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Genetics/ Original Article

Genetic cause and effect interrelationships for grain quality attributes of irrigated rice

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Abstract – The objective of this work was to determine the genetic correlations and the direct and indirect associations of agronomic traits and grain quality attributes with the percentage of whole grains in flood irrigated rice. The experiment was carried out in two environments, in a randomized complete block design with three replicates, using 23 irrigated rice genotypes. The evaluated traits were: percentage of whole grains, caryopsis length, caryopsis width, panicle length, panicle weight, 1,000 grain weight, days to flowering, percentage of chalky grains with white belly, total chalky area, total whiteness, vitreous whiteness, and defects in coloring. The percentage of grains with white belly and total chalky area were positively correlated, whereas the percentage of grains with white belly and vitreous whiteness were negatively correlated. The traits caryopsis width, percentage of chalky grains with white belly, panicle weight, and 1,000 grain weight showed indirect effects on whole-grain yield response according to total chalky area and total whiteness. Total chalky area and total whiteness are the factors that most negatively influence the percentage of whole grains according to the genotypic correlations and direct effects.

Index terms: *Oryza sativa*, indirect selection, whole grains.

Inter-relações genéticas de causa e efeito para atributos de qualidade de grãos de arroz irrigado

Resumo – O objetivo deste trabalho foi determinar as correlações genéticas e as associações diretas e indiretas de caracteres agronômicos e atributos de qualidade de grãos com a percentagem de grãos inteiros em arroz irrigado por inundação. O experimento foi conduzido em dois ambientes, em delineamento de blocos ao acaso, com três repetições, tendo-se utilizado 23 genótipos de arroz irrigado. Os caracteres avaliados foram: percentagem de grãos inteiros, comprimento da cariopse, largura da cariopse, comprimento da panícula, peso da panícula, peso de mil grãos, dias para floração, percentagem de grãos com "barriga branca" e grãos gessados, área gessada total, brancura total, brancura vítrea e defeitos de coloração. A percentagem de grãos com "barriga branca" e área gessada total correlacionaram-se positivamente, enquanto a percentagem de grãos com "barriga branca" e gessada e brancura vítrea correlacionaram-se negativamente. Os caracteres largura da cariopse, percentual de grãos com "barriga branca" e gessada, peso da panícula e peso de mil grãos apresentaram efeitos indiretos sobre a resposta de rendimento de grãos inteiros de acordo com área total gessada e brancura total. Área total gessada e brancura total são os fatores que mais influenciam negativamente a percentagem de grãos inteiros de acordo com as correlações genotípicas e os efeitos diretos.

Termos para indexação: *Oryza sativa*, seleção indireta, grãos integrais.

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Introduction

In genetic breeding programs, the development of superior genotypes of rice (*Oryza sativa* L.), a staple food and the second most produced cereal worldwide (FAO, 2021), has been taking new directions. In addition to the selection of genotypes with genetic constitutions of high yield potential, the search for grains with quality attributes has become an important standard for the launch of new cultivars (Rangel et al., 2000).

In flood irrigated rice, grain quality attributes are considered quantitative traits, strongly influenced by the environment and its interaction with the genotype (Silva Junior et al., 2022). The early selection and setting of these attributes in segregating generations are difficult due to a low heritability and the use of destructive methods to measure some traits, such as the percentage of whole grains, which requires grain polishing that damages the embryo and makes the sample unusable as a seed (Facchinello et al., 2022). In these cases, Nardino et al. (2016) recommend using indirect selection, in which selection is applied to a secondary trait to improve a desired one through a correlated response between both of them. However, Falconer (1987) added that, for a more efficient result, the direct and indirect methods should be used concomitantly.

An alternative is the path analysis method of Wright (1921) that proposes unfolding the estimated linear correlation in direct and indirect effects of several traits in relation to a main one, which can facilitate the understanding of existing correlations. However, for this method, it is important to verify the degree of multicollinearity between explanatory variables (Cruz & Carneiro, 2006), since a high degree of multicollinearity can generate an overestimation of direct and indirect effects, without any biological meaning (Toebe & Cargnelutti Filho, 2013). If a high degree of multicollinearity is detected, the path analysis may be either carried out under multicollinearity (crest path analysis), with the addition of a k-value to the diagonal elements of the correlation matrix, or traditionally, with the elimination of highly correlated variables (Cruz & Carneiro, 2006).

The path analysis under multicollinearity has been used very effectively in the genetic phyto-improvement of crops such as peanut (*Arachis hypogaea* L.) (Luz et al., 2011), maize (*Zea mays*, L.) (Toebe & Cargnelutti Filho, 2013), and kale [*Brassica oleracea* subsp. *acephala* (DC.) Metzg] (Azevedo et al., 2016), showing the possibility of selecting main traits through indirect selection. In rice, this methodology can be used to clarify how agronomic traits and grain quality attributes influence the percentage of whole grains, which may contribute to indirect selection and the development of rice genotypes with more whole grains.

The objective of this work was to determine the genetic correlations and the direct and indirect associations of agronomic traits and grain quality attributes with the percentage of whole grains in flood irrigated rice.

Materials and Methods

The experiment was carried out in the 2015/2016 harvest, in the two following locations in the state of Rio Grande do Sul, Southern Brazil: the experimental field of Estação de Terras Baixas of Embrapa Clima Temperado, in the municipality of Capão do Leão (31°46'3"S, 52°26'55"W); and a property in the municipality of Nova Esperança do Sul (29°23'40"S, 54°50'32"W).

The following rice genotypes (cultivars), developed by the improvement program of Embrapa alone or in partnership with other programs, were evaluated: BR/IRGA 409, BR/IRGA 410, BR/IRGA 411, BR/IRGA 412, BR/IRGA 413, BR/IRGA 414, BRS 6, BRS 7, BRS Sinuelo CL, BRS Agrisul, BRS Pampa, BRS Pampeira, BRS Pelota, BRS Fronteira, BRS Querência, BRS Ligeirinho, BRS 358, BRS AG, BRS Bojuru, BRS Firmeza, SCSBRS 113 - Tio Taka, BRSCIRAD 302, and IAS 12-9 (Formosa). The adopted cultural practices were standardized in both environments according to the recommendations for Southern Brazil (Reunião..., 2018).

To obtain the genotypes in the field, sowing was carried out at a density of 100 kg ha^{-1}, using a mechanical plot seeder, under a no-tillage system. Base fertilization consisted of 300 kg ha^{-1} NPK (formula 5-20-20) and 90 kg ha^{-1} nitrogen, in the form of urea, half applied at the V4 stage (collar formed on the fourth leaf of the main stem) and the other half at the R0 stage (panicle initiation). The permanent flooding irrigation system was adopted until the final stage of genotype maturation.

The experimental design was a randomized complete block with three replicates, in which the plots consisted of four rows of 5.0 m in length, spaced at 0.17 m. The useful area of the plot were the four central meters of the two inner rows, to exclude any border effect.

The evaluated agronomic traits were: percentage of whole grains; caryopsis length (mm); caryopsis width (mm); panicle length (cm); panicle weight (g); 1,000 grain weight (g); and days to flowering, considering the number of days from emergence to 50% exposed panicles. The following physical attributes of intrinsic grain quality were also analyzed: sum of the percentage of chalky grains with white belly (%), total chalky area (%), total whiteness, vitreous whiteness, and sum of the percentage of defects in coloring (stained, streaked, moldy, and yellow grains). These attributes were determined with the aid of the S21 rice statistical analyzer (S21 Solutions, Santa Cruz do Rio Pardo, SP, Brazil), based on the analysis of digital images of each sample.

The results were subjected to statistical analyzes using the GENES software (Cruz, 2013). Individual analysis of variance and the F-test were performed for each studied variable, in order to verify the existence of variability between genotypes and to check for homogeneity of variances. This way, the following estimates of genetic parameters were obtained: environmental, genotypic and phenotypic variances; coefficient of variation; and heritability.

For the path analysis, multicollinearity was detected in the matrices of genotypic and phenotypic correlations according to the criteria of Montgomery & Peck (1981) by determining the ratio (condition number) between the highest and lowest eigenvalues of the X'X matrix. The variance inflation factor obtained for each variable on the inverse diagonal of the correlation matrix (X'X) was also considered as an indicator of multicollinearity.

If severe multicollinearity was detected, to avoid the exclusion of variables, a procedure similar to the crest regression analysis was used, where a constant (k) is added to the diagonal of the X'X correlation matrix, in order to reduce the variance of the trail analysis least squares estimator (Cruz & Carneiro, 2006). The selected k-value (between 0 and 1) should be the best value that minimizes multicollinearity, considering the lowest constant for the stabilization of the trail coefficients, a variance inflation factor lower than 10, and a condition number lower than 100 (Hair et al., 2009). Cruz et al. (2014) highlighted that the higher the k-value used, the more biased the information obtained by the trail analysis will be.

A moderate to strong degree of multicollinearity was detected, with a condition number between 100 and 1,000 eigenvalues of the matrix, as well as values of the variance inflation factor higher than 10. The constant k = 0.0860 was used to minimize multicollinearity since it was the lowest constant that allowed of the stabilization of trail coefficients and showed a variance inflation factor lower than 10 and a condition number lower than 100.

Subsequently, phenotypic and genotypic correlations were obtained through the bootstrap test with 10,000 simulations, determining the existence of a significant linear correlation between the studied variables. The phenotypic correlations were analyzed by obtaining an n number of correlation estimates across the original permuted (unstructured) dataset. For the estimation of genotypic correlation, empirical distributions were constructed to verify significance by the Mantel test, which requires a higher number of cultivars (Oliveira et al., 2013), as used in the present study. After verifying the existence of a significant correlation between pairs of traits, the trail analysis was carried out to indicate the direct and indirect effects of the evaluated agronomic traits in relation to the percentage of whole grains.

Results and Discussion

A significant difference as to genotype effect was observed by the F-test among 11 of the analyzed variables (Table 1). Regarding environmental variance, only caryopsis width and percentage of defects in coloring showed significant differences, whereas, for the genotype x environment interaction effect, most variables differed significantly. The coefficients of variation of the studied traits ranged from 1.47% for caryopsis width to 19.01% for chalky area, which means there was a good experimental precision. However, the sum of the percentage of chalky grains with white belly (111.68%) and the percentage of defects in coloring (51.64%) showed high values, an effect mainly due to the nature of these variables. Moreover, there was a high heritability from 66.62 and 99.63% for the evaluated traits, which shows an adequate efficiency in the selection process.

A total of 32 pairs of significant genotypic correlations between the studied traits were obtained for the 23 evaluated cultivars (Table 2). The highest positive magnitude of 0.967 was observed between the sum of the percentage of chalky grains with white belly and total chalky area, which was already expected since both are a result of the variation of the same defect caused by the air spaces generated by disturbances at the time of the accumulation of starch and protein molecules in the grains (Shen, 2000). The highest negative magnitude was found between the sum of the percentage of chalky grains with white belly and vitreous whiteness, which were inversely proportional.

Regarding whole grains, six significant genetic correlations were observed, with negative effects for caryopsis width, sum of the percentage of chalky grains with white belly, chalky area, total whiteness, panicle weight, and 1,000 grain weight, with values ranging from -0.373 to -0.756 for caryopsis width and total whiteness, respectively. The relationship between the sum of the percentage of chalky grains with white belly and chalky area confirm the finding of Liu et al. (2009) that chalky grains, due to air spaces, break easily during processing. Zhou et al. (2009) added that these characteristics are among the greatest challenges in rice cultivation, as they directly affect rice quality and price, together with the percentage of whole grains. Therefore, simultaneous selection considering these two traits, resulting from this high genetic correlation, could generate considerable genetic gains for grain quality attributes.

For panicle weight and 1,000 grain weight, the negative correlations in relation to whole grains (Table 2) is attributed to the japonica subspecies of the cultivars, whose grains are rounder and have a different composition and inferior grain quality than those of the indica subspecies, as shown by

Table 1. Summary of the analysis of variance and estimates of the genetic and phenotypic parameters of the agronomic traits evaluated in 23 flood irrigated rice (*Oryza sativa*) genotypes in two locations in the state of Rio Grande do Sul, Brazil[(1)].

SV	DF	Mean square											
		WG	CL	CW	WB+C	CA	DC	WHT	WHV	PL	PW	TGW	DF
G	22	125.15**	1.76**	0.25**	822.41**	446.83^{ns}	100.75**	154.85**	83.99**	32.06**	5.04**	481.12**	550.85**
E	1	123.37^{ns}	0.22^{ns}	0.37**	14.41^{ns}	387.44^{ns}	1,290.89**	40.64^{ns}	418.09^{ns}	0.12^{ns}	0.13^{ns}	131.48^{ns}	165.22^{ns}
GxE	22	33.21**	0.13**	0.004**	3.03^{ns}	10.05^{ns}	33.63**	12.20**	19.63**	3.01**	0.42**	7.70**	46.12**
r	88	7.42	0.01	0.00	16.52	8.47	10.01	5.89	5.10	1.45	0.16	2.24	5.03
μ	-	60.70	6.34	2.14	3.64	15.31	6.13	131.63	121.53	23.86	3.61	29.78	77.51
CV (%)	-	4.49	1.91	1.47	111.68	19.01	51.64	1.84	1.86	5.05	11.10	5.03	2.89
σ^2_g	-	15.32	0.27	0.04	136.56	72.80	11.19	23.78	10.73	4.84	0.77	78.90	84.12
σ^2_i	-	8.59	0.04	0.00	0.00	0.53	7.87	2.10	4.85	0.52	0.09	1.82	13.70
h (%)	-	73.47	92.67	98.25	99.63	97.75	66.62	92.12	76.62	90.61	91.72	98.40	91.63

[(1)]SV, sources of variation; DF, degrees of freedom; WG, whole grain yield (%); CL, caryopsis length (mm); CW, caryopsis width (mm); WB+C, sum of the percentage of chalky grains with white belly (%); CA, total chalky area; DC, percentage of defects in coloring (%); WHT, total whiteness; WHV, vitreous whiteness, PL, panicle length (cm); PW, panicle weight (g); TGW, 1,000 grain weight (g); DF, days to flowering; G, genotype; E, environment; G×E, genotype × environment interaction; r, residue; μ, mean; σ^2_g, genetic variance, σ^2_i, variance of the G×E interaction; and h, heritability.**Significant by the F-test, at 1% probability. ^{ns}Nonsignificant.

the significant negative correlations between these traits and vitreous whiteness (-0.726 and -0.802, respectively). The intrinsic characteristics of grain type and plant architecture, for example, led BRS AG to be the first rice cultivar intended for uses other than human consumption, such as alcohol production or animal feed, explaining its high genetic distance in relation to other commonly used cultivars, with a practically double average 1,000 grain weight of 52 g (Streck et al., 2017).

Panicle length did not present significant correlations with whole grain yield (Table 2), contrasting with the finding of Jongkaewwattana & Geng (2002), who concluded that this character could be a useful selection index for the improvement of whole grain yield. These different results can be explained by the small amplitude variation for this character in the estimates of genetic correlations in the present study, since only cultivar BRS Querência showed higher panicle length values.

Days to flowering was the only variable that did not present a significant correlation with the explanatory variable percentage of whole grains, nor relationships with the other analyzed variables (Table 2). Similar results were reported in other studies with rice, where no correlation or few low-magnitude correlations were found between days to flowering and several other traits (Nandan et al., 2010; Kishore et al., 2015). Therefore, for an efficient response of indirect selection in breeding, it is important to identify which characters with a high correlation with the main trait present the greatest direct effect in a direction favorable to selection (Cruz & Carneiro, 2006).

In this sense, total whiteness and chalky area presented high negative magnitudes regarding the direct effect on whole grain yield, explaining much of the correlation between these traits (Table 3). In addition, indirect effects via chalky area and total whiteness were detected for caryopsis width, sum of the percentage of chalky grains with white belly, panicle weight, and 1,000 grain weight, with negative correlations in relation to the response variable whole grain yield.

Chalky area, sum of the percentage of chalky grains with white belly, and total whiteness were the factors that showed the greatest direct and indirect losses in terms of percentage of whole grains (Table 3). Several studies have sought to minimize these effects, both through genetic improvement and through different management methods, in order to avoid possible problems related to the occurrence of chalky grains (Marchezan et al., 1992; Ishimaru et al., 2009; Gu et al., 2015; Londero et al., 2015).

Table 2. Genotypic correlations between agronomic traits evaluated in 23 flood irrigated rice (*Oryza sativa*) genotypes in two locations in the state of Rio Grande do Sul, Brazil(1).

	WG	CL	CW	WB+C	CA	DC	WHT	WHV	PL	PW	TGW	DF
WG	1	-0.039	-0.373*	-0.563**	-0.702**	-0.192	-0.756**	0.382	0.220	-0.423*	-0.516*	0.215
CL		1	-0.588**	0.117	0.079	-0.763**	0.156	0.025	0.431*	0.335*	0.188	0.066
CW			1	0.562*	0.599**	0.865**	0.589**	-0.472	-0.533**	0.294	0.605**	0.044
WB+C				1	0.967**	0.286	0.883**	-0.913*	0.014	0.805*	0.956*	-0.017
CA					1	0.328	0.950**	-0.838*	-0.045	0.769*	0.927*	-0.115
DC						1	0.271	-0.298	-0.513**	-0.039	0.275	-0.114
WHT							1	-0.639$^+$	-0.119	0.707*	0.899**	0.002
WHV								1	-0.093	-0.726*	-0.802*	0.153
PL									1	0.239	-0.048	0.153
PW										1	0.841**	-0.009
TGW											1	0.095
DF												1

(1)WG, whole grain yield (%); CL, caryopsis length (mm); CW, caryopsis width (mm); WB+C, sum of the percentage of chalky grains with white belly (%); CA, total chalky area (%); DC, percentage of defects in coloring (%); WHT, total whiteness; WHV, vitreous whiteness; PL, panicle length (cm); PW, panicle weight (g); TGW, thousand grain weight (g); and DF, days to flowering. **and *Significant by the Mantel test, at 1 and 5% probability, respectively, with the bootstrap method with 10,000 simulations.

Table 3. Estimation of direct and indirect effects of trail coefficients, estimated from phenotypic correlations, on percentage of whole grains in 23 irrigated rice (*Oryza sativa*) genotypes[(1)].

Effect	Variable	Estimation	VIF	Variable	Estimation	VIF	Variable	Estimation	VIF
		------ CL ------			------ CW ------			------ WB+C ------	
Direct on	WG	0.1453	3.8633	WG	0.1836	7.2118	WG	-0.0179	9.9635
Indirect via	CW	-0.1078	2.1108	CL	-0.0854	1.1307	CL	0.0170	0.0449
Indirect via	WB+C	-0.0021	0.1157	WB+C	-0.0100	2.6645	CW	0.1031	1.9286
Indirect via	CA	-0.0397	0.0508	CA	-0.2996	2.9003	CA	-0.4828	7.5324
Indirect via	DC	-0.0542	2.3316	DC	0.0614	2.9965	DC	0.0203	0.3282
Indirect via	WHT	-0.1039	0.1365	WHT	-0.3935	1.9588	WHT	-0.5896	4.3975
Indirect via	WHV	-0.0044	0.0028	WHV	0.0824	1.0271	WHV	0.1592	3.8343
Indirect via	PL	0.0721	0.3114	PL	-0.0892	0.4766	PL	0.0024	0.0003
Indirect via	PW	-0.0174	0.3675	PW	-0.0152	0.2813	PW	-0.0417	2.1174
Indirect via	TGW	0.0530	0.2770	TGW	0.1711	2.8854	TGW	0.2702	7.1930
Indirect via	DF	0.0074	0.0055	DF	0.0050	0.0026	DF	-0.0019	0.0004
Total		-0.0392^{ns}			-0.3735*			-0.5631**	
		------ CA ------			------ DC ------			------ WHT ------	
Direct on	WG	-0.4994	9.5043	WG	0.0710	4.7209	WG	-0.6677	6.6518
Indirect via	CL	0.0115	0.0206	CL	-0.1109	1.9081	CL	0.0226	0.0793
Indirect via	CW	0.1101	2.2007	CW	0.1588	4.5776	CW	0.1082	2.1237
Indirect via	WB+C	-0.0173	7.8963	WB+C	-0.0051	0.6927	WB+C	-0.0158	6.5869
Indirect via	DC	0.0233	0.4303	CA	-0.1637	0.8663	CA	-0.4745	7.2761
Indirect via	WHT	-0.6344	5.0923	WHT	-0.1807	0.4134	DC	0.0192	0.2934
Indirect via	WHV	0.1461	3.2299	WHV	0.0519	0.4080	WHV	0,1116	1.8840
Indirect via	PL	-0.0075	0.0034	PL	-0.0858	0.4412	PL	-0.0198	0.0235
Indirect via	PW	-0.0398	1.9313	PW	0.0020	0.0049	PW	-0.0366	1.6308
Indirect via	TGW	0.2619	6.7577	TGW	0.0776	0.5934	TGW	0.2541	6.3595
Indirect via	DF	-0.0130	0.0169	DF	-0.0129	0.0166	DF	0.0002	0.0000
Total		-0.7017**			-0.1917^{ns}			-0.7559**	
		------ WHV ------			------ PL ------			------ PW ------	
Direct on	WG	-0.1744	5.4249	WG	0.1674	1.9786	WG	-0.0518	3.8489
Indirect via	CL	0.0037	0.0020	CL	0.0626	0.6080	CL	0.0487	0.3688
Indirect via	CW	-0.0867	1.3654	CW	-0.0978	1.7372	CW	0.0539	0.5271
Indirect via	WB+C	0.0163	7.0422	WB+C	-0.0003	0.0017	WB+C	-0.0144	5.4810
Indirect via	CA	0.4185	5.6587	CA	0.0224	0.0161	CA	-0.3842	4.7691
Indirect via	DC	-0.0211	0.3550	DC	-0.0364	1,0527	DC	-0.0027	0.0060
Indirect via	WHT	0.4273	2.3101	WHT	0.0791	0.0790	WHT	-0.4720	2.8183
Indirect via	PL	-0.0156	0.0146	WHV	0.0162	0.0400	WHV	0.1266	2.4250
Indirect via	PW	0.0376	1.7205	PW	-0.0124	0.1867	PL	0.0400	0.0960
Indirect via	TGW	-0.2268	5.0671	TGW	-0.0135	0.0181	TGW	0.2376	5.5638
Indirect via	DF	0.0173	0.0298	DF	0.0173	0.0298	DF	-0.0010	0.0001
Total		0.3815^{ns}			0.2196^{ns}			-0.4232*	
		------ TGW ------			------ DF ------				
Direct on	WG	0.2826	9.2826	WG	0.1132	1.5096			
Indirect via	CL	0.0273	0.1153	CL	0.0096	0.0141			
Indirect via	CW	0.1111	2.2417	CW	0.0082	0.0122			
Indirect via	WB+C	-0.0171	7.7206	WB+C	0.0003	0.0025			
Indirect via	CA	-0.4627	6.9191	CA	0.0575	0.1064			
Indirect via	DC	0.0195	0.3018	DC	-0.0081	0.0520			
Indirect via	WHT	-0.6002	4.5571	WHT	-0.0013	0.0000			
Indirect via	WHV	0.1399	2.9613	WHV	-0.0266	0.1072			
Indirect via	PL	-0.0080	0.0039	PL	0.0255	0.0391			
Indirect via	PW	-0.0435	2.3070	PW	0.0005	0.0003			
Indirect via	DF	0.0107	0.0115	TGW	0.0269	0.0708			
Total		-0.5165**			0.2150^{ns}				
	Coefficient of determination					0.6478			
	k-value					0.0860			
	Residual variable effect					0.3522			

(1)VIF, variance inflation factor; CL, caryopsis length (mm); WG, whole grain yield (%); CW, caryopsis width (mm); WB+C, sum of the percentage of chalky grains with white belly (%); CA, total chalky area (%); DC, percentage of defects in coloring (%); WHT, total whiteness; WHV, vitreous whiteness; PL, panicle length (cm); PW, panicle weight (g); TGW, 1,000 grain weight (g); and DF, days to flowering. ** and *Significant by the Mantel test, at 1 and 5% probability, respectively, with the bootstrap method with 10,000 simulations. ^{ns}Nonsignificant.

In this context, equipment and software for measuring grain quality attributes were developed to facilitate and generate results with a greater precision, processing information obtained from images of small amounts of rice (Yoshioka et al., 2007; Botelho, 2012; Marschalek et al., 2017). The practicality and accuracy of this procedure make it more feasible to use samples from families in segregating generations of rice to obtain genotype selection criteria for grain quality attributes.

For variables with a high correlation, Cruz & Carneiro (2006) concluded that the best strategy to be used is simultaneous selection, with emphasis on characters whose indirect effects are significant, as was the case for the sum of the percentage of chalky grains with white belly and 1,000 grain weight in the present study, with a genotypic correlation equal to -0.563 and -0.516, respectively, but a low direct effect on the response variable.

Indirect selection through the correlations shown in the present work, mainly of chalky area and total whiteness, can be effective to increase the percentage of whole grains.

Conclusions

1. Total chalky area, together with total whiteness, is the factor that most negatively influences the percentage of rice (*Oryza sativa*) whole grains according to the genotypic correlations and direct effects.
2. The variables caryopsis width, percentage of chalky grains with white belly, panicle weight, and 1,000 grain weight have indirect effects on whole-grain yield response according to total chalky area and total whiteness.

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References

AZEVEDO, A.M.; SEUS, R.; GOMES, C.L.; FREITAS, E.M. de; CANDIDO, D.M.; SILVA, D.J.H. da; CARNEIRO, P.C.S. Correlações genotípicas e análise de trilha em famílias de meios-irmãos de couve de folhas. **Pesquisa Agropecuária Brasileira**, v.51, p.35-44, 2016. DOI: https://doi.org/10.1590/S0100-204X2016000100005.

BOTELHO, N. Tecnologias pós-colheita de arroz. **Agrotec**, n.3, p.78-80, 2012.

CRUZ, C.D. Genes: a software package for analysis in experimental statistics and quantitative genetics. **Acta Scientiarum. Agronomy**, v.35, p.271-276, 2013. DOI: https://doi.org/10.4025/actasciagron.v35i3.21251.

CRUZ, C.D.; CARNEIRO, P.C.S. **Modelos biométricos aplicados ao melhoramento genético**. 2.ed. Viçosa: Ed. da UFV, 2006. 586p.

CRUZ, C.D.; CARNEIRO, P.C.S.; REGAZZI, A.J. **Modelos biométricos aplicados ao melhoramento genético**. 3.ed. rev. e ampl. Viçosa: Ed. da UFV, 2014. v.2, 668p.

FACCHINELLO, P.H.K.; STRECK, E.A.; AGUIAR, G.A.; OLIVEIRA, V.F. de; GOVEIA, J.; FEIJÓ, M.; VASCONCELLOS, M.L.; FAGUNDES, P.R.R.; CARVALHO, I.R.; MAIA, L.C. da; MAGALHÃES JÚNIOR, A.M. de. Adaptability and stability of irrigated rice elite lines for grain quality. **Brazilian Journal of Agriculture**, v.97, p.137-153, 2022. DOI: https://doi.org/10.37856/bja.v97i2.4277.

FALCONER, D.S. **Introdução à genética quantitativa**. Viçosa: UFV, 1987. 279p. Tradução de Martinho de Almeida e Silva e José Carlos Silva.

FAO. Food and Agriculture Organization of the United Nations. **World Food and Agriculture:** Statistical Yearbook. Rome, 2021. 368p. Available at: <https://www.fao.org/3/cb4477en/cb4477en.pdf>. Accessed on: Sept. 13 2023.

GU, J.; CHEN, J.; CHEN, L.; WANG, Z.; ZHANG, H.; YANG, J. Grain quality changes and responses to nitrogen fertilizer of *japonica* rice cultivars released in the Yangtze River Basin from the 1950s to 2000s. **The Crop Journal**, v.3, p.285-297, 2015. DOI: https://doi.org/10.1016/j.cj.2015.03.007.

HAIR, J.F.; BLACK, W.C.; BABIN, B.J.; ANDERSON, R.E.; TATHAM, R.L. **Análise multivariada de dados**. 6.ed. Porto Alegre: Bookman, 2009. 688p.

ISHIMARU, T.; HORIGANE, A.K.; IDA, M.; IWASAWA, N.; SAN-OH, Y.A.; NAKAZONO, M.; NISHIZAWA, N.K.; MASUMURA, T.; KONDO, M.; YOSHIDA, M. Formation of grain chalkiness and changes in water distribution in developing rice caryopses grown under high-temperature stress. **Journal of Cereal Science**, v.50, p.166-174, 2009. DOI: https://doi.org/10.1016/j.jcs.2009.04.011.

JONGKAEWWATTANA, S.; GENG, S. Non-uniformity of grain characteristics and milling quality of California rice (*Oryza sativa* L.) of different maturities. **Journal of Agronomy and Crop Science**, v.188, p.161-167, 2002. DOI: https://doi.org/10.1046/j.1439-037X.2002.00552.x.

KISHORE, N.S.; SRINIVAS, T.; NAGABHUSHANAM, U.; PALLAVI, M.; SAMEERA, S.K. Genetic variability, correlation and path analysis for yield and yield components in promising rice

(*Oryza sativa* L.) genotypes. **SAARC Journal of Agriculture**, v.13, p.99-108, 2015. DOI: https://doi.org/10.3329/sja.v13i1.24184.

LIU, Q.-H.; ZHOU, X.-B.; YANG, L.-Q.; LI, T. Effects of chalkiness on cooking, eating and nutritional qualities of rice in two indica varieties. **Rice Science**, v.16, p.161-164, 2009. DOI: https://doi.org/10.1016/S1672-6308(08)60074-8.

LONDERO, G.P.; MARCHESAN, E.; PARISOTTO, E.; COELHO, L.L.; ARAMBURU, B.B.; FLORES, C.S.; SILVA, A.L. da; Qualidade industrial de grãos de arroz decorrente da supressão da irrigação e umidade de colheita. **Irriga**, v.20, p.587-601, 2015. DOI: https://doi.org/10.15809/irriga.2015v20n3p587.

LUZ, L.N. da; SANTOS, R.C. dos; MELO FILHO, P. de A. Correlations and path analysis of peanut traits associated with the peg. **Crop Breeding and Applied Biotechnology**, v.11, p.88-93, 2011. DOI: https://doi.org/10.1590/S1984-70332011000100013.

MARCHEZAN, E.; DARIO, G.J.A.; TORRES, S. Ocorrência de grãos gessados em três cultivares de arroz. **Scientia Agricola**, v.49, p.87-91, 1992. DOI: https://doi.org/10.1590/S0103-90161992000400012.

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.

MONTGOMERY, D.C.; PECK, E.A. **Introduction to linear regression analysis**. New York: J. Wiley, 1981. 504p.

NANDAN, R.; SWETA; SINGH, S.K. Character association and path analysis in inter-racial hybrids in rice (*Oryza Sativa* L.). **World Journal of Agricultural Sciences**, v.6, p.201-206, 2010.

NARDINO, M.; SOUZA, V.Q. de; BARETTA, D.; KONFLANZ, V.A.; CARVALHO, I.R.; FOLLMANN, D.N.; CARON, B.O. Association of secondary traits with yield in maize F_1's. **Ciência Rural**, v.46, p.776-782, 2016. DOI: https://doi.org/10.1590/0103-8478cr20150253.

OLIVEIRA, O.M.S. de; SILVA, J.F. da; FERREIRA, F.M.; KLEHM, C. da S.; BORGES, C.V. Associações genotípicas entre componentes de produção e caracteres agronômicos em feijão-caupi. **Revista Ciência Agronômica**, v.44, p.851-857, 2013. DOI: https://doi.org/10.1590/S1806-66902013000400023.

RANGEL, P.H.N.; PEREIRA, J.A.; MORAIS, O.P. de; GUIMARÃES, E.P.; YOKOKURA, T. Ganhos na produtividade de grãos pelo melhoramento genético do arroz irrigado no meio-norte do Brasil. **Pesquisa Agropecuária Brasileira**, v.35, p.1595-1604, 2000. DOI: https://doi.org/10.1590/S0100-204X2000000800012.

REUNIÃO TÉCNICA DA CULTURA DO ARROZ IRRIGADO, 32., 2018, Farroupilha. **Arroz irrigado**: recomendações técnicas da pesquisa para o Sul do Brasil. Cachoeirinha: SOSBAI, 2018. 205p.

SHEN, B. Observation on the starch grain development in endosperm of early indica rice during chalkiness formation with scanning electronic microscope. **Chinese Journal of Rice Science**, v.14, p.225-228, 2000.

SILVA JUNIOR, A.C. da; SANT'ANNA, I. de C.; PEIXOTO, M.A.; TORRES, L.G.; SIQUEIRA, M.J.S.; COSTA, W.G. da; AZEVEDO, C.F.; SOARES, P.C.; CRUZ, C.D. Multiple-trait model through Bayesian inference applied to flood-irrigated rice (*Oryza sativa* L). **Euphytica**, v.218, art.124, 2022. DOI: https://doi.org/10.1007/s10681-022-03077-x.

STRECK, E.A.; AGUIAR, G.A.; MAGALHÃES JÚNIOR, A.M. de; FACCHINELLO, P.H.K.; OLIVEIRA, A.C. de. Variabilidade fenotípica de genótipos de arroz irrigado via análise multivariada. **Revista Ciência Agronômica**, v.48, p.101-109, 2017. DOI: https://doi.org/10.5935/1806-6690.20170011.

TOEBE, M.; CARGNELUTTI FILHO, A. Multicollinearity in path analysis of maize (*Zea mays* L.). **Journal of Cereal Science**, v.57, p.453-462, 2013. DOI: https://doi.org/10.1016/j.jcs.2013.01.014.

WRIGHT, S. Correlation and causation. **Journal of Agricultural Research**, v.20, p.557-585, 1921.

YOSHIOKA, Y.; IWATA, H.; TABATA, M.; NINOMIYA, S.; OHSAWA, R. Chalkiness in rice: potential for evaluation with image analysis. **Crop Science**, v.47, p.2113-2120, 2007. DOI: https://doi.org/10.2135/cropsci2006.10.0631sc.

ZHOU, L.; CHEN, L.; JIANG, L.; ZHANG, W.; LIU, L.; LIU, X.; ZHAO, Z.; LIU, S.; ZHANG, L.; WANG, J.; WAN, J. Fine mapping of the grain chalkiness QTL *qPGWC-7* in rice (*Oryza sativa* L.). **Theoretical and Applied Genetics**, v.118, p.581-590, 2009. DOI: https://doi.org/10.1007/s00122-008-0922-0.