ADAPTABILITY AND STABILITY OF IRRIGATED RICE ELITE LINES FOR GRAIN QUALITY

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ABSTRACT

The objective of this work was to investigate the interaction of irrigated rice genotypes in different environments, based on the genotypic evaluation of grain quality traits, through the adaptability and stability analysed by mixed models. These parameters were obtained from cultivation trials in eight cultivation environments of irrigated rice in Southern Brazil. The experimental design was randomized complete blocks, with 14 genotypes for each one and four repetitions. The genotypic values were estimated using REML/BLUP, based on the harmonic mean methods of the genotypic values, the relative performance of the predicted genotypic values through the environments and the harmonic mean of the relative performance of the genotypic values. The high accuracy values obtained for the most studied variables, show a great experimental quality and safety in the selection of these traits. The lines AB11502 and AB10501 showed a better agronomic performance in the milling yield. AB13008, AB13002 and AB13003 stood out for chalky traits, showing higher adaptability and stability. These inbred lines revealed high potential for grain quality attributes and have potential to be released.

Keywords: *Oryza sativa*, mixed models, genotype, environment, interaction

INTRODUCTION

The use of genetically superior rice genotypes is only possible through extreme efforts in labor and investment, as this is a slow and long term process. However, researchers are not looking only for genetic potential, but also for their performance when facing environmental changes. According to Colombari Filho et al. (2013) this variation is due to genotype x environment interaction (G x E), affecting mainly quantitative variables. Therefore the elite lines should be evaluated in different environments and the obtained data should be analyzed for yield, adaptability and stability, in order to select adapted cultivars to different cultivation regions.

Several authors defined the concepts about adaptability and stability. The most accepted are Mariotti et al. (1976), that defined adaptability as being the ability of the genotype to respond in a favorable way to environmental changes, while stability as being the ability of a genotype to achieve predictable performance under different environmental conditions.

When the breeders goal is to select the lines with high homeostasis and adaptability, as well as genotypes coupled with high yield and stability production, these evaluations are the most important (BALESTRE et al., 2010). However, one needs to use accurate measurement tools for the response of these lines to multiple testing environments (YAN et al., 2007).

Recently, there are several methods applied for the adaptability and stability analysis. Among them, the mixed models analysis, such as REML/BLUP, proposed for information analysis of several perennial and annual crops (RESENDE, 2004). The Restricted Maximum Likelihood (REML), procedure which has the purpose of estimating the variance components that are necessary to the model, and the Best Linear Unbiased Prediction (BLUP) which in turns estimates the genotypic value (REGITANO NETO et al., 2013).

The mixed models analysis allows the consideration of correlated errors within the locals, as well as the identification of adaptability and stability in order to select superior genotypes (TORRES et al., 2015). However, provides genetic values not considering the instability, and can be applied to several environments, in order to generate results in the unit or scale of the evaluated trait, with the possibility of direct interpretations as genetic values, differing from other methods. This model provides results such as genotype selection per local; stable genotype selection across sites by the harmonic mean method of the genotypic values (HMGV), according to Resende (2004); selection of genotypes with high adaptability, responsive to favorable environments, by the relative performance method of the predicted genotypic values (RPGV), based on the Annicchiarico (1992) method; and the selection for productivity, stability and adaptability, by the harmonic mean of the genotypic values relative performance method (HMGVRP), similar to the Lin and Binns (1988) method, but in the genotypic context not in the phenotypic one.

Several studies using HMGV, RPGV and HMGVRP methods were develop for different species, as rubber tree (GOUVÊA et al., 2011), cassava (FARIAS NETO et al., 2013), eucalyptus (PUPIN et al. 2015), beans (TORRES et al., 2015; CORRÊA et al., 2016), cotton (FARIAS et al., 2016), coffee (SILVA et al., 2017), upland (BORGES et al., 2010; COLOMBARI FILHO et al., 2013; REGITANO NETO et al., 2013), and irrigated rice (STRECK et al., 2018), for grain yield. However, for irrigated rice there are few studies regarding G x E, especially when referring to the attributes of grain quality, which are quantitative traits involving a lot of gens where the phenotypic expression is highly influenced by the environment, even when is the main objectives of the breeding programs.

Therefore, this study had the objective to investigate the G x E of irrigated rice in the main soil/climate regions of Rio Grande do Sul State irrigated rice agricultural zoning, based on the genotypic evaluation of grain quality, adaptability and stability attributes by REML/BLUP method.

MATERIAL AND METHODS

Eight experiments of cultivation and use value were conducted, where three of them in the 2014/15 season and five in the 2015/16 season. The locals comprised municipalities located in different irrigated rice producing regions of Rio Grande do Sul State, Brazil, whose edaphoclimatic characteristics are presented (Table 1). Each experiment was composed of 14 genotypes, 10 elite lines and/or hybrid and four control cultivars of irrigated rice, however some of these elite lines were changed from one season to another (Table 2). The experimental design was randomized complete blocks, with 14 treatments and four repetitions. The experimental unit consisted of nine rows of 5.0 m in length, spaced in 0.17 m between the rows. The useful harvest area was composed by 4 m in the center of four internal seven rows, to exclude some incident effect on the border.

The sowing density was 100 kg ha⁻¹, using a mechanical plot seeder, under no-tillage system. The base fertilization was 300 kg ha⁻¹ of NPK (formula 05-20-20) and 90 kg ha⁻¹ of nitrogen as urea, being 50% applied in the V4 stage (start of tillering) and the rest in R1 stage (differentiation of the floral primordium). The irrigate system was adopted by permanent inundation until R9 stage (genotype final maturation).

Grains were harvested manually, avoiding possible undesirable mixture among the genotypes, with a moisture of the grains approximately 22%. After, the grains were placed in a dryer for the reduction of relative humidity to 13%. Therefore, the grains underwent to a mini testing machine, (Suzuki – MT) for the husking and the polishing process, thus generating the percentual of total polished grains (TPG - %), percentual of whole grains (WG - %) and percentual of broken grains (BG - %) after milling. Subsequently, the inner physical quality attributes of the grains were evaluated with help of S21 grain statistical analyzer, based in the digital image analysis of each sample, showing the following parameters: CL- caryopsis length (mm); CW – caryopsis width (mm); P+WB - percentual chalky grains and with white belly (%); CD – general grain color defects (burnt, moldy, squashed, stained and yellow grains) (%); and PA – total chalky area (%).

Table 1. Geographic environmental traits, season, location, latitude, longitude and altitude, of the

Table 2. List of the 14 genotypes evaluated in each season in different environments of cultivation and use tests, their respective classifications totalling 21 different genotypes. Pelotas, Rio Grande do Sul State, Brazil, 2014/15 and 2015/16.

Genotypes

From the phenotypic data, the genetic traits estimated under analysis were made through the mixed linear models, being evaluated using the 54 statistical models of the software Selegen - REML/BLUP (RESENDE, 2016), corresponding the $y = Xr + Zg + Wi + and$, where "y" is the data vector, "r" is the vector of repeating effects (assumed as fixed) plus the general mean, "g" is the vector of genotypic effects (assumed as random), "i" is the vector of G x E effects (random) and "e" is the vector of the errors or residues (random). Capital letters represent incidence matrices

for these purposes. The same way as Torres (2015), the distributions, mean structures (E) and

variances (Var), were assumed as:
$$
E\begin{pmatrix} y \\ g \\ i \\ e \end{pmatrix} = \begin{pmatrix} Xr \\ 0 \\ 0 \\ 0 \end{pmatrix}, Var\begin{pmatrix} g \\ i \\ e \end{pmatrix} = \begin{pmatrix} I\hat{\sigma}_g^2 & 0 & 0 \\ 0 & I\hat{\sigma}_i^2 & 0 \\ 0 & 0 & I\hat{\sigma}_e^2 \end{pmatrix}.
$$

From the equations of the mixed models, we obtained the model fit: 1 2 From the equations of the mi
 $X'X'Z = X'W$ \hat{r} \hat{r} \hat{r} $\begin{pmatrix} X & X'Z & X'W \\ X & Z'Z + I\lambda_1 & Z'W \end{pmatrix}$ $x \begin{pmatrix} \hat{r} \\ \hat{g} \end{pmatrix} = \begin{pmatrix} X' \\ Z' \end{pmatrix}$ $\begin{array}{ccc} X & Z'Z + I\lambda_1 & Z'W \\ YX & W'Z & W'W + I\lambda_2 \end{array}\begin{bmatrix} x \\ x \\ \hat{i} \end{bmatrix} = \begin{bmatrix} Z' \\ W' \end{bmatrix}$ From the equations of the mixe $X'X = X'Z = X'W$ $\left(\begin{array}{cc} \hat{r} \end{array}\right) = \begin{pmatrix} X'y \end{pmatrix}$ $\begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + I\lambda_1 & Z'W \end{bmatrix}$ $x \begin{bmatrix} \hat{r} \\ \hat{g} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$ $Z'X$ $Z'Z + I\lambda_1$ $Z'W$
 $W'X$ $W'Z$ $W'W + I\lambda_2$ $\begin{pmatrix} x \\ \hat{i} \end{pmatrix} = \begin{pmatrix} Z'y \\ W'y \end{pmatrix}$ From the equations of the mixed mod
 $(X'X - X'Z - X'W)$ $\begin{pmatrix} \hat{r} \\ \hat{r} \end{pmatrix}$ $\begin{pmatrix} X'y \\ \hat{r} \end{pmatrix}$ $\begin{pmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + I\lambda_1 & Z'W \\ W'X & W'Z & W'W + I\lambda_2 \end{pmatrix} x \begin{pmatrix} \hat{r} \\ \hat{g} \\ \hat{i} \end{pmatrix} = \begin{pmatrix} X'y \\ Z'y \\ W'y \end{pmatrix},$ w , where 2 $1-h^2-i^2$ $1 = \frac{1}{2^2} = \frac{1}{2^2}$ $\hat{\sigma}^2_{\rho}$ 1 ˆ $e = \frac{1 - \mu_g}{g}$ n_g n_g $h_{\varrho}^{2}-i$ *h* $\lambda = \frac{\sigma}{\sqrt{2}}$ $=\frac{\hat{\sigma}_{e}^{2}}{\hat{\sigma}^{2}}=\frac{1-h_{g}^{2}-i^{2}}{h^{2}}$ and

2 $1-h^2-i^2$ $v_2 = \frac{1}{2^2} = \frac{1}{2^2}$ $\hat{\sigma}^2$ 1 ˆ *e g i* $h_{\varrho}^{2} - i$ *i* $\lambda = \frac{\sigma}{\sqrt{2}}$ σ $-h_{\rm e}^2 - i^2$ $=\frac{\sigma_e^2}{\sigma_s^2}=\frac{1-n_g-l}{l}$; being the broad sense heritability in the block: 2 2 2 \approx 2 \approx 2 ˆ $\hat{\sigma}^2_{\scriptscriptstyle{\alpha}}+\hat{\sigma}^2_{\scriptscriptstyle{i}}+\hat{\sigma}$ *g g* $_g$ + o_i + o_e $h_s^2 = \frac{\sigma_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_i^2 + \hat{\sigma}_e^2}$; the

coefficient of determination of the G x E effects: $\hat{\sigma}^2_i$ 2 \approx 2 \approx 2 ˆ $\hat{\sigma}^2_{\scriptscriptstyle{\alpha}} + \hat{\sigma}^2_{\scriptscriptstyle{i}} + \hat{\sigma}$ *i* $_g$ + σ _i + σ _e $i^2 = \frac{\sigma}{\sqrt{2}}$ $=\frac{\sigma_i}{\hat{\sigma}_{\hat{g}}^2 + \hat{\sigma}_i^2 + \hat{\sigma}_{\hat{g}}^2}$; $\hat{\sigma}_{g}^2$ is the genotypic variance

among the irrigated rice genotypes; $\hat{\sigma}_i^2$ is the G x E variance; $\hat{\sigma}_e^2$ is the residual variance among the plots; genotypic correlation of the genotypes, across environments is determined by

$$
r_{ga} = \frac{\hat{\sigma}_i^2}{\hat{\sigma}_g^2 + \hat{\sigma}_i^2} = \frac{h_g^2}{h_g^2 + i^2}.
$$

However, the estimaton of components of variance by REML, in EM algorithm corresponds to :

$$
\hat{\sigma}_e^2 = \frac{\left[y' y - \hat{r}' X' y - \hat{g}' Z' y - \hat{i} W' y \right]}{\left[N - r(x) \right]}; \quad \hat{\sigma}_g^2 = \frac{\left[g' g + \hat{\sigma}_e^2 tr C^{22} \right]}{q}; \quad \hat{\sigma}_i^2 = \frac{\left[i' i + \hat{\sigma}_e^2 tr C^{33} \right]}{s}; \quad \text{where } C^2
$$
\n
$$
\left(C_{11} - C_{12} - C_{13} \right)^{-1} \left(C_{11} - C_{12} - C_{13} \right)
$$

and C³ correspond to $I_1 = \begin{pmatrix} C_{11} & C_{12} & C_{13} \ C_{21} & C_{22} & C_{23} \end{pmatrix}^{-1} = \begin{pmatrix} C_{11} & C_{12} & C_{13} \ C_{21} & C_{22} & C_{23} \end{pmatrix}$ $\begin{array}{cccc} C_{31} & C_{32} & C_{33} \end{array}$ $\begin{array}{cccc} \begin{array}{cccc} C_{31} & C_{32} & C_{33} \end{array} \end{array}$ $C^{-1} = \begin{pmatrix} C_{11} & C_{12} & C_{13} \ C_{21} & C_{22} & C_{23} \end{pmatrix}^{-1} = \begin{pmatrix} C_{11} & C_{12} & C \ C_{21} & C_{22} & C \end{pmatrix}$ $\begin{array}{cc} C_{21} & C_{22} & C_{23} \ C_{31} & C_{32} & C_{33} \end{array}$ = $\begin{array}{cc} C_{21} & C_{22} & C \ C_{31} & C_{32} & C \end{array}$ - $\begin{bmatrix} C_{11} & C_{12} & C_{13} \\ C_{21} & C_{22} & C_{23} \\ C_{31} & C_{32} & C_{33} \end{bmatrix}^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} \\ C_{21} & C_{22} & C_{23} \\ C_{31} & C_{32} & C_{33} \end{bmatrix}$, where $=\begin{pmatrix} C_{11} & C_{12} & C_{13} \ C_{21} & C_{22} & C_{23} \ C_{31} & C_{32} & C_{33} \end{pmatrix}^{-1} = \begin{pmatrix} C_{11} & C_{12} & C_{13} \ C_{21} & C_{22} & C_{23} \ C_{31} & C_{32} & C_{33} \end{pmatrix}$, wher , where the coefficient matrix of

the mixed models is denominated by C; tr is the dot matrix operator; $r(x)$ the matrix post X; N is the total number of data, q number of genotypes and s is the number of the G x E combinations.

Thus, with this model empirical BLUP predictors was obtained (eBLUP or REML/BLUP) of the genotypic values without interaction, given by $\hat{\mu} + \hat{g}_i$, where the $\hat{\mu}$ is the total mean of the environments and \hat{g}_i is the genotypic effect without G x E interaction. The genotypic values (Vg),

for each environment j, were predicted by $\hat{\mu}_j + \hat{g}_i + (\hat{g}e)_{ij}$, where $\hat{\mu}_j$ is the mean of environment j, \hat{g}_i is the genotypic effect of the genotype i, in the environment j, and $(\hat{g}e)_{ij}$ is the G x E interaction relative to the genotype i.

The prediction of genotypic values capitalizing the mean interaction ($\hat{g}e_m$) in the different

environments is given by $\hat{\mu}_j + \hat{g}_i + \hat{g}e_m$, calculated by: $2 + \hat{\sigma}^2$ 2 $\hat{\sigma}^2_{\varrho} + \hat{\sigma}^2_{i}$ \hat{u} + $\frac{n}{\hat{s}^2}$ \hat{g}_i be ˆ $\sigma_{g}^{\tau}+\sigma_{i}^{\tau}$ $i_j = \mu + \frac{2}{\Delta^2} g_i$ *g* $Vg_{ij} = \hat{\mu} + \frac{(n-\lambda)^2}{2} \hat{g}$ $\hat{\sigma}_{\varrho}^2 + \hat{\sigma}_{i}^2$ $\mu + \frac{\Delta}{\hat{\sigma}}$ $\left(\hat{\sigma}_{\scriptscriptstyle\mathcal{G}}^2 + \hat{\sigma}_{\scriptscriptstyle i}^2\right)$ = $\hat{\mu}$ + $\left(\frac{\sigma_s^2 + \sigma_i^2}{n} \right)$
= $\hat{\mu}$ + $\left(\frac{\sigma_s^2 + \sigma_i^2}{n} \right)$ \hat{g}_i being $\hat{\mu}$ the overall

mean of all environments; n is the number of environments; and \hat{g}_i the genotypic effect of the genotype i.

The results regarding the genotypic stability by the harmonic mean method of the genotypic values were calculate by: 1 $i=\frac{n}{n}$ 1 *j ij* $MHVG = \frac{n}{n}$ \mathbf{V} *y* $=$ \sum .

The results regarding the genotypic adaptability by the relative performance method of the

predicted genotypic values across the environments were calculated by: $PRVG_i = \frac{1}{1-\frac{1}{2}}$ *n ij j i j Vg* $PRVG_i = \frac{1}{n} \left(\frac{\sum_{j=1}^{n} Vg_{ij}}{M_i} \right).$ $=\frac{1}{\sqrt{2}}\left|\frac{\sum_{j=1}^{3}S_{ij}}{S_{ij}}\right|$. $\left| \frac{1}{M_i} \right|$ $\begin{pmatrix} M & j \\ & \end{pmatrix}$ \sum .

The model that simultaneously considers the yield, adaptability and stability of irrigated rice genotypes is given by the harmonic mean method of relative performance of the genotypic values: 1 $i = \frac{n}{2}$ 1 *j* $MHPRVG_i = \frac{n}{r}$ \mathcal{I}_1 *PRVG* $=$ \sum . Where n is the number of the environments that genotype i was

evaluated; "Vg_{ij}" the genotypic value of the genotype i in the environment j, expressed as a proportion of the environment mean; M_i is the general mean of each j environment.

To obtain the results in scale or unit of measurement of the studied variables, both PRGV and HMMPGV were multiplied by the overall mean $(\hat{\mu})$, generating mean genotypic values (PRGVμ) capitalized by the interaction, and genotypic values of each genotype (HMMPGVμ) penalized by the instability and capitalized by the G x E interaction.

RESULTS AND DISCUSSION

The predictions of variance components estimate (Table 3) refer to the unfolding of the genetic structure of one plant population, in order to answer how much the phenotypic proportion is due to genetic, environmental or genotype x environment interaction effects. According to Maia et al. (2009) the importance of this information for the breeding programs in the direct use as a more practical way for the selection, besides serving as theoretical reference in support for recommendations of new cultivars.

Some grain quality traits evaluated, are not only related to genotypic variance but also under significant environmental influence (HAKATA et al., 2012; LI et al., 2014; XU et al., 2015). The high CV^e values are expected. However, *only* three showed this behavior with 26.40% for WG, 58.45% for P+WB, and 29.50% for Cd. The other traits analyzed presented low CV_e ranging from 1.01 to 9.53%.

The accuracy results refer to join assessments of CV_g and CV_e (RESENDE & DUARTE, 2007), showing the experimental quality. High accuracy values were obtained for all studied traits, with exception of total percentage of polished grains that presented 45.50%. The other traits ranging from 83.50% to 98.50%, for whole grains percentage and grains width respectively, revealing a great experimental quality and safety in selection.

Grain length and width (GL and GW) are high σ_{g}^{2} traits, showing a h_{g}^{2} $h_g²$ (total genotypic heritability effects) of 53.40 and 77.00% respectively, not demonstrating significant influences from σ_e^2 and σ_i^2 . Therefore, they can be considered less complex traits to select, as they do not change significantly among the environments. These attributes do not determine the grain quality, however, Castro et al. (1999) demonstrate the consumption pattern of white and polished rice in Brazil, being long and thin grain according to the results of the general with CL of 6.628 mm and CW of 2.040 mm (length/width relation $= 3.249$).

This consumption pattern was introduced with Bluebelle, an american cultivar being gradually replaced by BR IRGA 409 and BR IRGA 410, cultivars released in the late 70s, directly responsible for the green revolution of irrigated rice in Brazil due to the new plant architecture (semi-dwarf). This new architecture allowed to increase the milling yield as well as the yield potential in the Rio Grande do Sul State (STRECK et al., 2017) and consequently the grain quality.

Table 3. Estimates of variance components (REML individual) in irrigated rice genotypes, cultivated

 σ_g^2 - genotypic variance; σ_i^2 - genotype x environment interaction variance; σ_e^2 - residual variance; σ_p^2 - phenotypic variance; h_g^2 h_g^2 - total genotypic effects heritability; h_m^2 h_{mg}^2 - heritability in the broad sense at the level of mean of the genotypes; Ac_g – Accuracy of the select of level of the mean of the genotypes; c_i^2 c_i^2 - coefficient of determination of the genotype x environment interaction effects; r_{ga} - genotypic correlation between genotype x environment; CV_g – coefficient of genetic variation; CV_e – coefficient of environmental variation; μ - overall mean.

The σ_g^2 represented by the h_g^2 $h_g²$ results for the other evaluated traits ranging from 20.10% and 34.50%, for para WG and PA respectively, except for TPG being of 2.80%. These heritability values are considered low to be use as criteria of direct selection in the breeding of these traits assuming that such results can include not only additive (fixable) but also dominance and epistasis (non-fixable) effects.

In general, the grain quality attributes (WG, BG, TPG, P+WB, CD and PA) were strongly influenced by G x E interaction, demonstrated by the c_i^2 c_i^2 results, which corresponds to the percentage of σ_i^2 compared to total σ_p^2 (38.80%, 34.20%, 48.00%, 23.60%, 34.70% and 21.40%, respectively) (Table 3). However, these physical attributes are quantitative traits, responsible for many factors. They are also controlled by maternal and cytoplasmatic effects with large genetic effects (ZHOU et al., 2009) and the G x E interaction ends up not being noticeable.

The genotypic correlation among the performance of many environments (r_{ga}) shows the behavior of the genotypes beyond the changing environments tested, a way to indicate the occurrence of constant or if whether there will be genotype classification according to the evaluated trait. The observed proportions of r_{ga} , for the physical attributes of grain quality ranging from 34.20 to 61.80% (WG and PA respectively), not being considered high when pointing out the variations in order of genotypes. This has also been observed in other studies in different species (MAIA et al., 2009; TORRES et al., 2015).

Based in the stability parameters of genetic values (HMGV), adaptability of genotypic values (PRGVμ) and simultaneously the adaptability and stability of genotypic values $(HMMPGV\mu)$, a small difference in the ranking of the genotypes among the methods was observed. These circumstances were reported in a rice yield study by Colombari Filho et al. (2013).

The percentage of whole grain attributes (WG), considered as major trait of grain quality in irrigated rice is extremely sought by breeding programs. It is of fundamental importance in the commercialization and the most required attribute by the industry segment in the rice chain. The more stable genotypes for WG by HMGV were in successive order AB11502, BR IRGA 409, AB13006, AB10501, AB14001, AB13003 and AB13715, maintaining means higher than 62.00% of whole grains, in the constant way among the environments this same genotypes showed a great stability for lowest percentage of broken grains except for AB14001 (thirteenth of the ranking).

The AB10501 elite line showed higher adaptability for the percentage of whole grains and percentage of broken grains, reaching the mean genotypic value of 66.61% and 5.23% respectively, beyond the favorable environments for both PRGVμ and HMMPGVμ methods. In addition, it surpassed all the control cultivars in these traits followed by BR IRGA 409, which was the control that demonstrated both adaptability and stability in relation to the environments in all proposed methods.

In general, the line AB11502, together with AB10501, proved to be better in all three methods (HMGV, PRGV and HMMPGV), with stability in different environments and great adaptability in favorable environments for the three milling process traits (WG, BG and TPG). It is worth mentioning that the line AB11502 was originated by selection within the cross between the cultivars IRGA 417 and BR IRGA 409, both excellent in grain quality.

About the control cultivars IRGA 417, rice denominated as type "premium" in grain quality (CHAMPAGNE et al., 2010), and BRS PAMPA a cultivar of high concept and acceptance by the producers in Rio Grande do Sul state because of its grain quality (MAGALHÃES JÚNIOR et al., 2012), which refers to stability and adaptability for the percentage of total and whole grains were higher in some elite lines (Table 4). However, beyond the P+WB, CD and PA attributes (Table 5), both remained among the best ranked means.

For these same (P+WB, CD and PA) attributes, when observed together the AB13008, AB13002 and AB13003 lines were the most stables among the environments studied and showed good adaptability in all three methods.

Recently, the adoption of rice hybrids is under discussion, because of their low grain quality, one of the restrictions present in some of these cultivars. A lot of studies show this difference between the conventional and hybrids cultivars (BLANCHE et al., 2009; LONDERO et al., 2015). However, in this study the H7 CL hybrid genotype demonstrated satisfactory adaptability and stability parameters unlike the control Avaxi CL hybrid (HMGV, PRGV and HMMPGV) against the grains quality attributes throughout the tested environments.

This hybrid such as BRSCIRAD 302 development through a collaborative research between EMBRAPA (Brazilian Agricultural Research Corporation) and CIRAD ("*Centre de Coopération Internationale en Recherche Agronomique pour le Développement*"). This partnership does rely on single crosses between Brazilian cultivars already established in the market, but the development through constant improvement of the lines corresponding to the parents (previous parental improvement) in order to obtain better results both yield and grain quality (NEVES, 2010). Therefore, the improvement of specific lines for the use in the development of rice hybrids specially for females which refers to physic attributes for grain quality (due to the effects already mentioned), is an alternative to be used to enhance this trait in order to break barriers for the use of this type of cultivars in southern Brazil.

All the methods (HMGV, PRGV and HMMPGV) demonstrated that the control AVAXI CL (hybrid) presented low levels of adaptability in favorable environments and among the least stables in may environments for all the physics attributes of grains quality assuming a small improvement only in the TPG and CD.

Analyzing all the physical traits of grain quality the elite line AB13003 has shown constant performance through the many environments (PRGV μ and HMMPGV μ), followed by the cultivar BR IRGA 409, with a small exception for CD.

The results of this work point to the existence of genetic variability in the irrigated rice in breeding program of Embrapa in Rio Grande do Sul, for grain quality attributes among the evaluated lines with potential for future releases or for variability maintaining in the germplasm bank.

Table 4. Stability of genotypic values (HMGV). adaptability of genotypic values (PRGVμ) and simultaneously adaptability and stability of the genotypic values (HMMPGVμ) of the 21 irrigated rice genotypes predicted by the analysis BLUP. for the variables of WG – percentual of wholes grains. BG - percentual of broken grains and TPG – total percentual of polished grains. with their respective classifications (rº - ranking); cultivated in eight environments in the Rio Grande do Sul State, Brazil, 2016.

	HMGV							$PRGV\mu$					HMMPGVµ					
GENOTYPE	WG	$r^{\rm o}$	BG	$r^{\rm o}$	TPG	$\rm r^o$	WG	\mathbf{r}^{o}	BG	$r^{\rm o}$	TPG	$\rm r^o$	WG	\mathbf{r}^{o}	BG	$r^{\rm o}$	TPG	\mathbf{r}^{o}
AB11502	66.6	1	4.26	$\overline{2}$	71.42	1	63.87	3	6.83	4	71.17		63.82	3	6.62	$\overline{4}$	71.15	$\mathbf{1}$
BR IRGA 409	65.08	2	3.76	1	70.2	7	64.67	2	5.23	2	70.14	6	64.56	2	5.02	$\mathbf{1}$	70.11	6
AB13006	64.2	3	5.48	4	70.34	6	61.57	7	8.56	6	70.09	7	61.55	7	8.45	8	70.08	7
AB10501	63.26	4	5.43	3	70.66	3	66.61		5.23	1	70.87	3	66.58		5.15	$\overline{2}$	70.87	$\overline{2}$
AB14001	62.8	5	7.51	13	71.12	2	60.3	11	11.75	18	70.9	2	60.24	11	11.68	18	70.86	3
AB13003	62.69	6	6.12	7	70.05	9	60.12	12	9.92	14	69.79	11	60.12	12	9.83	14	69.79	11
AB13715	62.49	7	6.11	6	69.36	15	59.92	13	9.56	11	69.11	18	59.87	13	9.24	11	69.1	18
IRGA 417	62.42	8	5.62	5	70.09	8	62.08	6	7.7	5	70.01	8	62.05	5	7.57	5	70.01	8
H7 CL	60.5	9	6.28	8	70.03	10	60.67	10	8.58	7	69.95	9	60.44	10	8.29	7	69.95	9
AB11551	60.2	10	6.81	9	68.74	21	63.34	4	6.36	3	68.94	20	63.26	4	6.25	3	68.94	20
BRS Pampa	60.08	11	7.29	10	69.77	11	59.84	14	9.81	13	69.71	12	59.79	14	9.78	13	69.68	12
AB13008	59.99	12	7.46	12	69.27	16	59.6	15	10.29	15	69.21	17	59.55	15	10.13	15	69.18	17
AB13720	59.95	13	7.31	11	69.02	19	57.57	20	11.96	19	68.78	21	57.51	19	11.73	19	68.76	21
AB13689	59.8	14	8.67	15	69.67	12	57.69	19	13.74	20	69.54	13	57.39	20	13.08	20	69.43	13
AB13002	59.31	15	8.01	14	69.38	14	59.05	16	10.46	17	69.3	15	59.02	16	10.34	17	69.29	15
AB12683	59.04	16	9.61	16	69.64	13	62.18	5	8.74	8	69.85	10	61.98	6	8.28	6	69.85	10
AB13012	58.13	17	9.91	17	70.56	4	61.36	8	9.17	10	70.76	4	61.35	8	9.14	10	70.76	4
AB12597	57.84	18	10.32	18	68.89	20	60.88	9	9.15	9	69.1	19	60.67	9	8.84	9	69.09	19
Avaxi CL	55.89	19	10.96	20	70.46	5	56.36	21	14.42	21	70.38	5	55.96	21	14.12	21	70.37	5
AB12625	55.82	20	11.48	21	69.2	17	58.83	17	10.32	16	69.4	14	58.83	17	10.27	16	69.4	14
AB10572	55.53	21	10.36	19	69.08	18	58.72	18	9.7	12	69.29	16	58.68	18	9.64	12	69.29	16

CONCLUSION

There are significant changes resulting by the genotype x environment interactions for grain quality attributes in irrigated rice.

The methodologies used to determine adaptability and stability for the irrigated rice genotypes were effective for the grain quality attributes.

The lines AB11502 and AB10501 presented a good agronomic performance, adaptability and stability in the beneficiation yield traits against the proposed methods.

The lines AB13008, AB13002 and AB13003 presented agronomic performance for the traits percentage of chalky grains and with white belly and total chalky area against the proposed methods showing a higher adaptability and stability.

Among the evaluated lines AB13002 was the one presenting a better agronomic

performance in terms of percentage of colors defects against the proposed methods revealing superior adaptability and stability.

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