TreeDimensional Journal, Vol. X, e023010, 1-11, 2022
DOI: `doi.org/10.55746/treed.2023.01.010`

Selection of superior *Eucalyptus "urograndis"* hybrid clones through genotype × environment analysis

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Abstract
The success of *Eucalyptus* cultivation in Brazil is partly due to the adaptation of its species to the different environmental and edaphic conditions present in the country. To improve performance, one must consider the interaction of individuals with the environment in which they are planted, since productivity can be maximized by choosing clones that are better adapted to certain environmental conditions. The objective of this study was to verify the effects of genotype × environment interaction and assess the possibility of recommending genetic materials for the evaluated environmental conditions. These interactions were assessed using the harmonic mean of the relative performance of genotypic values and GGE biplot methods, so as to rank the best clones in each location and across all locations. We found low levels of variation between genotypes, resulting in low heritability and coefficients of variation, and the existence of GE interaction. The influence of the environment on the genotypic variation of the clones was very clear in the evaluated tests. Methods such as GE analysis are important and advantageous for tree breeding programs and success in the forest sector, since it enables the evaluation and definition of which genetic materials can be considered more suitable for different conditions and the potential gains of the studied traits.

Keywords
Tree breeding, clonal test, urograndis hybrid, genotype × environment

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1. Introduction

Year over year, the area of planted forests has grown consistently in Brazil. Planted forests currently cover about 9.55 million hectares (ha), of which about 7.47 million ha are cultivated with species of the *Eucalyptus* genus (IBÁ, 2021). The success of this forest crop is related to its adaptation to the different environmental and edaphic conditions of the country. This is due to the fact that *Eucalyptus* species have extensive genetic variability and morphological differences, which can be modified with the development of *Eucalyptus sp.* breeding programs, improving growth, wood productivity, and ecological adaptation (Alfenas et al., 2009).

Through a genetic improvement program, the *Eucalyptus grandis* W. Hill ex Maiden × *Eucalyptus urophylla* S.T.Blake hybrid was developed in Brazil. This hybrid was created to obtain plants with good wood and trunk development and diameter and height similar to its parent species, enabling an increase in yield as well as improved cellulose and wood quality properties. *E. urophylla* is currently planted on a total of 600,000 ha in Brazil and is one of the most important for clonal silviculture (Faria et al., 2014; Dos Santos et al., 2018).

A factor that must be taken into account when planting *Eucalyptus sp.*, is the interaction of individuals with the environment in which they are planted, as the phenotype of a given trait is the result of the combination of the effects of the genotype and the environment (Vencovsky & Barriga, 1992; Araujo et al., 2019). Thus, maximum productivity can be achieved due to better adaptation to the environmental conditions (Mori et al., 1986). As such, genotype × environment (GE) interaction should be considered in species improvement programs, since the success of the program depends on identifying superior genotypes with good performance and plasticity in terms of their adaptability (Pires et al., 2011).

Merely estimating GE interaction variance components is insufficient to understand the performance of individuals in certain places. Therefore, analyses of adaptability, stability, and productivity must be conducted using standard methods to identify the behavior of genotypes

Received: 2022/11/07 | **Accepted:** 2023/01/09 | **Online published:** 2023/02/07

that are responsive to the conditions in which they are planted (Cruz et al., 2004).

The harmonic mean of the relative performance of genetic values (HMRPGV) method, proposed by Resende (2007), allows for the selection of individuals based on their genetic values, simultaneously considering their productivity, stability, and adaptability in different locations. Thus, it enables the selection of genotypes with better productivity for each environment, those that are stable (with similar productivity) between environments, as well as offering information about how well genotypes adapt to different environmental conditions.

The harmonic mean of genotypic values (HMGV), relative performance of genotypic values (RPGV), and joint analysis of the two (HMRPGV), can be used to interpret the attributes of perennial plants. In breeding programs, they can inform selection for productivity, stability, and adaptability (Rosado et al., 2012). These methods do not allow for a graphical representation of genotype productivity, stability, and adaptability in different locations; however, the GGE biplot method (Yan et al., 2000) based on a data matrix can be used to represent the genotypes and their interactions with different environments (Silva et al., 2012).

In the present study, using genotype × environment analyses together with the environmental conditions of the evaluated sites, we sought to identify the best clones and genetic material of a *urograndis* hybrid, based on comparative methods of ranking by HMRPGV and GGE biplot analyses.

2. Matherials and Methods

The experiment was carried out in the *E. urograndis* experimental center that belongs to the Eldorado Brasil company, in the state of Mato Grosso do Sul (MS), Brazil. The climate of the region is considered Aw (tropical), according to the Köppen and Geiger classification (1928), with more rainfall in the summer than the winter, and an average temperature in the hottest month of 26.7 °C and in the coldest month of 21.2 °C.

Data were used from three clonal tests established to evaluate the silvicultural characteristics of *E. urograndis* hybrids in three locations (Canoas, Lagoa Bonita, and Rancharia), located in the cities of Selvíria and Aparecida do Taboado (Table 1).

For the analyses, measurements of diameter at breast height (DBH, cm) and height (m) were collected when the trees were between 34 and 36 months. The three experiments were installed using a randomized block design (RBD), with a total of four blocks containing 25 plants per plot, spaced 3.4 m × 2.3 m.

After data collection, the analysis of the materials was performed individually and jointly for the three sites, using the lme4 package (Bates et al. 2015) in the R statistical software environment (R Core Team, 2020). The variance components were estimated according to the following mixed model for cloned individuals:

$$Y_{ijk} = \mu + b_j + g_i + e_{ijk}$$

where:

μ = overall average; b_j= fixed effect of the *j*-th block; g_i= random effect of the *i*-th clone; e_{ijk}= residual error.

For the joint analyses, the variance components were estimated according to the following mixed model, considering the genotype × environment interaction:

$$Y_{ijk} = \mu + g_i + \ b_{jk} + ge_{ik} \ + \ e_{ijk}$$

where:

μ = overall average; g_i = random effect of the *i*-th clone; b_{jk} fixed effect associated with the *j*-th block within the *k*-th environment; ge_{ik} = random effect associated with the interaction between the *i*-th clone and the *k*-th environment; e_{ijk} = residual error.

With the adjustment of the mixed model, it was possible to obtain the genotypic variance, the genotype × environment interaction variance, residual variance, and phenotypic variance. Along with the variance estimates, it was possible to estimate the following genetic parameters:

a) Broad-sense heritability;

$$h_g^2 = \frac{\widehat{\sigma}_g^2}{\widehat{\sigma}_g^2 + \widehat{\sigma}_e^2}$$

b) Average heritability of clones;

$$h_m^2 = \frac{\widehat{\sigma}_g^2}{\widehat{\sigma}_g^2 + \frac{\widehat{\sigma}_{ge}^2}{nenv} + \frac{\widehat{\sigma}_d^2}{nb}}$$

c) Coefficient associated with the effects of the GE interaction;

$$c_{ge}^2 = \frac{\widehat{\sigma}_{ge}^2}{\widehat{\sigma}_g^2 + \widehat{\sigma}_{ge}^2 + \widehat{\sigma}_e^2}$$

d) Genotypic correlation of clones between environments;

Table 1. Edaphoclimatic data for the cities of Selvíria and Aparecida do Taboado, MS, with their respective geographic location.

City	Average Temperature (C°)	Average Rainfall (mm)	Climate	Latitude (°)	Longitude (°)	Elevation (m)	Soil Type
Selvíria	23.5	1370	Tropical Aw	-20.3696	-51.4191	345	Dystrophic Red Latosol
Aparecida do Taboado	23.5	1595	Tropical Aw	-20.089	-51.103	392	Red Yellow Latosol

$$rg_{loc} = \frac{h_a^2}{h_a^2 + c_{ge}^2}$$

e) Accuracy in clone selection;

$$\widehat{r}_{aa} = \sqrt{h_m^2}$$

f) Coefficient of genotypic variation;

$$C\widehat{V}_g(\%) = \frac{\sqrt{\widehat{\sigma}_g^2}}{\bar{x}}$$

g) Coefficient of environmental variation;

$$C\widehat{V}_e(\%) = \frac{\sqrt{\widehat{\sigma}_e^2}}{\bar{x}}$$

where:

$\widehat{\sigma}_g^2$ = genotypic variance; $\widehat{\sigma}_e^2$ = residual variance; $\widehat{\sigma}_d^2$ = variance within the plots; $\widehat{\sigma}_{ge}^2$ = variance of genotype × environment interaction; $\bar{x}$ = overall average; $nenv$ = number of environments; nb = number of blocks.

2.1 Genotype ranking

To perform the ranking of the genotypes, the best linear unbiased prediction method (BLUP) was used to predict the genotypic value for each clone, where the following formulas were used:

a) Selection of genotypes for all locations considering the GE interaction:

$$\mu + g_i + ge_m$$

where:

μ = average of all environments; g_i = genotypic BLUP associated with genotype effect (free of GE interaction); ge_m= mean BLUP of the effect of the GE interaction, where $ge_m = g_{ik}/n_k$, g_{ik} is the effect of the *i*-th genotype in the *k*-th environment, and n_k is the number of environments.

b) Selection of genotypes by location considering the GE interaction in each environment:

$$\mu_k + g_i + ge_{ik}$$

where:

μ = environment mean; *k*; g_i = genotypic BLUP associated with the effect of genotype *i* (free of GE interaction); ge_{ik} = BLUP associated with the interaction effect between genotype *i* in environment *k*.

c) Selection by values of productivity and stability (harmonic mean of genotypic values – HMGV), adaptability (relative performance of genotypic values – RPGV) and productivity, stability, and adaptability (harmonic mean of relative performance of genotypic values – HMRPGV).

$$HMGV_i = \frac{n_{ik}}{\sum_{k=1}^{n_{ik}} \frac{1}{GV_{ik}}}\ ; RPGV_i = \frac{1}{n_{ik}}\left(\frac{\sum GV_{ik}}{\mu_k}\right)\ ; HMRPGV_i = \frac{n_{ik}}{\sum_{k=1}^{n_{ik}} \frac{1}{RPGV_{ik}}}$$

where:

n_{ik} = number of environments *k* in which genotype *i* was evaluated; GV_{ik} = genotypic value of genotype *i* in environment *k*, predicted as: $\mu_k + g_i + ge_{ik}$; μ_k = average of environment *k*.

After estimating the BLUPs of the genotypes, it was possible to construct the GGE biplot analysis graphs (Yan et al., 2000) with the aid of the metan package (Olivoto et al., 2020) in R (R Core Team, 2020). These graphs enable a more detailed analysis of the GE interactions, confirming the productivity, stability, and adaptability of the genotypes in the environmental conditions of each area.

The package makes use of the singular value partitioning (SVP) method, which is the basis for principal component-based interaction analysis techniques. It summarizes the variation contained in an n × m matrix into vectors that contain most of the variation, resulting in a biplot (Peixouto, 2013). The following GGE model was used in the double-entry matrix *g + ge* created from the estimated BLUPs:

$$g+ge_{(g+gxa)} = [(g+ge)] = \sum_{j=1}^{n} \lambda_j \gamma_{ij} \delta_{kj} + \varepsilon_{ik}$$

where:

$g+ge_{(g+gxa)}$= matrix of the effects of *g* genotypes added to the effect *ge* of the interactions between *g* genotype and *a* environment; λ_j= singular value of the *j*-th axis of principal components analysis; γ_{ij}= eigenvector of genotype *i* in the *j*-th principal component; δ_{kj}= eigenvector of environment *k* in the *j*-th principal component; ε_{ik}= residual error.

3. Results and Discussion

After estimating the variance components, it was possible to assess the genetic parameters, both for the individual tests (Table 2) and for the joint analysis of genotype × environment (Table 3). In the analysis of clonal tests, broad-sense heritability (h_g^2) is one of the main parameters that indicates the success of selection, as it measures how much phenotypic variation is explained by the individual genotype, and how much of it can be used in subsequent generations through selection (Rosado et al., 2012).

Based on the classification by Ziegler and Tambarussi (2022), heritability estimates are considered low when they present values from 0.01 to 0.55, moderate from 0.55 to 0.73, and high greater than 0.73. Thus, the values of h_g^2 were all considered low, obtaining estimates of 0.028, 0.085, and 0.038 for Canoas, Lagoa Bonita, and Rancharia, respectively. The phenotypes of the individuals present in the experiments are strongly influenced by the environments in which they are planted, demonstrating poor environmental control in the experiments. These low values of h_g^2 were due to low genotypic variance of the clones ($\widehat{\sigma}_g^2$ = 0.135, 0.310, and 0.186).

Table 2. Estimates of variance and genetic parameters for DBH (cm) in the individual analysis of *E. urograndis* located in Canoas, Lagoa Bonita, and Rancharia, Mato Grosso do Sul, at three years of age.

Parameters	Canoas	Lagoa Bonita	Rancharia
$\widehat{\sigma}_g^2$	0.135	0.310	0.186
$\widehat{\sigma}_e^2$	4.664	3.343	4.728
$\widehat{\sigma}_f^2$	4.799	3.653	4.913
h_g^2	0.028	0.085	0.038
h_m^2	0.080	0.218	0.105
$\widehat{CV}_g(\%)$	2.839	4.447	3.508
$\widehat{CV}_e(\%)$	16.663	14.596	17.707
$\widehat{r}_{aa}$	0.283	0.467	0.325
$\bar{\mathbf{x}}$	12.960	12.526	12.280

$\widehat{\sigma}_g^2$: genotypic variance of clones; $\widehat{\sigma}_e^2$: residual variance; $\widehat{\sigma}_f^2$: phenotypic variance; h_g^2 : broad-sense heritability; h_m^2 : average heritability of clones; $\widehat{CV}_g(\%)$: coefficient of genotypic variation; $\widehat{CV}_e(\%)$: environmental variation coefficient; $\widehat{r}_{aa}$: accuracy in clone selection; $\bar{\mathbf{x}}$: trait average.

Rosado et al. (2012) also found low values of h_g^2 (0.238) for clones of *Eucalyptus spp.* in Sabinópolis, Minas Gerais State, Brazil, at 36 months, which emphasizes the influence of the effects of GE interaction, since DBH for the clonal test was more affected by the environment. On the other hand, Garcia and Nogueira (2005), carried out an experiment with *E. grandis, E. urophylla,* and *E. urograndis* at seven years of age in Eunápolis, Bahia, Brazil, and found estimates of h_g^2 for DBH of 0.462. This result shows better genetic control over the trait with some potential to explore selection within the experiment, and good results for genetic advancement. Tolfo et al. (2005) obtained high h_g^2 values (0.69) for clones of *E. grandis, E. urophylla, E. urograndis,* and *E. saligna* at 80 months of age in the municipality of Guatapará, São Paulo State, Brazil, considering the trait DBH.

The mean heritability of clones (h_m^2) is used when we want to consider the means of the selection. The parameter is chosen to predict values in the selection of clones where genotypic values are obtained according to the means of the experiment (Maia et al., 2009). In the present study, the values of h_m^2 were also considered low (0.080, 0.218 and 0.105), indicating limited potential to perform selection within each experiment. The accuracy in the selection of clones ($\widehat{r}_{aa}$) was low (0.283, 0467, 0.325), due to the low values of h_g^2 and $\widehat{\sigma}_g^2$.

For the estimates of the genetic parameters of the GE joint analysis (Table 2), we found values of h_g^2 that can be considered of low magnitude for both traits, DBH and height (0.031 and 0.161, respectively), according to the

Table 3. Estimates of variance and genetic parameters in the GE joint analysis for E. urograndis located in Canoas, Lagoa Bonita, and Rancharia, Mato Grosso do Sul at three years of age, for DBH and height.

Parameters	Trait	
	DBH (cm)	Height (m)
$\widehat{\sigma}_g^2$	0.085	0.257
$\widehat{\sigma}_{ge}^2$	0.092	0.046
$\widehat{\sigma}_e^2$	2.604	1.291
$\widehat{\sigma}_f^2$	2.781	1.593
h_g^2	0.031	0.161
h_m^2	0.211	0.618
c_{ge}^2	0.033	0.029
rg_{loc}	0.481	0.849
$\widehat{r}_{aa}$	0.459	0.786
$\widehat{CV}_g(\%)$	2.253	2.708
$\widehat{CV}_e(\%)$	12.442	6.075
$\bar{\mathbf{x}}$	12.968	18.702

$\widehat{\sigma}_g^2$: genotypic variance of clones; $\widehat{\sigma}_{ge}^2$: variance of the genotype × environment interaction; $\widehat{\sigma}_e^2$: residual variance; $\widehat{\sigma}_f^2$: phenotypic variance; h_g^2 : broad-sense heritability; h_m^2 : average heritability of clones; c_{ge}^2 : coefficient associated with the effects of the genotype × environment interaction; rg_{loc} : genotypic correlation of clones between environments; $\widehat{r}_{aa}$: accuracy in clone selection; $\widehat{CV}_g(\%)$: coefficient of genotypic variation; $\widehat{CV}_e(\%)$: environmental variation coefficient; $\bar{\mathbf{x}}$: trait average.

classification by Ziegler and Tambarussi (2022).

Therefore, a significant part of the phenotypic variation in terms of DBH is strongly influenced by the environment. Although minimal, greater genetic control was found for height. With low values, the importance of improving the GE interaction to maximize gains in clonal selection is highlighted (Rosado et al., 2012). Castro et al. (2018) found similar values of h_g^2 for the same traits in clones of *Eucalyptus dunnii* aged three to nine years, in three municipalities in Rio Grande do Sul State, Brazil (0.12 for DBH and 0.06 for height). Santos et al. (2015) found different values in a study at four different locations in Rio Grande do Sul, with three-year-old *Eucalyptus* hybrid clones, with h_g^2 values of 0.176 for DBH and 0.070 for height.

The h_m^2 observed for the three sites was considered low and moderate, with a value of 0.211 for DBH. This indicates little genetic control in the expression of the trait, but some potential to perform selection within each experiment. Rosado et al. (2012) found similar values of h_m^2 for height of *Eucalyptus sp.* clones at three years (0.775) in clonal tests established in Sabinópolis, Minas Gerais. Thus, the present experiment was able to distinguish the environmental effects, enabling an estimation of the true genotypic values.

In a study conducted by Castro et al. (2018), values of h_m^2 of 0.41 and 0.67 for DBH and height, respectively, were found for *E. dunnii* from three to nine years of age. Thus, it appears that h_m^2 produces values that are considered of low to moderate accuracy ($\widehat{r}_{aa}$) in the selection of clones (0.459). The low value of the genotypic variance for DBH also implies a low accuracy and, consequently, low h_g^2 (0.031).

According to Ziegler and Tambarussi (2022), the values of the coefficients of genotypic variation ($\widehat{CV}_g(\%)$) can be considered low for both traits (2.253 and 2.708, respectively). However, the values of the coefficients of environmental variation ($\widehat{CV}_e(\%)$) were high for DBH (12.442) and moderate for height (6.075). According to Sebben et al. (1999), $\widehat{CV}_g(\%)$ is an important parameter for breeding programs, as it indicates how much genotypic variation there is between clones, thus aiding in selection. It is also a parameter that is highly influenced by the environment. Therefore, due to the low values of $\widehat{CV}_g(\%)$, there is poor genotypic variation between the clones, indicating strong variation of the environment in this experiment.

Finally, the parameter of genotypic correlation of clones between environments (rg_{loc}) is considered one of the main parameters in the analysis of GE interaction. This parameter indicates how genotypes behaved in different environments, where the closer the value is to 1, the more similar the values are across two or more locations. According to Resende (2002), values of rg_{loc} between 0.70 and 0.90 indicate that the genotypes tend to have similar performance in the evaluated environments, which means high stability. The value found for DBH can be considered moderate (0.481), and for height it was high (0.849). Thus, a strategy that can be adopted is the selection of specific clones for each environment, aiming at maximizing the expected gains (Vencovsky & Barriga, 1992).

The ranking of the clones (Figure 1) considers the effect of the genotypes analyzed together in the three locations (Canoas, Lagoa Bonita, and Rancharia), accounting for the average effect of the interaction for DBH.

In Table 4, the genotypic value of the clones was ranked in relation to the GE interaction for selection, considering each location separately. Thus, it was possible to compare the adaptability of the 10 best clones in each location, as well as identify the clones that performed similarly in the three environments.

In Canoas, the genotype that showed the best performance was clone 80, even though Canoas is the only environment in which it was ranked in the top 10. This is followed by clones 51 and 111, which performed well

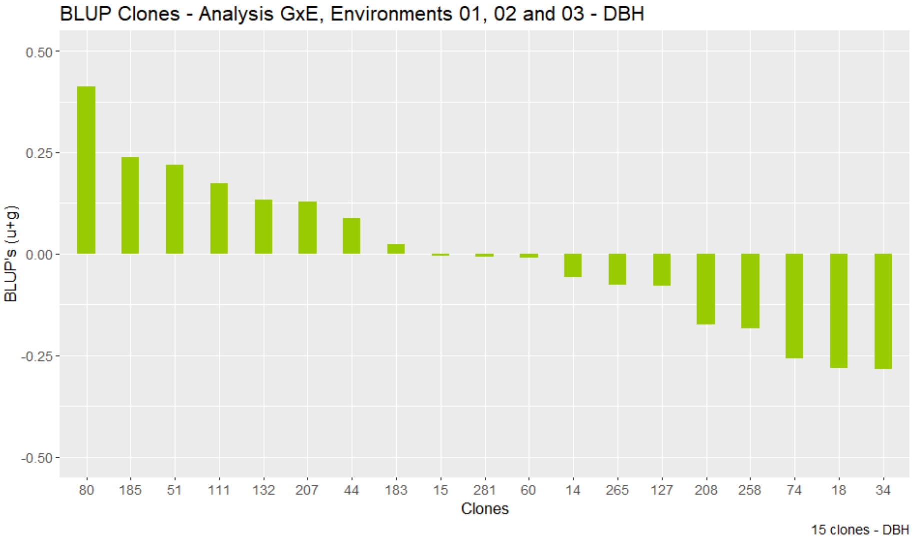

Figure 1. Ranking of the genotypic values for DBH of the 19 *E. urograndis* clones in Canoas, Lagoa Bonita, and Rancharia, Mato Grosso do Sul, at three years of age, considering the three environments.

in the three environments and obtained high ranking in the BLUPs. Clone 14, in turn, performed well in Lagoa Bonita but was not productive in Canoas.

In Lagoa Bonita, the genotype that performed best was clone 132, which is also present in the ranking of the 10 best clones across the three locations simultaneously. In this environment, clone 14 also performed well, which indicates the existence of GE interaction in the tests, explaining its poor ranking in Canoas.

According to the ordering obtained at Rancharia (Table 4), the influence of the GE interaction is evident, considering that the genotypic correlation value between environments (rg_{loc}) was moderate (0.481) for DBH, as we can see a difference in the ranking between the three environments. It is worth highlighting the performance of clones 51 and 111 which placed high in the ranking, with good results across the analyzed environments.

Clone 74 did not obtain good results in any of the three analyzed locations and was always ranked poorly.

The ranking of the best clones following the three criteria of productivity, stability, and adaptability (Table 5) was similar between the evaluated environments, as the same clones perform comparably in the rankings. Thus, it is important to evaluate genotypes that have stability in their performance and that are productive, that is, that respond favorably to different environments.

For example, clone 80 performed best in the three rankings, but this clone is only ranked highly in the first environment (Canoas). However, it performed so well in that environment that it managed to remain at the top of the joint analyses. Similarly, clone 207 is ranked highly in environments 1 and 3 (Canoas and Rancharia), and clone 185 is only found in the top 10 for Rancharia.

Clone 51, ranked highly in the three locations and maintained a high position for productivity, stability, and adaptability, thus indicating it as a material that performed well in the three environments. Clones 111 and 132, which were among the best in the environmental conditions of Lagoa Bonita, also had good results for the three sites simultaneously.

Table 4. Ranking of the genotypic values for DBH of the 10 best E. urograndis clones, at three years of age, in Canoas, Lagoa Bonita, and Rancharia, Mato Grosso do Sul, considering each environment separately.

Rank	**Canoas**		**Lagoa Bonita**		**Rancharia**	
	Clone	GV**	**Clone**	GV	**Clone**	GV
1	80	14.08	**132**	13.38	185	13.31
2	**51**	13.63	**111**	13.15	**111**	13.15
3	**111**	13.38	51	13.10	**51**	13.13
4	**183**	13.34	14	13.02	207	13.10
5	207	13.34	281	13.02	60	13.02
6	60	13.24	44	13.00	44	13.02
7	15	13.22	**183**	12.99	**132**	12.94
8	**132**	13.20	127	12.81	14	12.78
9	127	13.16	258	12.77	208	12.74
10	18	13.01	74	12.76	**183**	12.73

* values in bold refer to genetic materials that are among the top 10 clones in the three environments. ** GV is the genetic value composed by $\mu + g + ge$.

The graphs presented below are related to the joint analysis of the *E. urograndis* tests established in Canoas, Lagoa Bonita, and Rancharia, based on DBH at 34 to 36 months. These are reliable results since the two components (PC1 and PC2) represent 94.27% of all the G + GE variation in the data.

The GGE biplot model divides the G+GE effects into two main components. The first component (PC1) is

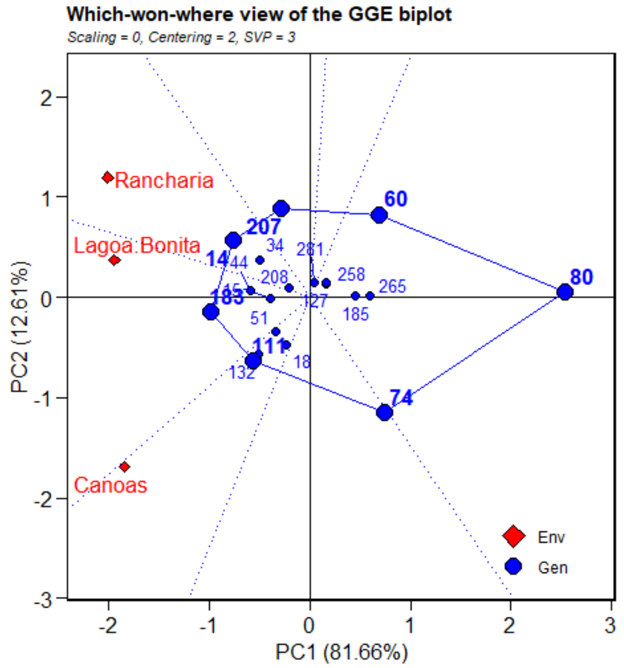

Figure 2. GGE biplot “which-won-where” with 19 *E. urograndis* genotypes evaluated in three environments, considering DBH.

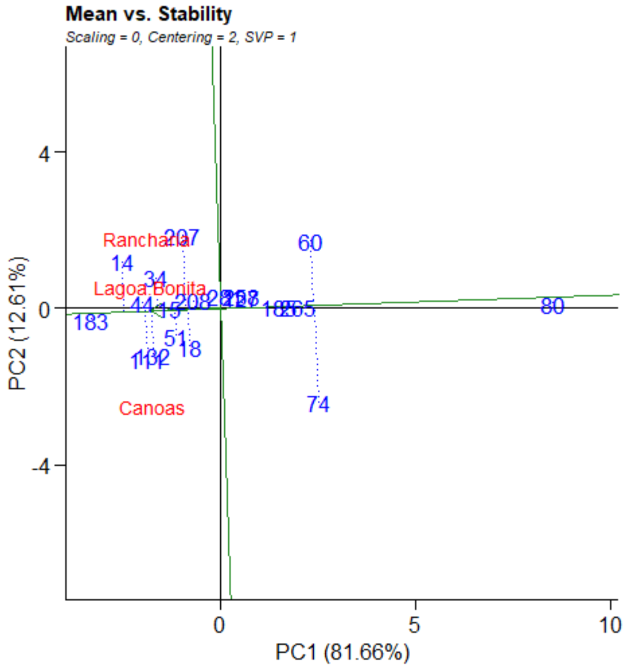

Figure 3. GGE biplot model “mean vs. stability” with 19 *E. urograndis* genotypes evaluated in three environments, considering DBH.

attributed to genotypic variation (G), which explained 81.66% of the variation. This demonstrates that most of the variation is the result of the genotypes. The second component (PC2) explained 12.61% of the variation, attributed to the GE effect.

Figure 2 represents the GGE biplot “which-won-where”. This biplot focuses on analyzing differences between environments (Column Metric Preserving – “SVP = 2”).

The “which-won-where” biplot forms an irregular polygon that includes all genotypes, at the vertices and within, and has two axes at right angles that signal the origin of the biplot. The genotypes that occur along the vertices of the polygon are the most distinct from the mean values of the population, either positively or negatively. All other genotypes occur within the polygon.

The dashed blue lines starting at the origin indicate mega-environments, which are formed based on the similarity of each site according to the performance of the genotypes in each. In this case, each site formed its own mega-environment. However, Canoas is almost on the edge of Lagoa Bonita, and Lagoa Bonita, in turn, is almost on the edge of Rancharia. Each mega-environment has a genotype that is located at the vertex of the polygon, indicating the genotype that performed best in each environment.

We can see in Figure 2 that the genotypes that performed best were 14 in the Rancharia mega-environment, 183 in Lagoa Bonita mega-environment, and 111 in the Canoas mega-environment. The genotypes present in the center of the polygon had similar results among them in each of the three locations. The genotypes that occur close to the origin are most similar to the general average of the three locations considered simultaneously.

As for the other genotypes that give rise to the other vertices of the polygon, such as genotypes 74, 60, and 80, these are considered unfavorable for the analyzed environments, along with the other genotypes in their corresponding sectors. In the case of genotype 80, it was ranked best for MHPRVG as it presented good results in the environment in which it was highly ranked. However, it is not ranked in the top 10 for all three locations, only in one. Thus, it is located inversely (negatively) to the mega-environments as there is no data for all environments to indicate the genotype as stable or productive.

The biplot shown in Figure 3 is called “mean vs. stability”. This biplot evaluates the productivity of a genotype in relation to the general average and expresses its stability in the environments.

This biplot demonstrates the differences between genotypes. The further the genotypes are from the y-axis in the direction of the arrow, i.e., the further to the left, the more productive they tend to be. Thus, genotypes 183, 14, 44, and 111 are more productive than the general average (represented by the y-axis). On the other

Table 5. Ranking of the 10 best E. urograndis clones, at three years of age, according to productivity and stability of genotypic values (HMGV), adaptability of genotypic values (RPGV), and productivity, stability, and adaptability simultaneously (HMRPGV) in the three environments.

Rank	Productivity and Stability		Adaptability			Productivity, Stability, and Adaptability		
	Clone	**HMGV**	**Clone**	**RPGV**	**RPGV + $\bar{x}$**	**Clone**	**HMRPGV**	**HMRPGV + $\bar{x}$**
1	80	14.0865	80	1.0645	13.8052	80	1.0645	13.8052
2	185	13.3194	185	1.0387	13.4701	185	1.0387	13.4701
3	51	13.2863	51	1.0227	13.2634	51	1.0227	13.2629
4	111	13.2298	111	1.0182	13.2052	111	1.0182	13.2047
5	207	13.2253	207	1.0153	13.1673	207	1.0153	13.1667
6	15	13.2212	132	1.0141	13.1516	132	1.0139	13.1485
7	132	13.1739	44	1.0106	13.1055	44	1.0105	13.1052
8	183	13.0201	183	1.0023	12.9979	183	1.0022	12.9974
9	44	13.0111	15	0.9991	12.9573	15	0.9991	12.9573
10	60	12.9763	281	0.9990	12.9559	281	0.9989	12.9549

hand, genotypes 60 and 74 are the most distant in the opposite direction, and are the least productive or stable. Again, clone 80 is further away because it is ranked in only one of the environments, thus there is insufficient information to be considered “above average” in other places.

The x-axis is called the average-environment axis (AEA), representing the average of the environments. The more distant the vector between the genotype and the AEA, the less stable it is in all environments. It is worth noting genotypes 111 and 132, which have distant vectors toward the Canoas environment. This indicates good performance in the given environment. The same occurs with genotype 14 for the Rancharia. The genotypes that are located along the AEA, not tending to either side, are genotypes that had similar results in the three locations and can be considered close to the average.

Another way to visualize the ranking of genotypes is the biplot called “ranking genotypes” (Figure 4). It is similar to “mean vs. stability” (Figure 3), and also includes the AEA, but with an absence of vectors linking the genotypes. This biplot shows concentric circles that facilitate ranking, where the center of the circles represents the ideal genotype (ideotype).

Again, genotypes 183, 14, 44, and 111 were the most productive, and occur closer to the center of the concentric circles. Genotype 183 can be considered the ideotype. As in Figure 3, clones 60 and 74 were the least productive/stable.

Figure 5 shows the biplot called “discrimination vs. representativeness”. This is used to verify the relationship between the environments.

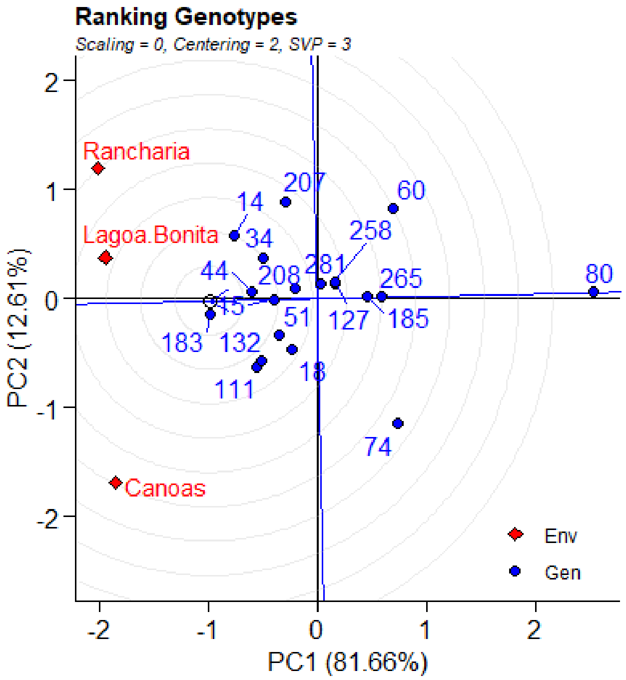

Figure 4. GGE biplot ”ranking genotypes” with 19 *E. urograndis* genotypes evaluated in three environments, considering DBH.

The environments that have long vectors in relation to the origin have high discriminating power. That is, the genotypes perform differently in such environments. In the case of this analysis, it was necessary to construct two biplots (A and B) for easier visualization, with biplot B on the right being an enlargement of the biplot on the left.

The cosine of the angle between the vector of an environment and the AEA is the same as the correlation value between the genetic values obtained in this environment and the average genetic values of all environments. Thus, a representative environment must occur at a small angle in relation to the AEA. As such, the Rancharia and

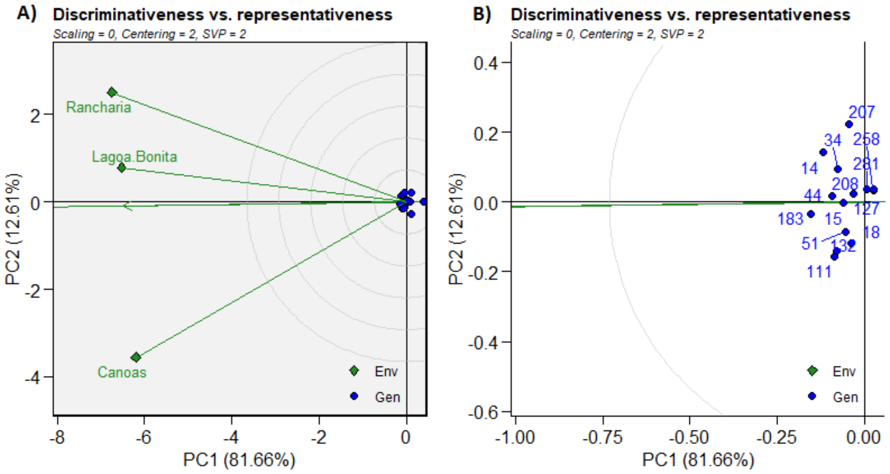

Figure 5. GGE biplot “discrimination vs. representativeness” with 19 *E. urograndis* genotypes evaluated in three environments considering DBH, where B) is an enlargement of biplot A).

Canoas environments do not represent an average environment, which is useful for the selection of genotypes with better performance in their own mega-environments. On the other hand, Lagoa Bonita is more suitable for identifying superior and stable genotypes within all environments.

We can see that the environment considered ”ideal” was Lagoa Bonita, this is due to the fact that this location had the greatest number of genotypes with better performance in DBH growth when compared to the other two, as shown in Figure 5A. The vector of the Lagoa Bonita environment had the smallest angle in relation to the AEA and is thus a more representative environment.

4. Conclusion

For the estimates of genetic parameters for the joint analysis of genotype × environment interaction, the values of broad-sense heritability were low for DBH. This indicates that a large part of the phenotypic variation that is expressed by the trait is strongly influenced by the environment. Therefore, the genetic control for DBH is low and will have little effect on selection among clones. The average heritability of clones was considered low for DBH and moderate for height, indicating greater potential than DBH to carry out selection within the experiment based on the averages of the clones. With low rg_{loc} values and high values of genotype × environment interaction, the importance of Identifying the interaction between genotype × environment to maximize gains in clonal selection is reinforced.

According to the ranking of the genotypic values by BLUP, MHPRVG, and the GGE biplots, we found that the best clones present in the three clonal tests were clones 51, 111, 132, and 183. These clones obtained good results, remaining productive and stable in all environments. One strategy that can be adopted is the selection of genotypes separately for each location, since the correlation of clones between environments was low for DBH, indicating that performance between the three locations is inconsistent.

Acknowledgements

We want to thank the company Eldorado Brasil for providing the data from their experiments.

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