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RESEARCH ARTICLE

Genetic trends and multivariate interrelationships for grain quality of irrigated rice genotypes

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ABSTRACT

For genetic improvement programs, researches with multivariate approaches in rice are fundamental, to define genetic trends, clusters and correlations of agronomic characters that together help selection procedures. This work aimed to reveal the agronomic performance, trends and genetic interrelationships of grain quality based on multivariate models applied to elite lines of irrigated rice. The experiment took place in the 2017/2018 harvest, held at Estação Experimental Terras Baixas (ETB), of Embrapa Clima Temperado. The study used randomized blocks design, with three replications. There were fifteen F6 lines and four control cultivars. Evaluation of intrinsic physical quality attributes with the aid of S21 grain statistical analyzer, as well as grain yield and mill yield (whole and broken grains). Performance of analysis of variance, genetic parameters and Scott Knott cluster test, linear correlation, canonical correlations, cluster analysis via generalized Mahalanobis distance, using the Toucher method, in addition to BIPLOT principal component analysis. The results showed that PH18502 and PH18701 strains presented better agronomic performance for the studied characters, by univariate analysis. The linear and canonical correlations presented demonstrate potential in the direction of selection of multiple characters and point to the possibility of indirect selection among the relevant agronomic characters for the production chain of irrigated rice.

Keywords: *Oryza sativa* L., elite lineages, Ideotype, early selection, main components, clustering methods, genetic distance estimating algorithms.

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INTRODUCTION

The rice quality grain is fundamental for its commercialization, since the whole and without defects have superior market value, considered by the producers as a critical factor in the production, harvest and post-harvest. Consumers have increased their demand for quality. Studies connecting price and product quality define that middle to upper class consumers show greater purchase interest for better quality rice (Cuevas, Pede, McKinley, Velarde, & Demont, 2016). It is challenging to produce rice with high yield and quality in its grains, which is the result prioritized in programs and improvement strategies in the most varied agricultural regions of the world (Lin et al., 2017). When the agronomic ideotype is obtained in the elite lines of the breeding program, they are directed to the selection, protection and registration of the new cultivar.

Studies indicate the possibility of early selections in segregating generations, showing quality traits, although this is a character controlled by many genes, has low heritability and high environmental effect, becoming effective strategies of classical genetic improvement and biotechnological tools can help the selection of transgressive strains. To help the breeder to carry out an effective selection over the segregating generations, it is necessary to understand the univariate and multivariate tendency of the characters of interest. In addition to using sophisticated methodologies capable of gathering the genetic and environmental effects, as well as estimating and predicting the ranking of the best genotypes (Carvalho et al., 2018; Szareski et al., 2019).

Among the viable options for this purpose are the univariate biometric approaches that separately direct the trends of the analyzed variables. Multivariate inferences are optimized and compile as much information as possible. In this way, they allow multiple combinations of information within and between experimental units (Moreira et al., 2009), interpret and simultaneously evaluate the characters, enabling multiple trends and classifications (Cruz, 2006). Among the approaches are the main components, clustering methods and genetic distance estimating algorithms.

Principal component analysis (PCA) allows compiling phenotypic matrices that will be standardized and rotated to obtain eigenvalues and eigenvectors that will manifest trends in a dimensional Cartesian plane (Morrison, 1978; Ferreira, 2011). The canonical correlations reveal the interrelationships of the variables of interest in two groups, in which the determination of the associations between the groups can be an indication for the indirect selection together with the information provided by the genetic parameters (Cruz et al., 2012; Carvalho et al., 2016). The estimation of genetic distances between genotypes is an indication of genetic variability (Hosan, Sultana, Iftekharudduala, Ahmed, & Mia, 2010), being promising to prove whether there was an increase in variability arising from the genetic recombination of contrasting parents (Streck et al., 2018). In this way, all these methods provide important and accurate information that can be vital for the action of breeders in the selection of ideotypes in genetic improvement programs (Carvalho et al., 2015).

Souza et al. (2009), Benitez, Rodrigues, Arge, Ribeiro and Braga (2011) and Panda, Sahu, Behera and Lenka (2020), who defined the genetic trends, clusters and correlations that together helped the selection procedures, presented researches with multivariate approaches in rice. There is a lack of accurate information for multivariate selection combined with genetic parameters aimed at the quality of irrigated rice. In this context, this work aimed to reveal the agronomic performance, trends and genetic interrelationships of grain quality based on multivariate models applied to irrigated rice genotypes.

MATERIAL AND METHODS

The experiment took place in the 2017/2018 harvest, carried out at the Estação Experimental Terras Baixas (ETB), of Embrapa Clima Temperado, in the municipality of Capão do Leão, in the state of Rio Grande do Sul, specifically located at the geographic coordinates, 31°48'. 49” S latitude and 52°28'20” W longitude, located in a traditional rice production area in the southern region of Brazil.

The experimental for this study used randomized blocks design, with three replications. Plots of 5 m in length formed the experimental units, with rows spaced at 0.17 m. The useful area of the plot consisted of the central four meters of the two inner rows, in order to exclude any border effect. The sowing density used was 100 kg ha^{-1}, using a mechanical plot seeder. Soil preparation for sowing took place according to the conventional system, following the manual of technical recommendations, as well as other crop management (Sosbai, 2016). The base fertilization took place with the sowing, with application corresponding to 300 kg ha^{-1} of NPK (formula 5-20-20). The topdressing nitrogen fertilization was 90 Kg ha^{-1} in the form of urea, with 50% of the dose applied at the V4 stage and the remainder at the R0 stage (panicle initiation). The irrigation system adopted was permanent flooding until stage R9 (end of genotype maturation). Controls of pests, weeds and diseases also carried out according to the technical recommendations for irrigated rice.

Evaluation of nineteen genotypes (Table 1). 15 were F6 lines specifically selected from the F3 generation for physical grain quality attributes of the Irrigated Rice Genetic Improvement Program – Melhor Arroz, from Embrapa, and four cultivars used as controls (BRS Pampa, BRS Pampeira, BR IRGA 409 and IRGA 417), all known for the high quality of grains, through Brazilian consumption patterns (Sociedade Sul-Brasileira de Arroz Irrigado [Sosbai], 2016).

Table 1. List of rice genotypes irrigated used and their parents.

Treatments	Genotypes	Genealogy
1	PH18101	BRS Pampa / 86014-TR891-7-2-1
2	BR IRGA 409	Cultivar control
3	PH18102	BRS Pampa / 86014-TR891-7-2-1
4	PH18103	BRS Pampa / 86014-TR891-7-2-1
5	PH18201	86014-TR891-7-2-1 / BR IRGA 409
6	PH18202	86014-TR891-7-2-1 / BR IRGA 409
7	BRS PAMPA	Cultivar control
8	PH18301	AB09025 / BRS Pampa
9	PH18302	AB09025 / BRS Pampa
10	PH18401	AB08020 / BRS Pampa
11	PH18402	AB08020 / BRS Pampa
12	PH18501	AB09025 / IRGA 417
13	IRGA 417	Cultivar control
14	PH18502	AB09025 / IRGA 417
15	PH18601	AB 10010 / BRS Pampa
16	PH18602	AB 10010 / BRS Pampa
17	PH18701	BRA 050151 / BRS Pampa
18	BRS PAMPEIRA	Cultivar control
19	PH18801	BRA 050151 / Puitá INTA CL

All plots were harvested manually and individually (separated by plot), and then placed in a grain dryer to reduce moisture to 13%. After drying, the mechanical threshing was carried out, followed by the processes of peeling and polishing of the grains of each plot, using the mini Suzuki rice proofing engine (Model MT2003). From these samples of the polished grains, the intrinsic physical quality attributes of the grains were evaluated with the aid of the S21 grain statistical analyzer (TakeshI, 2019), based on the analysis of digital images of each sample.

The following characters were determined: CA - total chalky area (%); WB - percentage of grains with white belly (%); DC - total defects of coloring (%); CL - caryopsis length (mm); CW - caryopsis width (mm); CLW - caryopsis length x width ratio (mm); WG - whole grain yield (%) and BG - broken grain yield (%); GY - grain yield (g); NG - number of grains per 60g sample of polished grains; CH - percentage of total chalky grains (%); YEL - percentage of yellow grains (%); ARM - percentage of arid and moldy grains (%); STA - percentage of stained grains (%); BRO - percentage of broken grains (%); WHT - total whiteness constant; and WHV - grain whiteness constant. The whiteness scale of S21 ranges from 0 to 200, where 200 is the maximum whiteness value. For vitreous whiteness, the mass considered chalky is discarded.

Data were subjected to analysis of variance, genetic parameters and subsequent Scott Knott cluster test at 5% probability ($p < 0.05$), linear correlation, canonical correlations. Cluster analyzes were conducted adopting the generalized distance of Mahalanobis as a dissimilarity measure and using the Toucher optimization clustering method. BIPLOT principal component analysis was also performed, using SAS statistical software (Khattree & Naik, 2018) and Rbio statistical software (Bhering, 2017).

RESULTS AND DISCUSSION

The analysis of variance (Table 2) revealed the significance of 5% of probability by the F test. It proved differences between the F6 genotypes and the irrigated rice controls for the characters of total chalky area (CA), percentage of grains with white belly (WB), total whiteness constant (WHT), grain vitreous whiteness constant (WHV), percentage of whole grains (WG), percentage of broken grains (BG), grain yield (GY), caryopsis length (CL), caryopsis width (CW), caryopsis length x width ratio (CLW), percentage of total chalky grains (CH) and percentage of stained grains (STA) in the F6 generation genotypes and irrigated rice controls.

The phenotypic variance (σ^2_p) which is composed of two components, the first being originated from the total environmental effects (environmental variance - σ^2_E) and the second resulting from the genetic effects (genetic variance - σ^2_G) that allow to evidence the genetic variability (Ramalho, Ferreira, & Oliveira, 2012).

The results of these parameters showed that the characters of total chalky area (CA), percentage of grains with white belly (WB), constant of total whiteness (WHT), constant of vitreous whiteness of grains (WHV), percentage of whole grains (WG), percentage of broken grains (BG), grain yield (GY), caryopsis length (CL), caryopsis width (CW), caryopsis length x width ratio (CLW) and percentage of total chalky grains (CH) in the F6 generation genotypes and irrigated rice checks have the phenotypic variance (σ^2_p) influenced mostly by genetic factors (σ^2_G) and presented low influence of environmental effects (σ^2_E), in the same way, being proven by the values of heritability in the broad sense (H^2), being classified as high (Hallauer, Carena, & Miranda Filho, 1988). This heritability represents the genetic variation involved in the phenotypic variability of the genotypes, however it does not represent the totality of the heritable effects, but expresses the reliability and representativeness of the phenotype in relation to genetic effects (Falconer, 1987).

Table 2. Summary of the analysis of variances and genetic parameters of the quality characters of irrigated rice grains of the F6 generation lines and controls.

SV	DF	CA[1]	WB	DC	WHT	WHV	WG	BG	GY	NG
Block	2	4.05	0.05	0.01	6.61	1.70	3.11	0.56	80004.85	25433.28
Treat	18	28.48^{**}	0.59^{**}	0.04^{ns}	9.62^{**}	7.73^{**}	67.50^{**}	34.87^{**}	83782.81^{**}	114661.90^{ns}
Res	36	3.31	0.04	0.04	1.93	0.45	9.22	4.52	11622.01	89055.89
Mean		16.03	0.55	0.50	130.37	122.37	55.32	11.80	350.09	1507.14
CV(%)		11.34	36.85	38.14	1.07	0.55	5.49	18.01	30.79	19.80
					Genetic parameters					
σ^2_p		9.49	0.20	0.01	3.21	2.58	22.50	11.62	27927.60	38220.63
σ^2_E		1.10	0.01	0.01	0.64	0.15	3.07	1.51	3874.00	29685.30
σ^2_G		8.39	0.18	0.00	2.56	2.43	19.43	10.12	24053.60	8535.34
H^2		88.38	93.05	11.91	79.92	94.15	86.34	87.05	86.13	22.33
CVg/CVe		1.59	2.11	0.21	1.15	2.32	1.45	1.50	1.44	0.31
SV	DF		CL	CW	CLW	CH	YEL	ARM	STA	BRO
Block	2		0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01
Treat	18		0.10^{**}	0.01^{**}	0.04^{**}	0.00^{**}	0.00^{ns}	0.00^{ns}	0.01^{**}	0.05^{ns}
Res	36		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
Mean			6.09	1.91	3.19	0.00	0.03	0.07	0.07	0.34
CV(%)			0.79	0.83	0.92	158.33	144.15	72.81	98.05	56.46
					Genetic parameters					
σ^2_p			0.032	0.002	0.014	0.00	0.00	0.00	0.0038	0.02
σ^2_E			0.001	0.000	0.000	0.00	0.00	0.00	0.0014	0.01
σ^2_G			0.031	0.002	0.013	0.00	0.00	0.00	0.0024	0.00
H^2			97.56	96.09	97.92	93.78	-	-	63.37	18.04
CVg/CVe			3.65	2.86	3.96	2.24	-	-	0.76	0.27

[1] CA - total chalky area (%); WB - percentage of grains with white belly (%); DC – total defects of coloring (%); WHT – total whiteness constant; WHV – grain vitreous whiteness constant; CL – caryopsis length (mm); CW - caryopsis width (mm); CLW – caryopsis length x width ratio (mm); WG – percentage of whole grains (%); BG – percentage of broken grains (%); GY – grain yield (g); NG – number of grains per 60g sample; CH – percentage of total chalky grains; YEL – percentage of yellow grains; ARM - percentage of arid and moldy grains; STA - percentage of stained grains; BRO – percentage of broken grains; SV – Source of Variation; Treat – treatment; Res - Residue; CV – Coefficient of variation; PV – Phenotypic Variation; EV – Environmental Variation; GV – Genetic Variation; and CVg/CVe – ratio of genetic and environmental variation coefficient. *Significant at 5% probability by F Test. **Significant at 1% probability by F Test. ns – not significant.

For percentage of stained grains (STA) it also presented as most of the genetic variance being 63.37%, however suffering a considerable environmental influence of 38.84%, thus being classified with heritability in the broad sense (H^2) intermediate. The other characters total defects of coloring (DC), number of grains (NG), percentage of yellow grains (YEL), percentage of arid and moldy grains (ARM), and percentage of broken grains (BRO) showed high environmental variance. This result was expected and can be explained due to the nature of the character, as well as the difficulty of measuring by very detailed data, with the exception of the number of grains where there were no significant differences between treatments with very similar data between the genotypes from the selection with focus on the thin long grain type.

The clustering test using the Scott Knott method (Table 3) at a 5% probability level differentiated the best genotypes for each individual character into groups. The total chalky area (CA) presented three groups, and only the lines PH18102 and PH18302 were classified as group "a" with average results of 11.05% and 8.94% respectively, being superior to the other lines and control cultivars. Lines PH18101, PH18301, PH18302, PH18501 and PH18502, in addition to cultivars IRGA 417 and BRS Pampeira, were classified as group “a”, higher for percentage of grains with white belly (WB).

In the constant of total whiteness of the grains (WHT), the lines PH18101, PH18301, PH18302, PH18601 and PH18601 stand out, being considered equal to the cultivar BRS Pampeira, this character represents the quantification of the opaque part of the grain sample represented by the shape of gypsum, thus, in terms of grain quality, Brazilian genetic improvement programs seek the lowest value of this constant. On the other hand, the constant of vitreous whiteness of the grains (WHV), refers to the factor of "transparency" (vitreous aspect) of the grains, seeking the highest value of the constant, highlighting the lines PH18202 and PH18401 as superior to the other genotypes studied.

The characters corresponding to the classification as to the type of grain, length (CL), width (CW) and length-to-grain width ratio (CLW), the cluster test differentiated in several groups, however, it is clear that the average results indicate that all strains fit as long fine grain (length ≥6 mm, width ≤1.90 mm and length-to-width ratio >2.75 mm), according to Magalhães Junior, Streck, Aguiar and Facchinello (2020). All genotypes were classified as group “a” for percentage of fully chalky grains (CH), with the exception of lineage PH18102. For the percentage of stained grains (STA) only 4 lines were grouped in group “b”, being PH18102, PH18302, PH18601 and PH18602.

Rice producers, industries and genetic improvement programs claim that the determining characters for the development of the production chain are the mill yield. Involving percentage of whole grains and broken grains, with the grain yield of the crop, directly affecting its value of marketing and acceptance of the product by the consumer (Streck et al., 2018; Magalhães Junior. et al., 2020).

Only BRS Pampa cultivar among the controls was classified as group “a” for the percentage of whole grains (WG), along with four lines, with emphasis on PH18102 and PH18502, whose average results were above 60% of whole grains (63.33% and 62.38% respectively), considered high values. Streck et al. (2018) showed similar results with BRS Pampeira average yield of 63% of whole grains, in addition to data from Magalhães Júnior et al. (2017) yields greater than 62% for polished whole grains. The cultivar BRS Pampa in the 2011/2012 harvest showed a yield of 65% of whole grains (Magalhães Júnior et al., 2012). For the percentage of broken grains (BG), the control cultivars BR IRGA 409 and BRS Pampa, in addition to six lines, were classified as superior (group "a"), highlighting PH18102 (6.44%) and PH18301 (6.35%).

For grain yield (GY) the genotypes were classified into 3 groups, considered superior (group “a”) the lines PH18402, PH18502, PH18601, PH18602, PH18701 and PH18801, as well as the control cultivars BRS Pampa, BRS Pampeira and IRGA 417. The average yields obtained in this group ranged from 4628 to 8008 kg ha^{-1}, where the Brazilian average is approximately 6000 kg ha^{-1} (CONAB, 2020), also demonstrated by Streck et al. (2018), Streck et al. (2019) and Sartori et al. (2011).

Important to note that all irrigated rice cultivars used as controls are widely known for presenting characteristics of agronomic interest, high productivity and high grain quality, being used in other research studies in irrigated rice (Champagne et al., 2010; Magalhães Júnior et al., 2017). Thus, the results obtained from the advanced strains (F6) demonstrate great potential.

Table 3. Mean grouping test by Scott Knott method for the 12 quality characters of irrigated rice grains of lines in F6 generation and controls with a significant difference at the 5% probability level by the F test.

TRE[1]	GEN	CA		WB		WHT		WHV		WG		BG	
1	PH18101	13.85	b[2]	0.31	a	129.30	a	122.49	b	55.06	b	11.23	a
2	BR IRGA 409	18.44	c	0.55	b	131.69	b	123.04	b	55.80	b	10.36	a
3	PH18102	11.05	a	0.56	b	130.45	b	121.91	c	63.33	a	6.44	a
4	PH18103	17.22	c	0.57	b	131.28	b	122.84	b	50.90	c	16.31	c
5	PH18201	19.82	c	0.57	b	133.61	b	122.77	b	48.97	c	13.64	b
6	PH18202	20.86	c	1.60	c	132.81	b	124.92	a	51.83	c	13.16	b
7	BRS PAMPA	17.91	c	0.57	b	131.15	b	122.32	c	58.54	a	8.86	a
8	PH18301	12.39	b	0.17	a	127.83	a	121.81	c	59.97	a	6.35	a
9	PH18302	8.94	a	0.19	a	127.70	a	117.61	e	57.47	b	9.65	a
10	PH18401	19.17	c	1.84	c	131.56	b	124.98	a	43.07	d	19.63	d
11	PH18402	16.69	c	0.53	b	131.13	b	123.01	b	56.69	b	12.25	b
12	PH18501	15.42	b	0.16	a	130.57	b	123.22	b	54.89	b	12.07	b
13	IRGA 417	17.45	c	0.32	a	131.52	b	123.30	b	56.54	b	11.62	b
14	PH18502	17.25	c	0.33	a	131.34	b	123.21	b	62.38	a	8.30	a
15	PH18601	14.52	b	0.41	b	127.38	a	121.50	c	53.68	b	12.90	b
16	PH18602	14.87	b	0.44	b	128.21	a	120.91	d	52.14	c	14.99	c
17	PH18701	17.02	c	0.61	b	130.89	b	122.63	b	59.24	a	8.66	a
18	BRS PAMPEIRA	13.60	b	0.14	a	128.10	a	120.58	d	55.17	b	15.58	c
19	PH18801	18.14	c	0.58	b	130.58	b	121.97	c	55.36	b	12.14	b
TREAT	GEN	CL		CW		CLW		CH		STA		GY	
1	PH18101	5.98	d	1.88	b	3.18	d	0.00	a	0.07	a	1721.0	c
2	BR IRGA 409	5.86	e	1.91	c	3.08	e	0.00	a	0.02	a	2046.0	c
3	PH18102	6.00	d	1.98	d	3.03	f	0.02	b	0.16	b	3392.5	b
4	PH18103	6.26	b	1.92	c	3.25	c	0.00	a	0.02	a	3351.0	b
5	PH18201	6.22	b	1.97	d	3.16	d	0.00	a	0.06	a	1852.9	c
6	PH18202	6.18	c	2.01	e	3.08	e	0.00	a	0.02	a	2970.1	b
7	BRS PAMPA	6.21	b	1.91	c	3.25	c	0.00	a	0.02	a	5497.2	a
8	PH18301	5.73	f	1.96	d	2.92	g	0.00	a	0.06	a	3911.2	b
9	PH18302	5.89	e	1.89	b	3.11	e	0.00	a	0.18	b	3482.0	b
10	PH18401	6.10	c	1.90	b	3.22	d	0.00	a	0.02	a	634.0	c
11	PH18402	6.25	b	1.89	b	3.30	b	0.00	a	0.03	a	7781.6	a
12	PH18501	6.35	a	1.86	a	3.41	a	0.00	a	0.08	a	3686.0	b
13	IRGA 417	6.23	b	1.91	c	3.26	c	0.00	a	0.07	a	6232.0	a
14	PH18502	6.12	c	1.89	b	3.24	c	0.00	a	0.03	a	5680.6	a
15	PH18601	5.87	e	1.84	a	3.18	d	0.00	a	0.22	b	6261.4	a
16	PH18602	5.90	e	1.84	a	3.21	d	0.00	a	0.13	b	8008.4	a
17	PH18701	6.22	b	1.90	c	3.28	c	0.00	a	0.01	a	6221.1	a
18	BRS PAMPEIRA	6.27	b	1.88	b	3.33	b	0.00	a	0.04	a	4628.9	a
19	PH18801	6.03	d	1.95	d	3.09	e	0.00	a	0.02	a	5788.3	a

[1] TRE – treatment; GEN – genotype; CA – total chalky area (%); WB – percentage of grains with white belly (%); WHT – total whiteness constant; WHV – grain vitreous whiteness constant; CL – caryopsis length (mm); CW - caryopsis width (mm); CLW – caryopsis length x width ratio (mm); WG – percentage of whole grains (%) and BG – percentage of broken grains (%); GY – grain yield (Kg ha-1); CH – percentage of total chaky grains; STA - percentage of stained grains. [2]Means followed by the same lowercase letter vertically do not differ statistically from each other, by the Scott Knott Cluster Test at the 5% probability level.

Pearson's linear correlation was performed in order to assess the degree of linear relationship between two characters (Figure 1). From the 19 irrigated rice genotypes, 51 pairs of significant genotypic correlations between the characters were obtained. However, only 18 pairs resulted in high magnitude correlations. The highest negative correlation was found between percentage of whole grains and percentage of broken grains, being -0.81, which was already expected, since both characters result from the inverse variation of the physical structure of the grains.

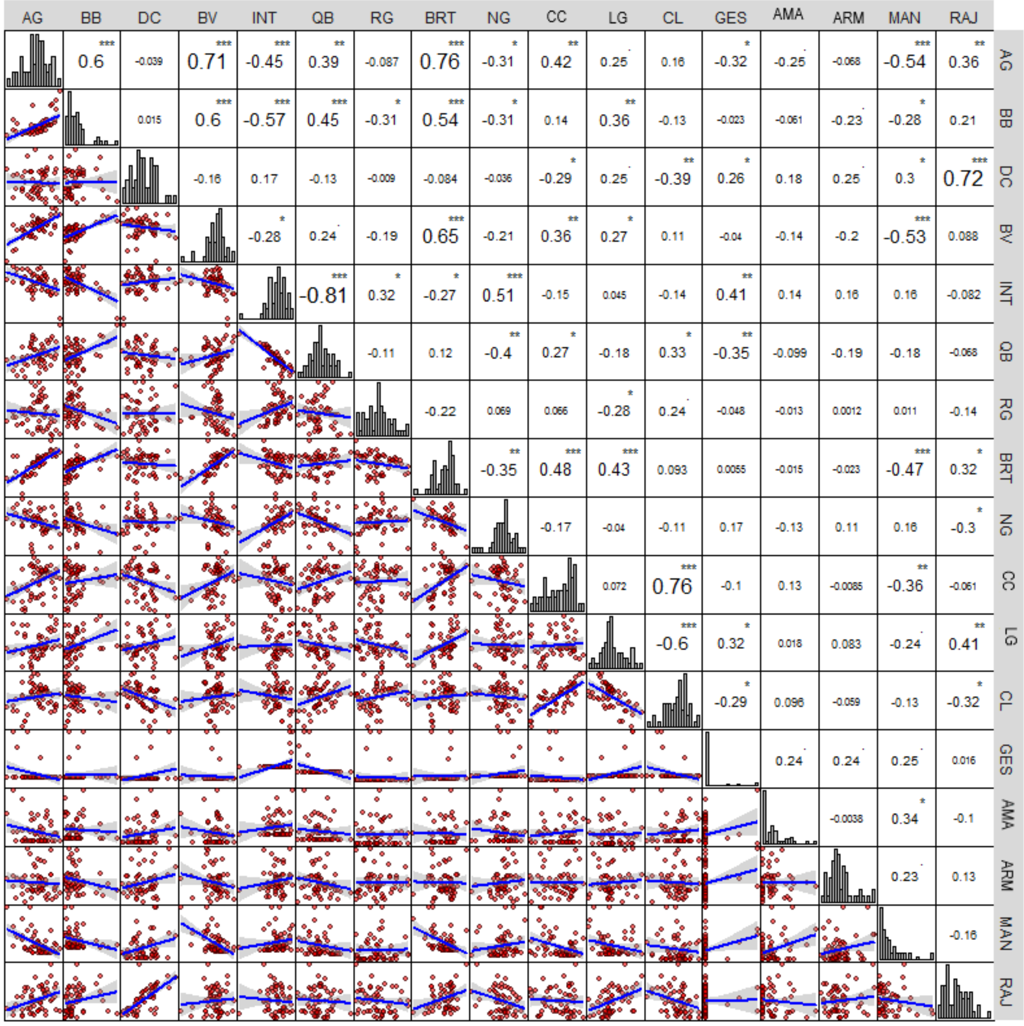

Figure 1. Pearson's linear correlation between irrigated rice grain quality traits of 19 irrigated rice genotypes. *, ** and *** indicate significant differences at levels of P<0.05, P<0.01 and P<0.001, respectively. CA - total chalky area (%); WB - percentage of grains with white belly (%); DC – total defects of coloring (%); WHT – total whiteness constant; WHV – grain vitreous whiteness constant; CL – caryopsis length (mm); CW - caryopsis width (mm); CLW – caryopsis length x width ratio (mm); WG – percentage of whole grains (%) and BG – percentage of broken grains (%); GY – grain yield (g); NG – number of grains per 60g sample; CH – percentage of total chalky grains; YEL – percentage of yellow grains; ARM - percentage of arid and moldy grains; STA - percentage of stained grains; and BRO – percentage of broken grains.

In addition, the percentage of whole grains (WG) showed high negative correlations with the characters related to plaster, total chalky area, white belly and total whiteness. These results corroborate what was proposed by Liu, Zhou, Yang and Li (2009) where the chalky grains make it easier to break the grains during processing. The gypsum grains occur by the arrangement between starch and protein molecules in a disorderly manner, developed under adverse conditions of climate and cultivation, as well as due to genetic factors. On the contrary, positive magnitude, these correlations occurred for the percentage of broken grains.

The grain size characters (CL, CW, CLW) showed significant correlations with each other, in addition, they resulted in positive correlations of intermediate magnitudes for the gypsum characters (CA, WB and WHT). However, according to Nikam, Takle, Patil, Mehta and Jadeja (2014), these characters, especially grain length, indicate an association of relative importance with the chemical composition of rice, used as a selection strategy to improve grain length along with cooking quality.

Important correlations were also found with grain yield (GY), being of positive function with the percentage of whole grains (WG) with magnitude of 0.32, and negative correlation with white belly with magnitude of -0.31, making it possible a complementary selection among these characters.

It is worth emphasizing the importance of analyzing linear correlations, as it allows the simultaneous selection for two characters with the presence of significant genetic correlation, in which it can generate potential genetic gains of great value for the genetic improvement program, considerably reducing the breeder's work time, as well as increasing efficiency.

In the analysis of canonical correlations (Table 4) the characters were divided into two groups, being group 1, the traits aimed at productivity, and in group 2 the traits aimed at grain quality in rice. Two canonical pairs between characters of group 1 and 2 were found for the rice genotypes under study, however only the first canonical pair proved to be significant. The high magnitude of the canonical correlation coefficients showed high dependence between the two groups of characters in the first canonical pair.

The results showed a correlation r=0.81 between the groups, through the first canonical pair. Grain yield and number of grains (group 1) were directly related to the percentage of whole grains, chalky grains and stained grains, however inversely related to total chalky area, white belly, total whiteness, vitreous whiteness, percentage of broken grains and defects of coloring (group 2). This correlation between grain yield and percentage of whole grains was of high magnitude and in a positive sense, being very important, considering that, these are the two main characters sought by breeders (Magalhães Junior et al., 2020).

Therefore, the selection of superior genotypes for productivity can be based on the choice of plants with high grain yield and number of grains per plant, obviously, contributing, indirectly, to better grain quality, mainly in the structuring of amylose and amylopectin molecules, with positive effects due to the reduction of gypsum areas, in addition to an increase in whole grain yield.

For the characters of grain size and shape (group 1) they were inversely correlated with the percentage of whole grains (group 2). These correlations corroborate the statements of Farias Filho and Ferraz Júnior (2009) and Maghelly, Ogliari, Souza, Reichert Júnior and Pinto (2020), where whole grain yield is affected by grain size and shape, concluding that genotypes with longer and shorter widths had the lowest whole grain yields.

Table 4. Canonical correlation between yield traits (group 1) and grain quality traits (group 2) of the 19 irrigated rice genotypes.

Character	Canonical Pair	
	1st	2nd
Group 1		
GY[1]	0.4144	0.3170
NG	0.6481	0.0505
CL	-0.3176	0.4715
CW	-0.2988	0.0834
CLW	-0.0562	0.3166
Group 2		
CA	-0.5283	0.3633
WB	-0.6176	0.0719
DC	-0.2134	-0.1186
WHV	-0.4648	0.1589
WG	0.6225	0.0347
BG	-0.4217	0.0139
WHT	-0.5201	0.3532
CH	0.1947	0.1644
YEL	-0.134	0.0078
ARM	0.0675	-0.0282
MAC	0.2782	-0.3034
BRO	-0.3454	-0.002
r	0.8012	0.6783
p	<.0001	0.0152

[1] GY – grain yield (g); NG – number of grains per 60g sample; CL – caryopsis length (mm); CW - caryopsis width (mm); CLW – caryopsis length x width ratio (mm); CA - total chalky area (%); WB - percentage of grains with white belly (%); DC – total defects of coloring (%); WHV – grain vitreous whiteness constant; WG – percentage of whole grains (%) and BG – percentage of broken grains (%); WHT – total whiteness constant; CH – percentage of total chalky grains; YEL – percentage of yellow grains; ARM - percentage of arid and moldy grains; MAC - magnitude of the coefficients and BRO – percentage of broken grains. r- canonical correlations; p- probability.

The dendrogram obtained by the generalized Mahalanobis distances (Figure 2) established six groups distinguishable from each other in terms of the genetic distances present, based on the relative contribution of the characters evaluated using the Toucher clustering method, with each group showing variations in the number of subgroups. It can be observed that the genotypes were grouped mainly by the characteristic of grain type, in which the lines with the presence of parents with grains not classified as long and fine, BR IRGA 409 (intermediate grains) and 86014-TR891-7-2 -1 (rounded grains), were grouped separately from the other genotypes (black, yellow and brown groups).

The largest grouping has nine genotypes (blue grouping), being composed of cultivars and lines originated mostly by the parents BRS Pampa, BRS Pampeira, Puitá Inta CL, IRGA 417, as well as other elite lines of the breeding program in which these cultivars in their genealogies. These four cultivars have similarities in terms of plant structure, being of the modern Filipino type, high capacity to produce tillers, robust and short stems (short height), and erect leaves, with long and thin grain, also known for their good physical attributes of grain quality, mainly due to the low incidence of gypsum characters. These similarity results for this group corroborate the analysis performed by Streck et al. (2017) in which these cultivars were grouped very closely, using an experiment with a dendrogram obtained from the dissimilarity matrix through the qualitative characters of 92 rice accessions, using the Intergroup Mean

Linkage (UPGMA) method.

While the smallest cluster had only one genotype (green cluster), the PH18602 strain, originated from the crossing of the elite strain of the Embrapa AB10010 breeding program and the cultivar BRS Pampa. Another grouping with three genotypes, the lines PH18402, PH18701 and the cultivar IRGA 417 (red group), followed this. These two groups are the most genetically distant from the other genotypes, and grain yield was the character that most contributed to the difference, being composed of the most productive genotypes.

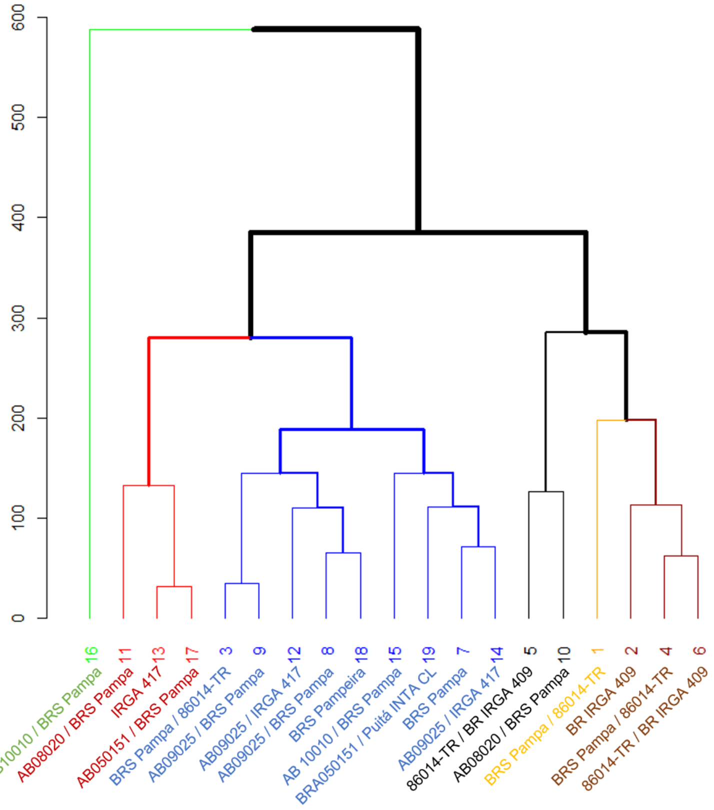

Figure 2. Dendrogram of the genetic distance of 19 irrigated rice genotypes for the studied characters in irrigated rice.

Principal Component Analysis (PCA) is a linear statistical method that finds the eigenvalues and eigenvectors of the covariance matrix of the data and, with this result, one can perform the dimensional reduction of the data and analyze the main patterns of variability present (Hongyu, Sandanielo, & Oliveira Junior, 2015). Figure 3 shows the weight plot for the first two principal components. Geometrically, the weights correspond to the cosines of the angles that the principal components (PC) make with the original characters, these weights in the linear combination are responsible for defining each Principal Component (Lyra, Silva, Araújo, Fragoso, & Veras, 2010).

Based on the results obtained by the principal components technique, the respective eigenvalues and percentages of the variance explained by each one were previously tested, the first two PCs were responsible for explaining 54.40% of the total variation, on the quality and yield traits of grains of the studied irrigated rice genotypes, in which PC1 was responsible for 33.50% and the second, PC2, for 20.90% of the data variations.

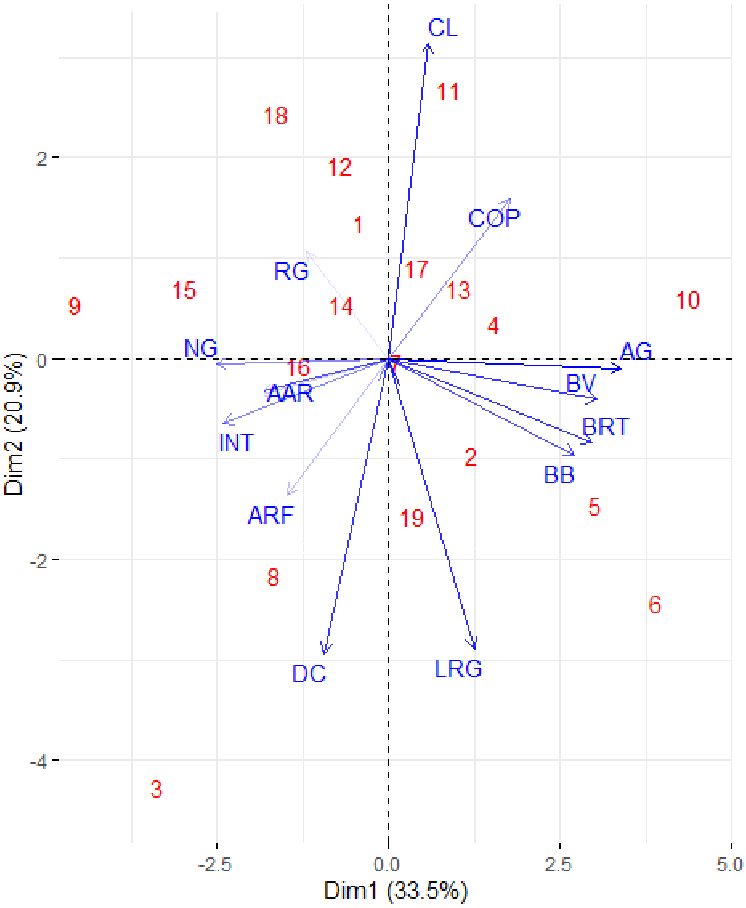

Figure 3. Graph of the weights of PC1 (Dim1) and PC2 (Dim2) for sixteen properties: CA – total chalky area (%); WB - percentage of grains with white belly (%); DC – total defects of coloring (%); WHT – total whiteness constant; WHV – grain vitreous whiteness constant; CL – caryopsis length (mm); CW - caryopsis width (mm); CLW – caryopsis length x width ratio (mm); WG – percentage of whole grains (%) and BG – percentage of broken grains (%); GY – grain yield (g); NG – number of grains per 60g sample; CH – percentage of total chalky grains; YEL – percentage of yellow grains; ARM - percentage of arid and moldy grains; STA - percentage of stained grains; and BRO – percentage of broken grains.

Liu et al. (2021) explained the variance of the study of identification of genetic loci that control the covariance between the mineral elements in the rice genome, PC1 and PC2 together resulted in the variance ratio of 34% (grains in a greenhouse) to 47% (roots grown in hydroponics). While Nihad et al. (2021) observed in seven rice yield components, morphological and by SSR (Simple Sequence Repeats), of 44 genotypes susceptible and resistant to rice tungro virus, PC1, PC2, PC3 and PC4 showed variations of 17.43%, 7.93%, 6.32% and 5.59%, respectively, and in the total implied a variation of 32.27% between genotypes. In this way, it can be seen that the value obtained with the results explains a value considered high in the variation of this study, even with only two main components.

The scatter plot between PC1 and PC2 (Figure 3) based on the biplot showed clustering of rice genotypes in relation to the characters of chalky grains (CA, WHV, WHT and WB) emphasizing the affinity between them. Treatment 5 (line PH18201) originated from the cross between 86014-TR891-7-2-1 and BR IRGA 409 showed the highest affinity with this grouping of plaster characters. Inversely to this grouping, in the opposite quadrant, only the grain yield is found, corroborating the other correlation analyzes of this study, in which it showed greater affinity with the PH18502 lineage.

Another affinity between characters observed in the scatter plot refers to the length x width ratio and the grain length, which is already expected. Inversely correlated, in the opposite quadrant, is the affinity grouping between the characters of percentage of whole grains, number of grains, percentage of stained grains and percentage of yellow grains. It is also worth mentioning the affinities of the characters in relation to the genotypes, the lineage PH18301 (treatment 8) had great affinity with the percentage of total chalky grains, the lineage PH18602 (treatment 16) with the percentage of yellow grains and the lineage PH18402 (treatment 11) with the grain length x width ratio. These results may provide background information for the conservation and use of the genotypic variability of these characters by rice genotypes in the breeding program.

CONCLUSIONS

There is phenotypic variability among the analyzed rice genotypes.

The PH18502 and PH18701 strains presented better desirable agronomic performance of the studied characters, by univariate analysis, being very promising for a future release as cultivars.

The linear and canonical correlations presented show potential in the direction of selection of multiple characters, in addition, they also point to the possibility of indirect selection between the characters of great agronomic importance and relevant to the production chain of irrigated rice.

Multivariate analyzes are a highly important tool to assist in the characterization of irrigated rice accessions.

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