Genetics/ Original Article

Predicted genetic gains weighted by selection pressures for grain quality in irrigated rice

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Abstract – The objective of this work was to analyze components of variances and heritabilities, estimate selection gain, and evaluate the different selection pressures for physical quality attributes of grains of families of segregating generations of irrigated rice (*Oryza sativa*), through the REML/BLUP methodology. The experiment was conducted in the state of Rio Grande do Sul, Brazil, where selections were made in the F3, F4, and F5 segregating generations, in the 2015/2016, 2016/2017, and 2017/2018 crop seasons, in eight segregating populations (families) from different crosses. Intrinsic physical quality attributes, genetic parameters, and response to selection were evaluated using different selection pressures. The obtained estimates showed genetic gains for the characters related to grain quality, mainly for total chalky area, vitreous whiteness, total whiteness, ratio between vitreous whiteness and total whiteness, and percentage of whole grains and broken grains, in selections in early generations. The used families show satisfactory results, being superior to the control cultivars. For most characters, the estimates of broad-sense heritability are considered intermediate, together with the other parameters, showing the possibility of genetic selection for grain quality attributes. The response to selection with a pressure of 10% is very promising for rice grain quality attributes.

Index terms: *Oryza sativa*, breeding, heritabilities, REML/BLUP methodology.

Ganhos genéticos previstos ponderados por pressões de seleção para qualidade de grãos em arroz irrigado

Resumo – O objetivo deste trabalho foi analisar componentes de variâncias e herdabilidades, estimar o ganho de seleção e avaliar as diferentes pressões de seleção para atributos físicos de qualidade de grãos de famílias de gerações segregantes de arroz (*Oryza sativa*) irrigado, por meio da metodologia REML/BLUP. O experimento foi conduzido no Rio Grande do Sul, Brasil, onde foram realizadas seleções nas gerações segregantes F3, F4 e F5, nas safras 2015/2016, 2016/2017 e 2017/2018, em oito populações segregantes (famílias) oriundas de diferentes cruzamentos. Foram avaliados atributos físicos de qualidade intrínsecos, parâmetros genéticos e resposta à seleção, tendo-se utilizado diferentes pressões de seleção. Foram obtidas estimativas que apresentaram ganhos genéticos para os caracteres de qualidade dos grãos, principalmente para área calcárea total, alvura vítrea, alvura total, relação entre alvura vítrea e alvura total, e percentual de grãos inteiros e quebrados, em seleções nas primeiras gerações. As famílias utilizadas apresentam resultados satisfatórios, sendo superiores às cultivares-controle. Para a maioria dos caracteres, as estimativas de herdabilidade em sentido amplo são consideradas intermediárias, junto com os demais parâmetros, o que mostra a possibilidade de seleção genética para os atributos de qualidade do grão. A resposta à seleção com pressão de 10% é muito promissora para os atributos de qualidade de grãos de arroz.

Termos para indexação: *Oryza sativa*, melhoramento genético, herdabilidade, metodologia REML/BLUP.

Introduction

The cultivation of irrigated rice (*Oryza sativa* L.) is important for human nutrition, since the cereal is responsible for supplying about 20% of the calories required in the diet of the worldwide population (Fukagawa & Ziska, 2019). Brazil is one of the crop's largest producers, yielding more than 7 thousand kilograms per hectare, on average, in the 2019/2020 season, with a production of 9.6 million tons of grains (Acompanhamento…, 2020). According to Magalhães Júnior et al. (2020), although productivity is the main aim of rice breeding programs, grain quality attributes can directly reflect the market value and consumer acceptance of the product, showing the importance of increasing the productivity and quality of the obtained grains.

However, the concept of rice quality is still considered abstract, with no current uniform and applicable definition of the agronomic ideotype referring to it, and there are also distortions in the used measurement and selection methods (Custodio et al., 2019). Anacleto et al. (2015) reported that the quality of rice grains can be determined considering four main aspects: nutritional value, industrial quality, adequacy of the product to commercialization standards, and culinary or sensory quality.

In Brazil, consumers have a preference for long, fine, and glassy grains (without chalky areas) that are mostly not broken or damaged (Rosa et al., 2021). Growers and cerealists seek an adequate processing, good whole grain yields, low breakage rate during grain processing, minimal damage to the product's market value, and high acceptance of new cultivars (Magalhães Júnior et al., 2020).

Among the traits of agronomic interest, stand out quantitative characters determined by several genes, presenting low expression and significantly influenced by the environment (Falconer, 1981), which is reflected in the quality characters of rice grains. Possible strategies for irrigated rice breeding programs to obtain the desired results in a short period and with accuracy include the choice of the method and selection index (selection pressure) to be used.

Families are usually selected when the characters of interest have low heritability. However, Rocha et al. (2013) found that the early selection of high potential families is crucial in a breeding program, maximizing human and financial resources.

Therefore, it is important to observe the progeny and its genetic effects on segregating generations and families. Peternelli & Resende (2015) pointed out that, by using methodologies based on mixed linear models, it is possible to include all sources of variation, which are estimates of precise genotypic values, without environmental effects. An alternative for the construction of indexes, which may result in a more precise selection, is the application of the restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) methodology, which allows obtaining estimates of the variance components extracted by REML, as well as predicting the genetic values through BLUP (Resende, 2002). However, studies with mixed models applied to different segregating generations of irrigated rice, specifically regarding grain quality characters, are still scarce.

The objective of this work was to analyze components of variances and heritabilities, estimate selection gain, and evaluate the different selection pressures for physical quality attributes of grains of families of segregating generations of irrigated rice, through the REML/BLUP methodology.

Materials and Methods

The experiment was carried out at the lowland experimental station of Embrapa Clima Temperado, located in the municipality of Capão do Leão, in the state of Rio Grande do Sul, Brazil (31°48'49"S, 52°28'20"W, at 21 m altitude). According to Köppen-Geiger, the climate is of the Cfa type, with no dry season and a hot summer. In 2015, 2016, 2017, and 2018, the minimum and maximum temperatures were, respectively: 14.5 and 23.4°C, 13.6 and 22.3°C, 14.7 and 23.6°C, and 14.2 and 23.6°C. More than 30 mm of rain were registered in the driest month, and annual rainfall was 1,557, 1,421, 1,500, and 1,237 mm in 2015, 2016, 2017, and 2018, respectively. The soil of the experimental area is classified as a Planosolo Háplico (Santos et al., 2018), i.e., a Haplic Planosol.

Selections were made in the F3, F4, and F5 segregating generations in the 2015/2016, 2016/2017, and 2017/2018 crop seasons, respectively, in eight segregating populations (families) from crosses between the parents obtained from the irrigated rice breeding program of Embrapa Clima Temperado (Table 1).

The experimental design of interim controls was composed of eight families from ten plants of the previous generation (treatments) and of ten plots of each, with three fixed-effect controls, which were cultivars BRS Pampa, BR/IRGA 409, and Puitá INTA-CL. The plots consisted of four rows of 5.0 m in length, spaced at 0.25 m from each other. The experimental unit was composed of ten plants, totaling 100 plants per family.

The area was prepared following the technical recommendations and other managements for the crop (Reunião…, 2016). Sowing density was 100 kg ha^{-1}, and a mechanical plot seeder was used. Basic fertilization was applied at sowing, corresponding to 300 kg ha^{-1} N-P$_2$O$_5$-K$_2$O (5-20-20). Topdressing was done using 90 kg ha^{-1} in the form of urea, with 50% of the rate being applied in stage V4 (start of tillering) and the remainder in stage R0 (panicle initiation). The irrigation system adopted throughout rice cultivation until the R9 stage (end of genotype maturation) was permanent flooding, with approximately 10 cm water depth. The control of pests, weeds, and diseases was carried out according to the technical recommendations for growing irrigated rice.

Panicles of all generations were harvested manually and individually (separated by plant), and then packed in a grain stationary dryer to reduce moisture to approximately 13%. After drying, a manual trail was performed, followed by the process of peeling and polishing the grains of each plant of all generations, using the MT 2003 mini rice mill machine (Suzuki, Santa Cruz do Rio Pardo, SP, Brazil). The samples of polished grains were used to evaluate intrinsic physical quality attributes, with the aid of the S21 statistical grain analyzer (S21 Solutions, Santa Cruz do Rio Pardo, SP, Brazil), using the digital images of each sample to determine the following parameters in the grains: total chalky area (%); white core (%); color defects (%); vitreous whiteness; total whiteness; ratio between vitreous whiteness and total whiteness (VW/TW ratio), where values closer to one indicate more vitreous grains; total mass of whole grains (g); and total mass of broken grains (g) from a sample of 10 g polished grains.

The obtained data were subjected to the analysis of variance, at 5% probability, in order to test the additivity of the model, normality of residues, and homogeneity of variances. Subsequently, the likelihood ratio test of the deviance analysis was carried out, also at 5% probability, using the chi-square test, in order to verify the significance of the variance components and genetic parameters by REML, based on the model $y = Xr + Zg + e$, where y is the data vector, r are the effects of replicates assumed to be fixed, g are the genetic effects assumed to be random, e corresponds to the effects of residues assumed to be random, and X and Z are the incidence matrices to orthogonalize model effects. Genetic variance, environmental variance, block or residual variance, individual phenotypic variance, broad-sense heritability, family effect coefficient, coefficient of determination of plot effects, accuracy, coefficient of genotypic variation between progenies (CVg), residual coefficient of variation (CVe), and general mean of the experiment were determined. Subsequently, the selection response analysis was performed, using different selection pressures, i.e., 1, 5, 10, 20, 30, and 50%. The analyzes were performed with the aid of the R statistical software (R Core Team, 2020), using scripts linked to three packages (metan, ExpDes.pt, and agricolae), and Selegen, with 76 models (Resende, 2016).

Results and Discussion

The estimates of the genetic parameters and components of variance, as well as the genotypic mean, for the quality attributes of rice grains are presented in Table 2. Total chalky area, total whiteness, vitreous whiteness, VW/TW ratio, percentage of whole grains, and percentage of broken grains showed higher genetic variance in all generations, enabling the identification of superior genotypes for rice grain breeding programs.

Table 1. Segregating populations (families) and parents of rice (*Oryza sativa*) evaluated in the 2015–2018 crop seasons, in the municipality of Capão do Leão, in the state of Rio Grande do Sul, Brazil.

Family	Genitors (♀ / ♂)
1	'BRS Pampa' / 86014-TR891-7-2-1
2	86014-TR891-7-2-1 / 'BR/IRGA 409'
3	AB09025 / 'BRS Pampa'
4	AB08020 / 'BRS Pampa'
5	AB09025 / 'IRGA 417'
6	AB 10010 / 'BRS Pampa'
7	BRA 050151 / 'BRS Pampa'
8	BRA 050151 / 'Puitá INTA-CL'

For the variables white core and color defects, values with a low magnitude were obtained, which can be attributed to the greater degree of kinship between the progenies in each treatment.

For the characters total chalky area, total whiteness, vitreous whiteness, VW/TW ratio, percentage of whole grains and of broken grains, the estimates of broad-sense heritability, according to Hallauer et al. (1988), were considered medium/intermediate, presenting values between 30 and 70% in the three studied generations; the exception was percentage of whole and broken grains in the F4 generation, which showed a low heritability. High heritability estimates increase the potential for genetic selection (Rosado et al., 2012). Therefore, since the heritability of white core and color defects was of low magnitude, the selection of both characters can be difficult, as well as their fixation as generations advance.

In irrigated rice, there was environmental influence for most grain quality characters (Hakata et al., 2012; Li et al., 2014; Xu et al., 2015), as they are quantitative, consisting of many genes, with high CVe values being expected and, consequently, a low CVg/CVe ratio. This fact should be taken into account to avoid selection due not to genetics but to environmental effects, which are noninheritable. According to Silva et al. (2020), the CVg/CVe ratio can be an indicator of the degree of ease in the selection of characters in genotypes. When the CVg/CVe ratio is greater than or equal to one ($\geq$1.0), the available genetic variation is responsible for the estimated variation of the evaluated characters (Leite et al., 2016). The variables total whiteness and vitreous whiteness showed this behavior in the F3 and F5 generations (Table 2). In addition, total chalky area, VW/TW ratio, whole grains, and broken grains had satisfactory values in these two same generations, allowing an adequate selection with genetic gains for these characters. In general, the lowest coefficient of genetic variation for all traits was found in the F4 generation, with a high influence of the environment due to an atypical year climatically, mainly attributed to an excessive rainfall – more than 200 mm concentrated in late September and early October according to the agroclimatological station of Empresa Brasileira de Pesquisa Agropecuária (Embrapa) – that delayed sowing.

Resende & Duarte (2007) concluded that accuracy results refer to the joint evaluation of CVg and CVe,

showing the quality of the experiment. Considering this ratio, average to high accuracy values were obtained for most of the studied characters, ranging from 37.6 to 83.7% for whole grains in F4 and total whiteness in F3, respectively, characterizing experimental quality and safety in selection (Table 2). The exception was white core and color defects, with results between 21.2 and 41.2% in all generations.

Accuracy, therefore, represents the quality of the results and statistical procedures applied to assume genetic values, being a very important parameter in the evaluation of precision in the access to true genetic variation (Cavalcante et al., 2019). According to Pimentel et al. (2014), the accuracy parameter is related to selection precision, directly linked to the correlation between the predicted genetic values and true genetic values of individuals. Following the classification of Resende & Duarte (2007), the accuracy (Acg) results were considered: very high, Acg $\geq$ 0.90; high, $0.70 \leq$ Acg < 0.90; moderate, $0.50 \leq$ Acg < 0.70; and low, Acg <0.50. In F3 and F4, total whiteness and vitreous whiteness were classified as high; chalky area, VW/TW ratio, and whole and broken grains were considered moderate; and white core and color defects were low (Table 2). In the F5 generation, the results were moderate accuracy for total chalky area and all characters of whiteness, but low for white core, color defects, and whole and broken grains.

According to Carvalho et al. (2020), the methodology used in the present work is based on components of variance and genetic parameters (REML), and the obtained estimates are used to determine genetic value (BLUP), which will be applied in the classification of the best genotypes, without any impact on the environment.

In the present study, the agronomic ideotype was predefined according to Brazilian consumer standards, aiming for long-fine grains. Therefore, genetic gain through the selection of families was sought, aiming low values (close to zero) for total chalky area, white core, color defects, total whiteness, and broken grains, i.e., estimates of negative genetic gains are expected. However, for vitreous whiteness, VW/TW ratio, and whole grains, the best values should be high. The individual average components of BLUP in the eight segregating families from crosses of irrigated rice and in the three controls – 'BRS Pampa', 'BR/IRGA 409', and 'Puitá INTA-CL' – for generations F3, F4,

Table 2. Genetic parameters and components of variance of grain quality characters from eight families of irrigated rice (*Oryza sativa*), in the F3, F4 and F5 generations[1], evaluated in the 2015–2018 crop seasons, in the municipality of Capão do Leão, in the state of Rio Grande do Sul, Brazil.

Genetic parameter	Grain quality characters							
	TCA (%)	WC (%)	Color (%)	TW	VW	VW/TW	WHO (g)	BRO (g)
	F3 generation							
$\sigma^2 g$	11.414	0.015	0.001	45.963	19.643	0.000208	0.158	0.111
$\sigma^2 b$	0.877	0.002	0.000	0.064	0.135	0.000008	0.025	0.011
$\sigma^2 e$	14.739	0.070	0.009	19.547	13.977	0.00028	0.284	0.202
$\sigma^2 p$	27.030	0.087	0.011	65.573	33.755	0.000496	0.467	0.325
H^2	0.422	0.169	0.139	0.701	0.582	0.419	0.338	0.343
$c^2 b$	0.032	0.024	0.000	0.001	0.004	0.017	0.055	0.034
CVg	0.740	0.105	0.030	0.360	0.164	0.000222	0.017	0.226
CVe	0.955	0.502	0.188	0.153	0.117	0.000299	0.030	0.411
CVg/CVe	0.774	0.210	0.161	2.351	1.405	0.743	0.556	0.550
Acg	0.650	0.412	0.372	0.837	0.763	0.648	0.581	0.586
Mean	15.434	0.140	0.048	127.826	119.683	0.937	9.329	0.492
	F4 generation							
$\sigma^2 g$	3.077	0.000	0.000	2.253	1.040	0.000036	0.011	0.012
$\sigma^2 b$	0.230	0.000	0.000	0.110	0.019	0.000004	0.000	0.000
$\sigma^2 e$	5.319	0.005	0.001	4.395	2.108	0.000075	0.069	0.059
$\sigma^2 p$	8.626	0.005	0.001	6.758	3.166	0.000115	0.080	0.071
H^2	0.357	0.087	0.045	0.333	0.328	0.311	0.141	0.171
$c^2 b$	0.027	0.014	0.008	0.016	0.006	0.033	0.000	0.000
CVg	0.165	0.002	0.000	0.017	0.009	0.0000389	0.001	0.029
CVe	0.285	0.022	0.007	0.033	0.017	0.0000811	0.007	0.142
CVg/CVe	0.578	0.096	0.047	0.513	0.493	0.480	0.164	0.207
Acg	0.597	0.295	0.212	0.577	0.573	0.557	0.376	0.414
Mean	18.677	0.214	0.083	131.880	121.917	0.925	9.285	0.414
	F5 generation							
$\sigma^2 g$	3.236	0.000	0.001	8.378	4.542	0.000029	0.040	0.042
$\sigma^2 b$	0.177	0.000	0.000	0.333	0.157	0.000003	0.001	0.002
$\sigma^2 e$	4.913	0.003	0.007	6.064	2.984	0.000069	0.058	0.051
$\sigma^2 p$	8.326	0.003	0.008	14.775	7.683	0.000101	0.099	0.094
H^2	0.389	0.082	0.095	0.567	0.591	0.288	0.401	0.444
$c^2 b$	0.021	0.000	0.009	0.023	0.020	0.029	0.015	0.018
CVg	0.284	0.008	0.011	0.066	0.037	0.0000304	0.004	0.094
CVe	0.432	0.090	0.105	0.047	0.025	0.0000724	0.006	0.114
CVg/CVe	0.659	0.089	0.106	1.382	1.522	0.420	0.686	0.824
Acg	0.623	0.286	0.308	0.753	0.769	0.537	0.633	0.666
Mean	11.382	0.031	0.070	127.699	121.784	0.953	9.453	0.446

[1]F3, F4, and F5, obtained by self-fertilization of selected plants of the F2, F3, and F4 generations, respectively, from eight different crosses between two rice cultivars. TCA, total chalky area (%); WC, white core (%); Color, color defects (%); TW, grain total whiteness; VW, grain vitreous whiteness; VW/TW, ratio between vitreous whiteness and total whiteness; WHO, mass of whole grains in the sample (g); BRO, mass of broken grains in the sample (g); $\sigma^2 g$, genotypic variance; $\sigma^2 b$, block variance; $\sigma^2 e$, environmental variance; $\sigma^2 p$, phenotypic variance; H^2, broad-sense heritability; $c^2 b$, family effect coefficient; CVg, coefficient of genetic variation; CVe, coefficient of environmental variation; CVg/CVe, ratio between coefficient of genetic determination and coefficient of environmental variation; and Acg, experimental accuracy.

and F5 are shown in Tables 3, 4, and 5, respectively. The genotypic values of each family were obtained by adding each genotype effect to the overall average of the experiment. The genetic gain was equivalent to the value of the predicted genetic effect vectors for the selected genotypes. The general average, plus genetic gain, results in the new expected average of the improved population; therefore, the selection of the best genotypes becomes reliable and accurate, with less distortions attributed to noncontrollable factors resulting from the environment (Carvalho et al., 2020).

Total chalky area was higher in 75% of the F3 segregating populations, when compared with the commercial controls, with families 8, 5, 1, 2, 3, and 6 standing out (Table 3). Greater genetic gains can be obtained by selecting population 8, which would result in an increase of -2.18% for this character, followed by plants in the subsequent generation, with a total chalky area of 15.43%. In generation F4, 62.5% of the families showed higher values than the controls, and the greatest predicted genetic gains can be obtained by selecting family 3, from the crossing between AB09025 and 'BRS Pampa', generating a new estimated average of 18.68% total chalky area (Table 4). In F5, for the same character, 50% of the families had higher values than the controls, and, again, the greatest genetic gains can be obtained in family 3, with a new estimated average of 11.38% chalky area (Table 5).

In the present study, genetic gain, together with the new estimated average, is equal to or higher than the average values obtained by Streck et al. (2018) for total chalky area of the commercial cultivars launched by the irrigated rice breeding program of Embrapa Clima Temperado.

For the characters white core and color defects, Magalhães Júnior et al. (2020) found that several defects are the result of the contamination of the product by foreign matter, moldy and rotten grains, presence of stained and stung grains – mainly by stink bugs, and yellow color and streaks (red rice). For both characters, 75% of the families in the F3 generation were superior to the controls, especially family 5, in relation to white core, and family 7, with few color defects. In the F4 generation, the superior families were 5 and 6 for white core and 7 and 8 for color, together with population 4 for both characters. These same families stood out in the F5 generation, with estimates of new averages close to zero for the occurrence of these defects, considered serious by the rice industry.

The BLUP estimates for the characters vitreous whiteness, total whiteness, and VW/TW ratio in the F3 segregating generation in family 6 were superior to those of the controls for all white characters. In generation F4, families 1 and 4 were also superior to the controls for the same characters. It should be emphasized that, once again, family 6 showed favorable results, but this time for vitreous whiteness and for the VW/TW ratio. In the F5 generation, no family stood out for the three whiteness characters together, but families 3 and 6 showed higher values for total whiteness and the VW/TW ratio, and family 7, for vitreous whiteness, with a gain of 2.61 of the vitreous constants of the grains.

When considering each character of whiteness separately in all studied generations, there were greater gains by selection for total whiteness in family 3, vitreous whiteness in family 4, and the VW/TW ratio in families 1, 3, and 6.

Despite these interesting results, few known studies use this measurement methodology, which allows analyzing quality characters through sample readings with digital technologies considered new; however, its implementation in rice research programs has been gaining space in recent years, together with the interest to increase the grain quality standards in the rice production chain (Sordi et al., 2021). On this topic, some surveys are being carried out in Brazil by Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina (Marschalek et al., 2017, 2020) and Embrapa (Streck et al., 2018), being directly linked to the breeding program or academic research in partnership with graduate programs, as is the case of the present work.

The genetic gain estimates of the attributes percentage of whole grains and of broken grains showed that more than 62.5% of the families were superior to the controls in all segregating generations. Those variables are considered the main quality characters of irrigated rice grains and, therefore, are extremely sought by breeding programs, being of fundamental importance at the time of commercialization, representing a large part of the requirements of the industrial segment of the rice chain (Szareski et al., 2018).

Considering the obtained results, family 5 – originating from the crossing of the elite strain AB09025 with the IRGA 417 cultivar – stands out, being classified at the top of the rank in practically all three generations studied and for both grain yield characters.

Table 3. Estimates and classification of the eight families of the F3 generation and of the three control cultivars (T1, T2, and T3)[1], predicted genotypic values (g), genotypic values (μ + g), and predicted new mean (NM) by the best linear unbiased prediction for the grain quality characters of rice (*Oryza sativa*) evaluated in the 2015/2016 crop season, in the municipality of Capão do Leão, in the state of Rio Grande do Sul, Brazil.

F3[2]		TCA					WC					Color					WHO			
Order	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM
1	8	-2.81	12.62	0.00	15.43	5	-0.13	0.01	0.00	0.14	7	-0.04	0.01	0.00	0.05	5	0.34	9.67	0.34	9.67
2	5	-2.76	12.68	0.28	15.72	1	-0.10	0.04	0.01	0.15	4	-0.02	0.03	0.00	0.05	1	0.27	9.60	0.30	9.63
3	1	-1.87	13.56	0.62	16.05	8	-0.06	0.08	0.03	0.16	2	-0.02	0.03	0.01	0.06	3	0.23	9.56	0.28	9.61
4	2	-1.47	13.96	0.93	16.36	2	-0.04	0.10	0.04	0.18	1	-0.02	0.03	0.01	0.06	8	0.20	9.53	0.26	9.59
5	3	-0.86	14.58	1.27	16.71	7	-0.02	0.12	0.05	0.19	5	-0.01	0.04	0.01	0.06	6	0.16	9.49	0.24	9.57
6	6	-0.05	15.39	1.63	17.06	3	-0.02	0.12	0.06	0.20	8	-0.01	0.04	0.02	0.07	T2	0.00	9.33	0.20	9.53
7	T1	0.00	15.43	1.96	17.40	T3	0.00	0.14	0.07	0.21	T2	0.00	0.05	0.02	0.07	T1	0.00	9.33	0.17	9.50
8	T3	0.00	15.43	2.46	17.89	T2	0.00	0.14	0.09	0.23	T1	0.00	0.05	0.03	0.08	T3	0.00	9.33	0.15	9.48
9	T2	0.00	15.43	3.27	18.71	T1	0.00	0.14	0.12	0.26	T3	0.00	0.05	0.04	0.09	2	-0.02	9.31	0.13	9.46
10	7	2.82	18.26	4.91	20.34	4	0.17	0.31	0.18	0.32	3	0.05	0.10	0.06	0.11	7	-0.37	8.96	0.08	9.41
11	4	7.00	22.43	7.00	22.43	6	0.19	0.33	0.19	0.33	6	0.06	0.11	0.06	0.11	4	-0.80	8.52	0.00	9.33

F3		TW					VW					VW/TW					BRO			
Order	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM
1	3	-3.94	123.89	0.00	127.83	4	10.26	129.95	10.26	129.95	6	0.01	0.95	0.01	0.95	3	-0.30	0.19	0.00	0.49
2	2	-3.77	124.06	0.39	128.22	6	0.90	120.58	5.58	125.26	8	0.01	0.95	0.01	0.95	5	-0.23	0.26	0.03	0.52
3	8	-3.58	124.25	0.86	128.68	T2	0.00	119.68	3.72	123.40	5	0.01	0.95	0.01	0.95	1	-0.19	0.30	0.06	0.55
4	1	-3.13	124.70	1.41	129.24	T1	0.00	119.68	2.79	122.47	1	0.01	0.94	0.01	0.95	8	-0.17	0.32	0.09	0.58
5	5	-1.67	126.16	2.06	129.89	T3	0.00	119.68	2.23	121.92	2	0.01	0.94	0.01	0.94	6	-0.15	0.34	0.13	0.62
6	6	-0.49	127.34	2.68	130.51	5	-0.23	119.46	1.82	121.51	T2	0.00	0.94	0.01	0.94	T3	0.00	0.49	0.18	0.67
7	T2	0.00	127.83	3.32	131.14	7	-0.36	119.32	1.51	121.19	T3	0.00	0.94	0.01	0.94	T2	0.00	0.49	0.21	0.70
8	T1	0.00	127.83	4.14	131.97	8	-1.99	117.70	1.07	120.76	T1	0.00	0.94	0.01	0.94	T1	0.00	0.49	0.26	0.75
9	T3	0.00	127.83	5.53	133.35	1	-2.07	117.62	0.72	120.41	3	0.00	0.93	0.00	0.94	2	0.04	0.53	0.35	0.84
10	7	0.30	128.13	8.29	136.11	2	-2.67	117.02	0.39	120.07	7	-0.01	0.93	0.00	0.94	7	0.42	0.91	0.51	1.00
11	4	16.28	144.10	16.28	144.10	3	-3.85	115.83	0.00	119.68	4	-0.03	0.90	0.00	0.94	4	0.60	1.09	0.60	1.09

[1]T1, T2, and T3, cultivars BRS Pampa, BR/IRGA 409, and Puitá INTA-CL, respectively. [2]Obtained by self-fertilization of selected plants of the F2 generation from eight different crosses between two rice cultivars. TCA, total chalky area (%); WC, white core (%); Color, color defects (%); WHO, mass of whole grains in the sample (g); Gen, genotype; TW, grain total whiteness; VW, grain vitreous whiteness; VW/TW, ratio between vitreous whiteness and total whiteness of the grains; and BRO, mass of broken grains in the sample (g).

Table 4. Estimates and classification of the eight families of the F4 generation and of the three control cultivars (T1, T2, and T3), predicted genotypic values (g), genotypic values (μ + g), and predicted new mean (NM) by the best linear unbiased prediction for the grain quality characters of rice (*Oryza sativa*) evaluated in the 2016/2017 crop season, in the municipality of Capão do Leão, in the state of Rio Grande do Sul, Brazil.

F4	TCA					WC					Color					WHO				
Order	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM
1	3	-2.09	16.59	0.00	18.68	6	-0.02	0.20	0.00	0.21	8	-0.01	0.08	0.00	0.08	5	0.09	9.38	0.09	9.38
2	4	-1.34	17.33	0.21	18.89	4	-0.01	0.20	0.00	0.22	4	0.00	0.08	0.00	0.08	6	0.07	9.36	0.08	9.37
3	1	-1.34	17.33	0.38	19.06	5	-0.01	0.20	0.00	0.22	7	0.00	0.08	0.00	0.08	8	0.07	9.36	0.08	9.36
4	5	-0.73	17.95	0.60	19.27	2	-0.01	0.20	0.01	0.22	5	0.00	0.08	0.00	0.09	3	0.06	9.35	0.07	9.36
5	6	-0.43	18.25	0.79	19.46	1	-0.01	0.21	0.01	0.22	6	0.00	0.08	0.00	0.09	1	0.03	9.32	0.07	9.35
6	T2	0.00	18.68	0.99	19.67	T1	0.00	0.21	0.01	0.22	T2	0.00	0.08	0.00	0.09	T3	0.00	9.29	0.06	9.34
7	T3	0.00	18.68	1.19	19.86	T3	0.00	0.21	0.01	0.23	T3	0.00	0.08	0.00	0.09	T1	0.00	9.29	0.05	9.33
8	T1	0.00	18.68	1.48	20.16	T2	0.00	0.21	0.01	0.23	T1	0.00	0.08	0.00	0.09	T2	0.00	9.29	0.04	9.33
9	2	1.29	19.97	1.98	20.65	3	0.00	0.22	0.02	0.23	3	0.00	0.09	0.01	0.09	7	-0.01	9.28	0.04	9.32
10	8	2.15	20.83	2.32	21.00	8	0.01	0.22	0.03	0.24	1	0.01	0.09	0.01	0.09	4	-0.16	9.13	0.02	9.30
11	7	2.49	21.17	2.49	21.17	7	0.05	0.26	0.05	0.26	2	0.01	0.09	0.01	0.09	2	-0.16	9.12	0.00	9.29

F4	TW					VW					VW/TW					BRO				
Order	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM
1	3	-2.47	129.41	0.00	131.88	2	1.39	123.31	1.39	123.31	3	0.01	0.93	0.01	0.93	8	-0.08	0.34	0.00	0.41
2	5	-0.81	131.07	0.25	132.13	7	0.94	122.86	1.17	123.09	1	0.01	0.93	0.01	0.93	5	-0.08	0.34	0.01	0.42
3	1	-0.53	131.35	0.36	132.24	4	0.47	122.39	0.94	122.85	4	0.00	0.93	0.01	0.93	3	-0.07	0.35	0.02	0.43
4	8	-0.26	131.62	0.48	132.36	1	0.25	122.17	0.77	122.68	5	0.00	0.93	0.00	0.93	6	-0.06	0.36	0.03	0.44
5	4	-0.14	131.74	0.58	132.46	6	0.21	122.13	0.66	122.57	6	0.00	0.93	0.00	0.93	7	-0.03	0.38	0.04	0.45
6	T1	0.00	131.88	0.70	132.58	T3	0.00	121.92	0.55	122.46	T3	0.00	0.93	0.00	0.93	1	-0.03	0.38	0.05	0.47
7	T3	0.00	131.88	0.84	132.72	T1	0.00	121.92	0.47	122.39	T1	0.00	0.93	0.00	0.93	T2	0.00	0.41	0.07	0.48
8	T2	0.00	131.88	1.05	132.93	T2	0.00	121.92	0.41	122.33	T2	0.00	0.93	0.00	0.93	T1	0.00	0.41	0.09	0.50
9	6	0.14	132.02	1.40	133.28	5	-0.66	121.26	0.29	122.21	2	0.00	0.92	0.00	0.93	T3	0.00	0.41	0.11	0.53
10	2	1.92	133.80	2.04	133.92	8	-1.09	120.83	0.15	122.07	8	-0.01	0.92	0.00	0.93	2	0.17	0.58	0.17	0.59
11	7	2.16	134.04	2.16	134.04	3	-1.53	120.39	0.00	121.92	7	-0.01	0.92	0.00	0.93	4	0.18	0.59	0.18	0.59

[1]T1, T2, and T3, cultivars BRS Pampa, BR/IRGA 409, and Puitá INTA-CL, respectively. [2]Obtained by self-fertilization of selected plants of the F3 generation from eight different crosses between two rice cultivars. TCA, total chalky area (%); WC, white core (%); Color, color defects (%); WHO, mass of whole grains in the sample (g); TW, grain total whiteness; VW, grain vitreous whiteness; VW/TW, ratio between vitreous whiteness and total whiteness of the grains; and BRO, mass of broken grains in the sample (g).

Table 5. Estimates and classification of the eight families of the F5 generation and of the three control cultivars (T1, T2, and T3)[1], predicted genotypic values (g), genotypic values (μ + g), and predicted new mean (NM) by the best linear unbiased prediction for the grain quality characters of rice (*Oryza sativa*) evaluated in the 2017/2018 crop year, in the municipality of Capão do Leão, in the state of Rio Grande do Sul, Brazil.

F5[2]	TCA					WC					Color					WHO				
Order	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM
1	3	-2.44	8.94	0.00	11.38	5	-0.02	0.01	0.00	0.03	7	-0.03	0.04	0.00	0.07	1	0.21	9.66	0.21	9.66
2	6	-1.94	9.44	0.24	11.63	6	-0.02	0.01	0.00	0.03	4	-0.02	0.05	0.00	0.07	5	0.19	9.64	0.20	9.65
3	2	-1.03	10.35	0.49	11.87	3	-0.01	0.02	0.00	0.04	8	-0.02	0.05	0.01	0.08	3	0.08	9.53	0.16	9.61
4	5	-0.47	10.91	0.68	12.06	2	0.00	0.03	0.01	0.04	5	-0.02	0.06	0.01	0.08	7	0.07	9.52	0.14	9.59
5	T3	0.00	11.38	0.84	12.22	T1	0.00	0.03	0.01	0.04	1	0.00	0.07	0.01	0.08	8	0.02	9.48	0.11	9.57
6	T2	0.00	11.38	0.98	12.36	T2	0.00	0.03	0.01	0.04	T2	0.00	0.07	0.01	0.08	2	0.02	9.47	0.10	9.55
7	T1	0.00	11.38	1.18	12.56	T3	0.00	0.03	0.01	0.04	T3	0.00	0.07	0.02	0.09	T3	0.00	9.45	0.08	9.54
8	1	0.60	11.98	1.47	12.85	4	0.00	0.04	0.01	0.04	T1	0.00	0.07	0.02	0.09	T2	0.00	9.45	0.07	9.53
9	4	1.09	12.48	1.76	13.14	1	0.00	0.04	0.01	0.05	6	0.01	0.08	0.03	0.10	T1	0.00	9.45	0.07	9.52
10	8	1.41	12.79	2.10	13.48	7	0.02	0.05	0.02	0.05	2	0.04	0.11	0.04	0.11	6	-0.22	9.23	0.04	9.49
11	7	2.79	14.17	2.79	14.17	8	0.02	0.05	0.02	0.05	3	0.04	0.11	0.04	0.11	4	-0.37	9.09	0.00	9.45

F5	TW					VW					VW/TW					BRO				
Order	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM	Gen	g	u+g	Gain	NM
1	6	-4.26	123.44	0.00	127.70	7	2.61	124.39	2.61	124.39	3	0.01	0.96	0.01	0.96	1	-0.21	0.23	0.00	0.45
2	3	-3.43	124.27	0.43	128.12	8	1.73	123.51	2.17	123.95	6	0.01	0.96	0.01	0.96	5	-0.15	0.30	0.02	0.47
3	2	-1.87	125.83	0.86	128.55	5	1.05	122.84	1.79	123.58	2	0.00	0.96	0.01	0.96	3	-0.12	0.33	0.04	0.49
4	T2	0.00	127.70	1.20	128.89	1	0.97	122.75	1.59	123.37	5	0.00	0.96	0.00	0.96	7	-0.06	0.39	0.06	0.51
5	T3	0.00	127.70	1.37	129.07	4	0.79	122.57	1.43	123.21	1	0.00	0.95	0.00	0.96	2	-0.05	0.39	0.08	0.52
6	T1	0.00	127.70	1.59	129.29	T3	0.00	121.78	1.19	122.97	T1	0.00	0.95	0.00	0.96	8	-0.03	0.42	0.10	0.54
7	5	0.80	128.50	1.91	129.61	T1	0.00	121.78	1.02	122.80	T2	0.00	0.95	0.00	0.96	T2	0.00	0.45	0.12	0.57
8	1	1.06	128.76	2.19	129.89	T2	0.00	121.78	0.89	122.68	T3	0.00	0.95	0.00	0.96	T1	0.00	0.45	0.15	0.60
9	4	1.36	129.06	2.57	130.27	2	-1.36	120.43	0.64	122.43	4	0.00	0.95	0.00	0.95	T3	0.00	0.45	0.21	0.65
10	8	2.46	130.15	3.17	130.87	3	-2.36	119.42	0.34	122.13	8	0.00	0.95	0.00	0.95	6	0.23	0.68	0.31	0.75
11	7	3.89	131.59	3.89	131.59	6	-3.42	118.36	0.00	121.78	7	-0.01	0.94	0.00	0.95	4	0.38	0.83	0.38	0.83

[1]T1, T2, and T3, cultivars BRS Pampa, BR/IRGA 409, and Puitá INTA-CL, respectively. [2]Obtained by self-fertilization of selected plants of the F4 generation from eight different crosses between two rice cultivars. TCA, total chalky area (%); WC, white core (%); Color, color defects (%); WHO, mass of whole grains in the sample (g); TW, grain total whiteness; VW, grain vitreous whiteness; VW/TW, ratio between vitreous whiteness and total whiteness of the grains; and BRO, mass of broken grains in the sample (g).

Specifically for whole grains, as a percentage unit, the following estimates of very satisfactory genetic gains were obtained: greater than 3.0% in F3, approximately 1.0% in F4, and greater than 2.0% in F5. These estimates show a significant increase, providing interesting genetic gains with selection carried out in early generations, mainly the increment of mill yields (whole and broken grains), essential for the industry and particularly for growers who suffer from price discounts when a minimum of 58% whole grains is not reached in a sample of paddy rice, as required by Brazilian legislation (Magalhães Júnior et al., 2020).

A better genetic gain response for each sought character may be obtained by choosing the most appropriate selection pressure or selection index. Varying responses to selection were observed under the six selection pressures evaluated (Table 6), ranging from 1 to 50% (highest and lowest values, respectively) in the F3, F4, and F5 segregating generations for all eight rice grain quality characters assessed.

With the increase in selection pressure, the estimated genetic gain of selection became greater for all rice grain quality characters in all studied generations. Silva et al. (2017) reported that, in a selection of favorable characters, the greater the selection pressure, the greater the selection differential and, consequently, the greater the genetic progress. However, the ideal selection pressure depends directly on the heritability of each

Table 6. Response to selection of eight families in the F3, F4, and F5 generations[1] for the grain quality characters of rice (*Oryza sativa*), at different levels of selection pressure (%), evaluated in the 2015–2018 crop seasons, in the municipality of Capão do Leão, in the state of Rio Grande do Sul, Brazil.

Quality characters	H^2	PV	PSD	Selection pressure (%)					
				1	5	10	20	30	50
Response in F3 seletion									
TCA (%)	0.422	27.030	5.199	5.851	4.529	3.853	3.074	2.547	1.756
WC (%)	0.169	0.087	0.295	0.133	0.103	0.088	0.070	0.058	0.040
Color defects (%)	0.139	0.011	0.103	0.038	0.029	0.025	0.020	0.017	0.011
TW	0.701	65.573	8.098	15.127	11.710	9.961	7.946	6.584	4.541
VW	0.582	33.755	5.810	9.010	6.975	5.934	4.733	3.922	2.705
VW/TW	0.419	0.000	0.022	0.025	0.019	0.016	0.013	0.011	0.007
WHO (g)	0.338	0.467	0.684	0.615	0.476	0.405	0.323	0.268	0.185
BRO (g)	0.343	0.325	0.570	0.521	0.403	0.343	0.274	0.227	0.156
Response in F4 seletion									
TCA (%)	0.357	8.626	2.937	2.792	2.161	1.839	1.467	1.215	0.838
WC (%)	0.087	0.005	0.073	0.017	0.013	0.011	0.009	0.007	0.005
TW	0.333	6.758	2.600	2.310	1.788	1.521	1.213	1.005	0.693
VW	0.328	3.166	1.779	1.557	1.205	1.025	0.818	0.678	0.467
VW/TW	0.311	0.000	0.011	0.009	0.007	0.006	0.005	0.004	0.003
WHO (g)	0.141	0.080	0.284	0.107	0.083	0.070	0.056	0.046	0.032
BRO (g)	0.171	0.071	0.267	0.122	0.094	0.080	0.064	0.053	0.037
Color defects (%)	0.045	0.001	0.025	0.003	0.002	0.002	0.002	0.001	0.001
Response in F5 seletion									
TCA (%)	0.389	8.326	2.886	2.989	2.314	1.968	1.570	1.301	0.897
WC (%)	0.082	0.003	0.056	0.012	0.009	0.008	0.006	0.005	0.004
TW	0.567	14.775	3.844	5.809	4.497	3.825	3.052	2.528	1.744
VW	0.591	7.683	2.772	4.367	3.381	2.876	2.294	1.901	1.311
VW/TW	0.288	0.000	0.010	0.008	0.006	0.005	0.004	0.003	0.002
WHO (g)	0.401	0.099	0.315	0.336	0.260	0.221	0.177	0.146	0.101
BRO (g)	0.444	0.094	0.307	0.363	0.281	0.239	0.191	0.158	0.109
Color defects (%)	0.095	0.008	0.091	0.023	0.018	0.015	0.012	0.010	0.007

[1]F3, F4, and F5, obtained by self-fertilization of selected plants of the F2, F3, and F4 generations, respectively, from eight different crosses between two rice cultivars. H^2, broad-sense heritability; PV, phenotypic variance; PSD, phenotypic standard deviation; TCA, total chalky area (%); WC, white core (%); TW, grain total whiteness; VW, grain vitreous whiteness; VW/TW, ratio between vitreous whiteness and total whiteness of the grains; WHO, mass of whole grains in the sample (g); and BRO, mass of broken grains in the sample (g).

character under consideration (Silva & Pereira, 2011), taking into account the broad-sense heritability of the characters that presented mostly average/intermediate values. The use of high pressures in selection reduces genetic variability in the subsequent generation. Besides raising the levels of inbreeding, which may result in the character not being fixed by self-fertilization, the response to selection over generations is, consequently, slower, minimizing phenotypic gains.

The obtained results indicate that the selection of families using intermediate pressure, such as 10%, provides a high genetic gain without significant loss of genetic variability, being a very promising tool for studies of quality attributes of irrigated rice.

Conclusions

1. The estimates obtained for quality characters of irrigated rice (*Oryza sativa*) grains show genetic gains, mainly for total chalky area, vitreous whiteness, total whiteness, ratio between vitreous whiteness and total whiteness, as well as percentage of whole grains and broken grains, with selection carried out in early generations, and the eight evaluated families present satisfactory results that are superior to those of the control cultivars BRS Pampa, BR/IRGA 409, and Puitá INTA-CL.

2. For most characters, the estimates of broad-sense heritability are considered intermediate, together with the other parameters, showing the possibility of genetic selection for grain quality attributes in rice.

3. The response to selection with a pressure of 10% is the most promising for grain quality attributes of irrigated rice.

References

ACOMPANHAMENTO DA SAFRA BRASILEIRA [DE] GRÃOS: safra 2019/20: sexto levantamento, v.7, n.6, mar. 2020. Available at: <http://www.conab.gov.br>. Accessed on: Mar. 20 2020.

ANACLETO, R.; CUEVAS, R.P.; JIMENEZ, R.; LLORENTE, C.; NISSILA, E.; HENRY, R.; SREENIVASULU, N. Prospects of breeding high-quality rice using post-genomic tools. **Theoretical and Applied Genetics**, v.128, p.1449-1466, 2015. DOI: https://doi.org/10.1007/s00122-015-2537-6.

CARVALHO, I.R.; SILVA, J.A.G. da; FERREIRA, L.L.; SZARESKI, V.J.; DEMARI, G.H.; LAUTENCHLEGER, F.; MENEGHELLO, G.E.; MATTER, E.M.; MAGANO, D.A.; SOUZA, V.Q. de. REML/BLUP applied to characterize important agronomic traits in segregating generations of bean (*Phaseolus vulgaris* L.). **Australian Journal of Crop Science**, v.14, p.391-399, 2020. DOI: https://doi.org/10.21475/ajcs.20.14.03.p1520.

CAVALCANTE, N.R.; VIANA, A.P.; ALMEIDA FILHO, J.E.; PEREIRA, M.G.; AMBRÓSIO, M.; SANTOS, E.A.; RIBEIRO, R.M.; RODRIGUES, D.L.; SOUSA, C.M.B. Novel selection strategy for half-sib families of sour passion fruit *Passiflora edulis* (Passifloraceae) under recurrent selection. **Genetics and Molecular Research**, v.18, gmr18305, 2019. DOI: https://doi.org/10.4238/gmr18305.

CUSTODIO, M.C.; CUEVAS, R.P.; YNION, J.; LABORTE, A.G.; VELASCO, M.L.; DEMONT, M. Rice quality: how is it defined by consumers, industry, food scientists, and geneticists? **Trends in Food Science & Technology**, v.92, p.122-137, 2019. DOI: https://doi.org/10.1016/j.tifs.2019.07.039.

FALCONER, D.S. **Introdução à genética quantitativa**. Viçosa: UFV, 1981. 279p.

FUKAGAWA, N.K.; ZISKA, L.H. Rice: importance for global nutrition. **Journal of Nutritional Science and Vitaminology**, v.65, p.S2-S3, 2019. DOI: https://doi.org/10.3177/jnsv.65.S2.

HAKATA, M.; KURODA, M.; MIYASHITA, T.; YAMAGUCHI, T.; KOJIMA, M.; SAKAKIBARA, H.; MITSUI, T.; YAMAKAWA, H. Suppression of α-amylase genes improves quality of rice grain ripened under high temperature. **Plant Biotechnology Journal**, p.1110-1117, 2012. DOI: https://doi.org/10.1111/j.1467-7652.2012.00741.x.

HALLAUER, A.R.; CARENA, M.J.; MIRANDA FILHO, J.B. **Quantitative genetics in maize breeding**. 2nd ed. Ames: Iowa State University, 1988. 650p.

LEITE, W. de S.; PAVAN, B.E.; MATOS FILHO, C.H.A.; ALCANTARA NETO, F. de; OLIVEIRA, C.B. de; FEITOSA, F.S. Estimativas de parâmetros genéticos, correlaçõese índices de seleção para seis caracteres agronômicosem linhagens F8 de soja. **Comunicata Scientiae**, v.7, p.302-310, 2016. DOI: https://doi.org/10.14295/cs.v7i3.1176.

LI, Y.; FAN, C.; XING, Y.; YUN, P.; LUO, L.; YAN, B.; PENG, B.; XIE, W.; WANG, G.; LI, X.; XIAO, J.; XU, C.; HE, Y. *Chalk5* encodes a vacuolar H$^+$-translocating pyrophosphatase influencing grain chalkiness in rice. **Nature Genetics**, v.46, p.398-404, 2014. DOI: https://doi.org/10.1038/ng.2923.

MAGALHÃES JÚNIOR, A.M. de; STRECK, E.A.; AGUIAR, G.A.; FACCHINELLO, P.H.K. Industrial quality. In: OLIVEIRA, A.C. de; PEGORARO, C.; VIANA, V.E. (Ed.). **The future of rice demand**: quality beyond productivity. Switzerland: Springer, 2020. p.47-67.

MARSCHALEK, R.; SILVA, M.C.; SANTOS, S.B. dos; MANKE, J.R.; BIEGING, C.; PORTO, G.; WICKERT, E.; ANDRADE, A. de. Image – Rice Grain Scanner: a three-dimensional fully automated assessment of grain size and quality traits. **Crop Breeding and Applied Biotechnology**, v.17, p.89-97, 2017. DOI: https://doi.org/10.1590/1984-70332017v17n1s15.

MARSCHALEK, R.; WICKERT, E.; SCHEUERMANN, K.K.; TERRES, L.R.; NOLDIN, J.A.; HICKEL, E.R.; VALE, M.L.C. do; ANDRADE, A. de. SCS124 Sardo: Brazilian rice cultivar with excellent milling quality. **Crop Breeding and Applied**

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Biotechnology, v.20, e28212017, 2020. DOI: https://doi.org/10.159 0/198470332020v20n1c7.

PETERNELLI, L.A., RESENDE, M.D.V. de. Experimental designs for next generation phenotyping. In: FRITSCHE-NETO, R.; BORÉM, A. (Ed.). **Phenomics**: how next-generation phenotyping is revolutionizing plant breeding. Cham: Springer, 2015. p.15-32. DOI: https://doi.org/10.1007/978-3-319-13677-6_2.

PIMENTEL, A.J.B.; GUIMARÃES, J.F.R.; SOUZA, M.A. de; RESENDE, M.D.V. de; MOURA, L.M.; ROCHA, J.R. do A.S. de C.; RIBEIRO, G. Estimação de parâmetros genéticos e predição de valor genético aditivo de trigo utilizando modelos misto. **Pesquisa Agropecuária Brasileira**, v.49, p.882-890, 2014. DOI: https://doi.org/10.1590/S0100-204X2014001100007.

R CORE TEAM. **R**: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing, 2020.

RESENDE, M.D.V. de. **Genética biométrica e estatística no melhoramento de plantas perenes**. Brasília: Embrapa Informação Tecnológica; Colombo: Embrapa Floresta, 2002. 975p.

RESENDE, M.D.V. de. Software Selegen-REML/BLUP: a useful tool for plant breeding. **Crop Breeding and Applied Biotechnology**, v.16, p.330-339, 2016. DOI: https://doi.org/10.1590/1984-70332016v16n4a49.

RESENDE, M.D.V. de; DUARTE, J.B. Precisão e controle de qualidade em experimentos de avaliação de cultivares. **Pesquisa Agropecuária Tropical**, v.37, p.182-194, 2007.

REUNIÃO TÉCNICA DA CULTURA DO ARROZ IRRIGADO, 31., 2016, Bento Gonçalves. **Arroz irrigado**: recomendações técnicas da pesquisa para o Sul do Brasil. Pelotas: SOSBAI, 2016. 200p.

ROCHA, G.S. da; CARNEIRO, J.E. de S.; REZENDE JÚNIOR, L. da S.; SILVA, V.M.P. e; MENEZES JÚNIOR, J.Â.N. de; CARNEIRO, P.C.S.; CECON, P.R. Effect of environments on the estimated genetic potential of segregating common bean populations. **Crop Breeding and Applied Biotechnology**, v.13, p.241-248, 2013. DOI: https://doi.org/10.1590/S1984-70332013000400004.

ROSA, T.D.A.; HELGUEIRA, D.B.; BASTIANI, M.O.; CARVALHO, I.R.; ROSA, M.M.; BENETTI, C.; ALMEIDA, A. da S.; AVILA, L.A. de; SZARESKI, V.J.; CONTE, G.G.; VILLELA, F.A. Effect of seeds dressingon the initial establishment of irrigated rice in different temperatures and sowing periods. **Revista Científica Rural**, v.1, p.94, 2021. DOI: https://doi.org/10.30945/rcr-v23i1.3242.

ROSADO, A.M.; ROSADO, T.B.; ALVES, A.A.; LAVIOLA, B.G.; BHERING, L.L. Seleção simultânea de clones de eucalipto de acordo com produtividade, estabilidade e adaptabilidade. **Pesquisa Agropecuária Brasileira**, v.47, p.964-971, 2012. DOI: https://doi.org/10.1590/S0100-204X2012000700013.

SANTOS, H.G. dos; JACOMINE, P.K.T.; ANJOS, L.H.C. dos; OLIVEIRA, V.Á. de; LUMBRERAS, J.F.; COELHO, M.R.; ALMEIDA, J.A. de; ARAÚJO FILHO, J.C. de; OLIVEIRA, J.B. de; CUNHA, T.J.F. **Sistema brasileiro de classificação de solos**. 5.ed. rev. e ampl. Brasília: Embrapa, 2018. 356p.

SILVA, B.E.D.; RIBEIRO, J.C.; SANTOS, W.B.R. dos; CESÁRIO, A.S.; OLIVEIRA, E.M.B.; VALENTE, T.N.P.; CAMARGOS, A. de S.; SOUZA, C.M. de. Comparações de métodos de seleção em populações simuladas de frangos caipiras. **Colloquium Agrariae**, v.13, p.129-134, 2017. DOI: https://doi.org/10.5747/ca.2017.v13. nesp2.00021.

SILVA, G.O. da; PEREIRA, A. da S. Seleção em gerações iniciais para caracteres agronômicos em batata. **Horticultura Brasileira**, v.29, p.449-455, 2011. DOI: https://doi.org/10.1590/S0102-05362011000400001.

SILVA, I.G. da; CASTOLDI, R.; CHARLO, H.C. de O.; MIRANDA, M. de S.; NUNES, T.D.C.; COSTA, L.L.; LEMES, E.M. Prediction of genetic gain in sweet corn using selection indexes. **Journal of Crop Science and Biotechnology**, v.23, p.191-196, 2020. DOI: https://doi.org/10.1007/s12892-019-0334-0.

SORDI, E.; NOVAKOWISKI, J.H.; REBESQUINI, R.; BENEDETTI, T.; CARVALHO, I.R.; LAUTENCHLEGER, F.; BORTOLUZZI, E.C. Agronomic biofortification of rice and wheat with zinc: a metanalytical study. **Research, Society and Development**, v.10, e39210615133, 2021.

STRECK, E.A.; MAGALHÃES JÚNIOR, A.M. de; AGUIAR, G.A.; FACCHINELLO, P.H.K.; PERIN, L.; FAGUNDES, P.R.R.; OLIVEIRA, A.C. de. Genetic progress of grain quality of flooded-irrigated rice cultivars in the state of Rio Grande do Sul, Brazil. **Pesquisa Agropecuária Brasileira**, v.53, p.453-463, 2018. DOI: https://doi.org/10.1590/s0100-204x2018000400007.

SZARESKI, V.J.; CARVALHO, I.R.; CORAZZA, T.C.; DELLAGOSTIN, S.M.; PELEGRIN, A.J. de; BARBOSA, M.H.; SANTOS, O.P. dos; MURARO, D.S.; SOUZA, V.Q. de; PEDÓ, T.; AUMONDE, T.Z.; PEGORARO, C. *Oriza* wild species: an alternative for rice breeding under abiotic stress conditions. **American Journal of Plant Sciences**, v.9, p.1093-1104, 2018.

XU, Q.; CHEN, W.; XU, Z. Relationship between grain yield and quality in rice germplasms grown across different growing areas. **Breeding Science**, v.65, p.226-232, 2015. DOI: https://doi.org/10.1270/jsbbs.65.226.