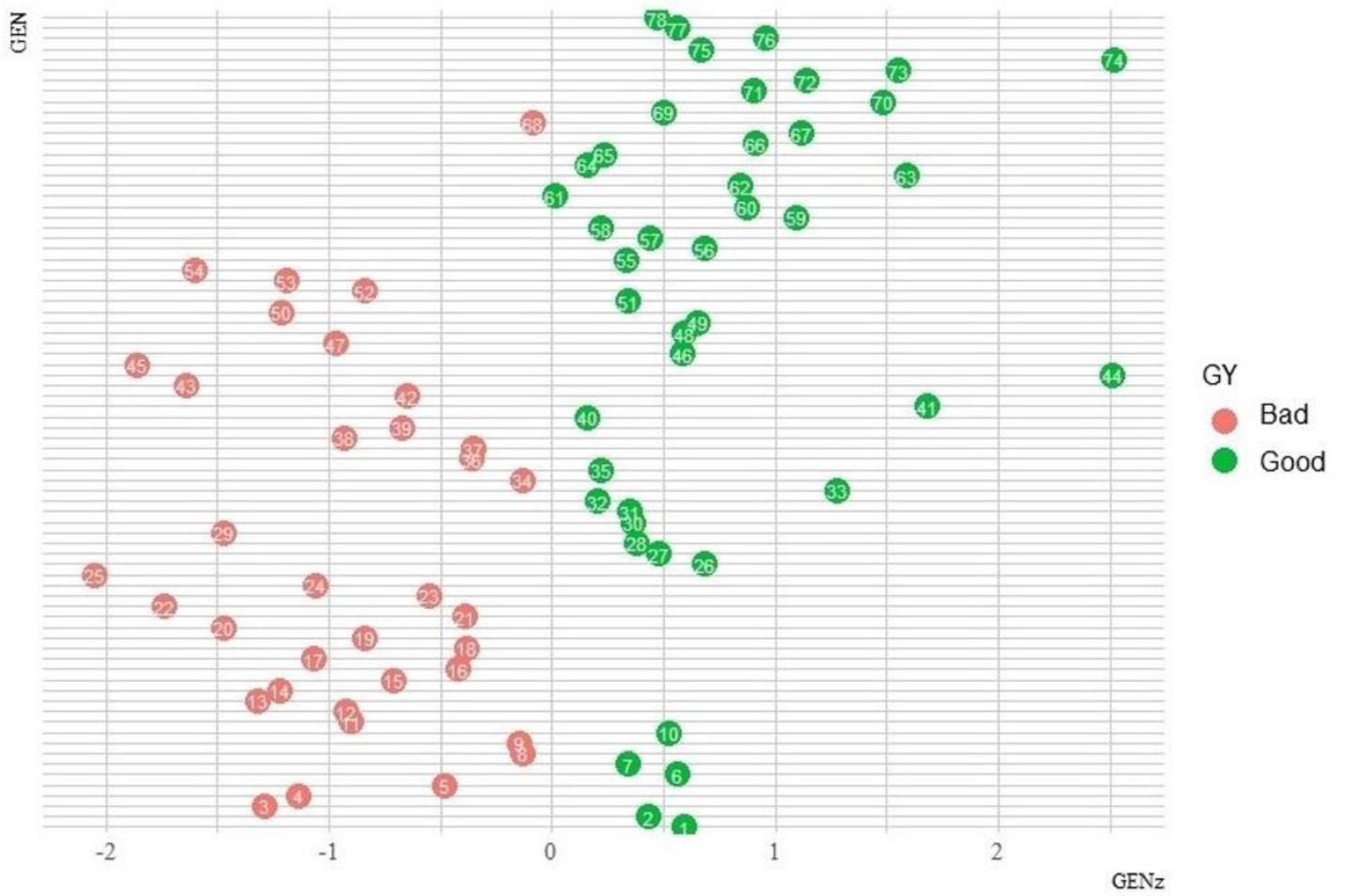


Figure 3

Rank of corn genotypes for their selection regarding grain yield (kg ha^{-1}) based on the averages of the genotypes adjusted by the BLUE of the model. GY: grain yield (kg ha^{-1}); GEN: genotypes; GENz: genotype means adjusted by BLUE-GY.

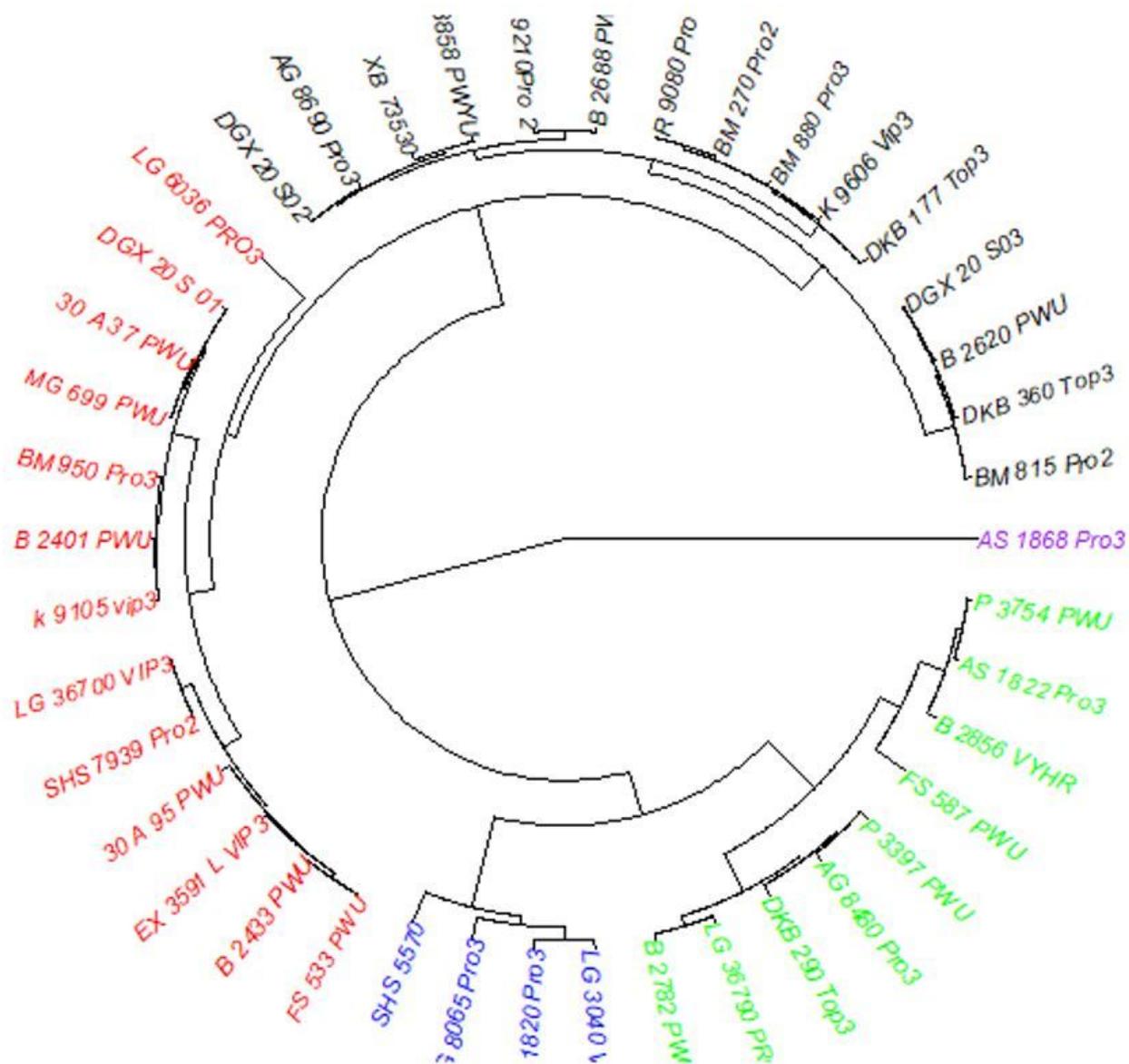


Figure 4

UPGMA cluster analysis and formation of crossing blocks based on estimated dissimilarity for the 43 selected genotypes. Black: BLOCK I; Purple: BLOCK II; Green: BLOCK III; Blue: BLOCK IV; and Red: BLOCK V.