

GENETIC PARAMETERS, CORRELATIONS AND PATH ANALYSIS IN UPLAND RICE GENOTYPES

PARÂMETROS GENÉTICOS, CORRELAÇÕES E ANÁLISE DE TRILHA EM GENÓTIPOS DE ARROZ DE TERRAS ALTAS

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ABSTRACT: Trying to obtain information relevant to the genetic improvement of rice, the aim of research was to estimate genetic parameters and identify agronomic characters directly and indirectly correlated with the grain yield of ten cultivars of upland rice. The experiment was conducted in the municipality of Aquidauana-MS, region of transition among the Savanna and Pantanal biomes. The experimental design was a randomized block with three replications. Treatments consisted of ten genotypes (BRS Aimoré, BRS Coringa, BRS Pepita, BRS Bonança, BRS Talento, BRS Maravilha, BRS Primavera, BRS Caiapó, BRS Monarca and BRS Aroma). The following variables were measured: days to flowering and maturity, plant height, number of stems and panicles, thousand grains mass and grain yield. It was determined the following genetic parameters: environmental, phenotypic and genotypic variances; coefficients of experimental and genotypic variation; heritability; b quotient; environmental, phenotypic and genetic correlations. Phenotypic correlations among traits and grain yield (principal dependent variable) were unfolded in direct and indirect effects. The population under study proved to be promising for improvement based on the traits plant height, days to flowering, thousand grains mass and grain yield. Plant height, number of panicles and thousand grains mass directly influence the yield, being recommended for direct selection of superior genotypes.

KEYWORDS: Agronomic characters. Direct and indirect effects. Genetic variability. *Oryza sativa*.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most cultivated cereal in the world, with production of 720 million tons and mean yield of 4,410 kg ha⁻¹ in the 2011/2012 harvest (FAO, 2012), having great social and economic importance for the Brazilian population (ALVAREZ et al., 2012; NASCENTE et al. 2011). In Brazil, data from Conab (2014) show that the cultivated area in 2013/2014 was 2.40 million hectares, with mean national yield of 5.096 kg ha⁻¹.

Study on genetic control of agronomic traits and heritage through genetic parameter estimates of a population allows inferring about its genetic variability and which can be expected of gain with the selection (FURTADO et al., 2002; CRUZ; CARNEIRO, 2003). The obtained estimates are used by the breeder for setting appropriate strategies in order to achieve superior genotypes, based on the most important traits (CRUZ et al., 2004; TEODORO et al., 2014).

In genetic breeding programs, it is essential the knowledge of correlations among grain yield components, since when selection is based on a trait, changes may occur in other traits of agronomic importance (SANTOS; VENCOVSKI, 1986). This

occurs because these correlations do not determine the relative importance of direct and indirect effects of the traits that make up grain yield (FURTADO et al., 2002; LYNCH; WALSH, 1998).

Path analysis proposed by Wright (1921) allows better understanding of the different trait association, through the unfolding of the correlation coefficients in direct and indirect effects on the main trait (CRUZ; CARNEIRO, 2003; CRUZ et al., 2004; HAIR et al., 2005; CORRAR et al., 2007). Estimates of these effects are obtained by regression equations, in which the variables are previously standardized. This analysis was initially used in plants by Dewey and Lu (1959). This approach has been used as an indirect criterion in the selection of several genotypes of maize (TEODORO et al., 2014), soybean (TEODORO et al., 2015), castor (TORRES et al., 2015) and cowpea (CORREA et al., 2015) for Cerrado/Pantanal ecotone region. However, for rice, researches on the traits which are directly or indirectly related to the grain yield are limited.

Thus, in order to obtain relevant information to rice crop genetic breeding, this study aimed to estimate genetic parameters and to identify agronomic traits directly and indirectly correlated with the grain yield of ten upland rice cultivars.

MATERIAL AND METHODS

The experiment was carried out in the municipality of Aquidauana, a region situated in the Savanna-Pantanal ecotone (20°27'S and 55°40'W), with average altitude of 170 m. The soil of the area is classified as Ultisol Dystrophic of sandy texture, according to the criteria established by Embrapa (2013). The chemical properties of the layer 0 - 0.20 m are: pH (H₂O) = 6.2; Al exchangeable (cmol_c dm⁻³) = 0.0; Ca+Mg (cmol_c dm⁻³) = 4.31; P (mg dm⁻³) = 41.3; K (cmol_c dm⁻³) = 0.2; Organic matter (g dm⁻³) = 19.74; V (%) = 45; m (%) = 0.0; Sum of bases (cmol_c dm⁻³) = 2.3; CEC (cmol_c dm⁻³) = 5.1. The regional climate, according to the classification of Köppen, is Aw (Savanna Tropical). The accumulated rainfall over the experiment was 433 mm, with maximum and minimum average temperatures of 28.1 and 20.4 °C, respectively.

The experimental design was randomized blocks with three replications. Treatments consisted of ten genotypes (BRS Aimoré, BRS Coringa, BRS Pepita, BRS Bonança, BRS Talento, BRS Maravilha, BRS Primavera, BRS Caiapó, BRS Monarca and BRS Aroma) from the Banco de Germoplasma da Embrapa – Centro Nacional de Pesquisa de Arroz e Feijão (Germplasm Bank of Embrapa – National Center of Research on Rice and Beans). The experimental unit consisted of four 3.0 m rows, spaced 0.40 m apart, with the two central rows of each plot as useful area.

Soil preparation consisted of a grader harrowing and two leveling harrowing. Subsequently, it was carried out mechanical opening of the grooves to a depth of 5-10 cm. Sowing was manually carried out in November 2013, with 70 seeds per meter. In order to control weeds in post-emergence, it was carried out hand weeding, from emergence until the closing of crop between lines. In the topdressing, it was applied 100 kg N ha⁻¹, whose ammonium sulphate source was applied in a continuous bead next to the lines at floral differentiation stage.

The following variables were measured: days to flowering and maturity, (DF and DM, respectively), plant height (PH), number of stems and panicles m⁻² (NS and NP, respectively), thousand grains mass (TGM), and grain yield (YIE). For determining DF and DM in the useful area of each plot, it was considered the period (days) between emergency and 50% flowering, and 90% of mature panicles, respectively. PH was measured in 15 plants per plot with the aid of a graduated scale, from the plant base on the soil surface to the extremity of the largest panicle. NS and NP were

determined by counting the number of stems and panicles in 1.0 m², within each plot. TGM was determined by manual counting, and was weighed and corrected to 13% moisture. Grain yield (YIE) was estimated in the useful area with correction to 13% wet basis, and values were extrapolated to 1 ha.

Initially, in order to verify the existence of variability among genotypes, it was carried out analyses of variance and F-test in each trait. The following genetic parameters were estimated: environmental, phenotypic and genotypic variances; coefficients of experimental and genotypic variation; coefficient of genotypic determination; heritability; b quotient; environmental, phenotypic and genotypic correlations, respectively (JOHNSON et al., 1955).

The \hat{r}_F were unfolded through path analysis, in direct and indirect effects, considering the following model: $Y = p_1X_1 + p_2X_2 + \dots + p_nX_n + p_eu$, wherein Y is the principal dependent variable; X₁, X₂, ..., X_n: are the explanatory independent variables; and p₁, p₂, ..., p_n: are the path analysis coefficients. The coefficient of determination was calculated by the expression $R^2 = p_{1y}^2 + p_{2y}^2 + \dots + p_{ny}^2$.

The matrix degree of multicollinearity X'X was established based on its number of conditions (NC), which is the ratio between the largest and the smallest eigenvalue of the matrix (Montgomery; Peck, 1981). If NC < 100, multicollinearity is weak and is not considered a problem for analysis; if 100 ≤ NC ≤ 1,000, multicollinearity is considered moderate to strong; and if NC > 1,000, the degree of multicollinearity is considered severe. All statistical analyses were carried out with the GENES software (CRUZ, 2013), according to the procedures recommended by Cruz et al. (2004).

RESULTS AND DISCUSSION

There were significant differences (p < 0.05) among the genotypes for the traits PH, DF, TGM and YIE (Table 1). Considering the existence of genetic variability in a population as a decisive factor in any breeding program (Cruz et al., 2004; Lynch and Walsh, 1998; Falconer and MacKay, 1996; Falconer et al., 1987; Falconer and MacKay et al., 1996), the studied population proved to be promising for selection and crossing works which aim at improving these traits. Similar results were obtained in other studies with rice crop (CARGNELUTTI FILHO et al., 2012; NASCENTE et al., 2011; REIS et al., 2007).

Table 1. Values of F calculated (Fc) and estimates of genetic parameters for plant height (PH), number of stems and panicles per m² (NS and NP, respectively), days to flowering and maturity (DF and DM, respectively), thousand grains mass (TGM) on grain yield (YIE) of 10 rice genotypes in Savanna-Pantanal ecotone.

Parameters	PH	NS	NP	DF	DM	TGM	YIE
Fc	8.04*	0.92 ^{ns}	1.66 ^{ns}	63.07*	1.00 ^{ns}	17.44*	16.37*
CV _e (%)	5.91	27.79	20.74	1.53	1.14	0.08	13.03
CV _g (%)	9.06	15.96	9.73	6.96	0.98	18.49	133.63
b	1.53	0.57	0.47	4.55	0.86	241.40	10.25
$\hat{\sigma}_E^2$	0.00	410.63	324.29	0.53	0.68	0.00	568.01
$\hat{\sigma}_G^2$	0.01	514.67	514.44	32.88	0.55	17.48	179,172.31
$\hat{\sigma}_F^2$	0.01	375.70	538.53	33.41	0.68	17.48	179,700.31
\hat{h}^2 (%)	87.57	23.44	39.78	98.41	25.77	99.99	99.68

^{ns} and * = not significant and significant at 5% by t-test.

In general, the estimated values of the coefficients of experimental variation denote moderate to high experimental precision (CARGNELUTTI FILHO et al., 2012), except for NP and NS, which obtained values above 20%. Coefficients estimates of genotypic variation ranged from 0.98 (DM) and 133.63% (YIE), indicating that among traits, YIE is that which shows greater variability, being highly promising for selection. This occurs due to its complex genetic inheritance resulting from the involvement of several small effect genes on the phenotype (CRUZ; CARNEIRO, 2003; FALCONER; MACKAY, 1996).

The estimate of b quotient was higher than 1.0 for PH, DF, TGM and YIE, indicating situations which enable selection for these traits according to the interpretation recommended by Vencovsky (1978). Following this trend, these traits showed heritability (\hat{h}^2) higher than 80%, reinforcing the possibility of genetic gain with selection of these traits.

It was noted that for all traits, the estimated values for variance ($\hat{\sigma}_G^2$) were close to those

obtained for phenotypic variance ($\hat{\sigma}_F^2$), and higher than those observed for environmental variance ($\hat{\sigma}_E^2$), except for the DM. This indicates greater influence of genetic components regarding environmental components in traits expression.

Estimates of negative and significant ($p < 0.05$) genotypic correlations (\hat{r}_G) were identified among PH x NS and DF x NP (Table 2). r_G showed equal sign, and in most cases, similar magnitude to its phenotypic correlations (\hat{r}_F), which indicates that the phenotypic expression is decreased before environmental influences (Cruz et al. 2004; Lynch and Walsh, 1998; Falconer and MacKay, 1996). Absence of significant r_F indicates that the selection of a trait will not result in an unwanted selection of other trait (Goldenberg, 1968; Johnson et al., 1955). Environmental correlations (\hat{r}_E) among traits with differences in magnitude and sign, regarding the respective r_G correlations, revealed that the environment favored one trait over the other (FALCONER et al., 1987; FALCONER; MACKAY et al., 1996).

Table 2. Estimates of phenotypic, genotypic and environmental correlations (r_F , r_G and r_E , respectively) among plant height (PH), number of stems and panicles per m² (NS and NP, respectively), days to flowering and maturity (DF and DM, respectively), thousand grains mass (TGM) on grain yield (YIE) of 10 rice genotypes in Savanna-Pantanal ecotone.

Traits		NS	NP	DF	DM	TGM	YIE
PH	r_F	-0.2110	-0.2398	-0.5170	0.1375	0.2596	0.0041
	r_G	-0.2980	-0.4333	-0.6453*	0.1465	0.2773	0.0000
	r_E	-0.0180	0.0585	0.3049	-0.2076	0.1068	0.2127
NS	r_F		0.4543	-0.2488	-0.1766	0.1054	0.2104
	r_G		0.5455	-0.3256	-0.2213	0.1456	0.2845
	r_E		0.5782	0.0929	0.3562	0.4187	-0.0239
NP	r_F			-0.4466	0.4387	-0.0215	-0.0826
	r_G			-0.6876*	0.4897	-0.0346	-0.1274

	r_E	-0.1673	0.3559	0.1565	-0.0539
	r_F		-0.2257	-0.5310	0.1794
DF	r_G		-0.2567	-0.5354	0.1813
	r_E		0.0247	0.2477	-0.0305
	r_F			-0.0251	-0.4083
DM	r_G			-0.1009	-0.4349
	r_E			0.0450	-0.3401
	r_F				0.2458
TGM	r_G				0.2462
	r_E				-0.4080

* = significant at 5% by t-test.

According to the criterion established by Montgomery and Peck (1982), the estimates matrix of \hat{r}_G showed weak multicollinearity, since the number of condition was equal to 24. In the presence of multicollinearity, the use of all variables in the path analysis is not an appropriate procedure,

since multicollinear traits are implicitly weighted with greater weight (CRUZ; CARNEIRO, 2003; CRUZ et al., 2004; HAIR et al., 2005; CORRAR et al., 2007). Thus, since multicollinearity was not detected, the seven traits evaluated in the path analysis were used (Table 3).

Table 3. Estimates of the direct and indirect effects of plant height (PH), number of stems and panicles per m² (NS and NP, respectively), days to flowering and maturity (DF and DM, respectively), thousand grains mass (TGM) on grain yield (YIE) of 10 rice genotypes in Savanna-Pantanal ecotone.

Effect	PH	NS	NP	DF	DM	TGM
Direct on YIE	0.7774	0.1056	0.8804	0.2367	-0.5863	0.6936
Indirect via PH	---	-0.1640	-0.1864	-0.4019	0.1069	0.2018
Indirect via NS	-0.2223	---	0.0480	0.6150	-0.0186	0.0111
Indirect via NP	-0.2111	0.4000	---	-0.3932	0.3862	-0.0189
Indirect via DF	-0.6394	-0.3077	-0.5523	---	-0.2791	-0.6567
Indirect via DM	-0.0806	0.1035	-0.2572	0.4911	---	0.0147
Indirect via TGM	0.1801	0.0731	-0.0149	-0.3683	-0.0174	---
Total (Pearson's correlation)	0.0041	0.2104	-0.0826	0.1794	-0.4083	0.2458
Coefficient of determination = 0.5844						

It is verified that selection of genotypes with higher PH, NP and TGM employ a direct effect in the increase of YIE. This fact may result in greater ease in the selection of rice genotypes, since these traits help identify the traits of interest. TGM is a highly stable trait, since the grain size is physically limited by the lemma and palea (MARCHEZAN, 1994), contributing to the obtained results. AP, in turn, directly affects grain yield, due to better utilization of light and nutrients. Similar results were obtained by Marchezan et al. (2005) and Zaffaroni et al. (1998), which observed that these are the traits that most influenced rice yield.

Coefficient of determination was 58.44%, showing similar magnitude to those obtained by

Marchezan et al. (2005). Although there is no pre-established classification for these values, it is considered as intermediaries. Thus, we recommend for future trials the assessment of a larger number of traits.

CONCLUSIONS

The population under study proved to be promising for improvement based on the traits plant height, days to flowering, thousand grains mass and grain yield. Plant height, number of panicles and thousand grains mass directly influence the yield, being recommended for the direct selection of superior genotypes.

RESUMO: Visando à obtenção de informações relevantes para o melhoramento genético da cultura do arroz, o objetivo do trabalho foi estimar os parâmetros genéticos e identificar quais caracteres agrônômicos estão correlacionados direta e indiretamente com a produtividade de grãos de dez genótipos de arroz sequeiro. O experimento foi realizado no município de Aquidauana, MS, região de transição entre os biomas Cerrado e Pantanal. O delineamento experimental foi o de blocos ao acaso com três repetições. Os tratamentos consistiram em dez genótipos (BRS Aimoré, BRS Coringa, BRS Pepita, BRS Bonança, BRS Talento, BRS Maravilha, BRS Primavera, BRS Caiapó, BRS Monarca e BRS Aroma). Foram mensuradas as seguintes variáveis: dias para o florescimento e maturação, altura de plantas, número de colmo e panículas, massa de mil grãos e produtividade de grãos. Foram estimados dos os seguintes parâmetros genéticos: variâncias ambiental, fenotípica e genotípica; coeficientes de variação experimental e genotípico; herdabilidade; quociente b; correlações ambientais, fenotípicas e genotípicas. As correlações fenotípicas entre os caracteres e a produtividade (variável dependente principal) foram desdobradas em efeitos diretos e indiretos. A população em estudo mostrou-se promissora para o melhoramento com base nos caracteres altura de plantas, dias para o florescimento, massa de mil grãos e produtividade de grãos. Os caracteres altura de plantas, número de panículas e massa de mil grãos influenciam diretamente a produtividade de grãos, sendo recomendados para a seleção direta de genótipos superiores.

PALAVRAS-CHAVE: Caracteres agrônômicos. Efeitos diretos e indiretos. *Oryza sativa*. Variabilidade genética.

REFERENCES

- ALVAREZ, R. C. F.; CRUSCIOL, C. A. C.; NASCENTE, A. S. Análise de crescimento e produtividade de cultivares de arroz de terras altas dos tipos tradicional, intermediário e moderno. **Pesquisa Agropecuária Tropical**, Goiânia, v. 42, n. 4, p. 397-406, 2012. <http://dx.doi.org/10.1590/S1983-40632012000400008>
- CARGNELUTTI FILHO, A.; MARCHESAN, E.; SILVA, L. S.; TOEBE, M. Medidas de precisão experimental e número de repetições em ensaios de genótipos de arroz irrigado. **Pesquisa Agropecuária Brasileira**, Brasília, v. 47, n. 3, p. 336-343, 2012. <http://dx.doi.org/10.1590/S0100-204X2012000300004>
- CONAB: Companhia Nacional de Abastecimento. Acompanhamento de safra brasileira: grãos, décimo levantamento, julho 2014.
- CORRAR, L. J.; PAULO, E.; DIAS FILHO, J. M. **Análise multivariada**. Atlas: FIPECAFI, 2007. 542p.
- CORREA, A. M.; BRAGA, D. C.; CECCON, G.; OLIVEIRA, L. V. A.; LIMA, A. R. S.; TEODORO, P. E. Variabilidade genética e correlações entre caracteres de feijão-caupi. **Agro@mbiente**, Boa Vista, v. 9, p. 42-47, 2015. <http://dx.doi.org/10.5327/Z1982-8470201500012252>
- CRUZ, C. D.; CARNEIRO, P. C. S. **Modelos biométricos aplicados ao melhoramento genético**. Viçosa: Editora UFV, 2003. 579p.
- CRUZ, C. D.; REGAZZI, A. J.; CARNEIRO, P. C. S. **Modelos biométricos aplicados ao melhoramento genético**. 3. ed. Viçosa: UFV, 2004. 480p.
- CRUZ, C. D. GENES - a software package for analysis in experimental statistics and quantitative genetics. **Acta Scientiarum Agronomy**, Maringá, v. 35, p. 271-276, 2013.
- DEWEY, D. R.; LU, K. H. A correlation and path coefficient analysis of components of crested wheatgrass seed production. **Agronomy Journal**, Madson, v. 51, n. 9, p. 515-518, 1959.
- EMBRAPA. **Sistema Brasileiro de Classificação de Solos**. Centro Nacional de Pesquisa em Solos, Brasília-DF: Embrapa-SPI; Rio de Janeiro: Embrapa-Solos, 2013. 353p.
- FALCONER, D. S. **Introduction to quantitative genetics**. New York: Longman, 1987. 279p.

- FALCONER, D. S.; MacKAY, T. F. C. **Introduction to quantitative genetics**. Essex: Longman Scientific and Technical, 1996. 435p.
- FAO. Food and Agriculture Organization of the United Nations. **Production – Crops**. Disponível em: <<http://faostat.fao.org>>. Acesso em: 27 de julho de 2014.
- FURTADO, M. R.; CRUZ, C. D.; CARDOSO, A. A.; COELHO, A. D. F.; PETERNELLI, L. A. Análise de trilha do rendimento do feijoeiro e seus componentes primários em monocultivo e em consórcio com a cultura do milho. **Ciência Rural**, Santa Maria, v. 32, n. 2, p. 217-220, 2002. <http://dx.doi.org/10.1590/S0103-84782002000200006>
- GOLDENBERG, J. B. El empelo de lá correlaciona em ele mejoramiento genético de las plantas. **Fitotecnia Latino Americana**, Caracas, v. 5, p. 1-8, 1968.
- HAIR JUNIOR, J. F.; ANDERSON, R. E.; TATHAM, R. L.; BLACK, W. C. **Análise multivariada de dados**. 5. ed. Porto Alegre: Bookman, 2005. 593p.
- JOHNSON, H. W.; ROBINSON, H. F.; COMSTOCK, R. E. Genotypic and phenotypic correlations in soybeans and their implications in selection. **Agronomy Journal**, Madson, v. 47, p. 477-483, 1955.
- LYNCH, M.; WALSH, B.; **Genetics and Analysis of Quantitative Traits**. MA: Sinauer Associates, 1998. 980p.
- MARCHEZAN, E. Avaliação de rendimento de engenho de arroz. **Lavoura Arrozeira**, Porto Alegre, v. 47, n. 415, p. 23, 1994.
- MARCHEZAN, E.; MARTIN, T.N.; SANTOS, F.M.; CAMARGO, E.R. Análise de coeficiente de trilha para os componentes de produção em arroz. **Ciência Rural**, Santa Maria, v. 35, n. 5, 2005.
- MONTGOMERY, D. C.; PECK, E. A. **Introduction to linear regression analysis**. 3 ed. New York: John Wiley & Sons, 2001. 504p.
- NASCENTE, A. S.; KLUTHCOUSKI, J.; RABELO, R. R.; OLIVEIRA, P.; COBUCCI, T.; CRUSCIOL, C. A. C. Produtividade do arroz de terras altas em função do manejo do solo e da época de aplicação de nitrogênio. **Pesquisa Agropecuária Tropical**, Goiânia, v. 41, n. 1, p. 60-65, 2011. <http://dx.doi.org/10.5216/pat.v41i1.6509>
- RAMALHO, M. A. P.; SANTOS, J. B.; PINTO, C. A. B. P. **Genética na Agropecuária**. 7ª ed. São Paulo: Editora Globo, 2000. 359 p.
- SANTOS, J.; VENCOVSKY, R. Correlação fenotípica e genética entre alguns caracteres agrônômicos do feijoeiro (*Phaseolus vulgaris* L.). **Ciência e Prática**, Bebedouro, v. 10, n. 3, p. 265-272, 1986.
- REIS, M. S.; SOARES, A. A.; CORNÉLIO, V. M. O.; SOARES, P. C.; GUEDES, J. C.; COSTA JÚNIOR, J. T. Comportamento de genótipos de arroz de terras altas sob sistemas de plantio direto e convencional. **Pesquisa Agropecuária Tropical**, Goiânia, v. 37, n. 4, p. 227-232, 2007.
- TEODORO, P. E.; SILVA JUNIOR, C. A.; CORRÊA, C. C. G.; RIBEIRO, L. P.; OLIVEIRA, E. P.; LIMA, M. F.; TORRES, F. E. Path analysis and correlation of two genetic classes of maize (*Zea mays* L.). **Journal of Agronomy**, New York, v. 13, n. 1, 2014. <http://dx.doi.org/10.3923/ja.2014.23.28>
- TEODORO, P. E.; RIBEIRO, L. P.; CORREA, C. C. G.; LUZ JUNIOR, R. A. A.; ZANUNCIO, A.; CAPRISTO, D. P.; TORRES, F. E. Path analysis in soybean genotypes as function of growth habit. **Bioscience Journal**, Uberlândia, v. 31, p. 794-799, 2015. <http://dx.doi.org/10.14393/BJ-v31n1a2015-26094>

TORRES, F. E.; TEODORO, P. E.; RIBEIRO, L. P.; CORREA, C. C. G.; HERNANDES, F. B.; FERNANDES, R. L.; GOMES, A. C.; LOPES, K. V. Correlations and path analysis on oil content of castor genotypes. **Bioscience Journal**, Uberlândia, v. 31, p. 1363-1369, 2015. <http://dx.doi.org/10.14393/BJ-v31n5a2015-26391>

VENCOVSKY, R. Herança quantitativa. In: PATTERNIANI E. (Ed.) **Melhoramento e produção de milho no Brasil**. Piracicaba: Marprint. p. 122-201, 2008.

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

ZAFFARONI, E.; TERRES, A. L.; BEVILAQUA, G. A. P.; ROBAINA, A. D.; LIMA, D.; SILVA FILHO, P. M. LOPES, R. Análise de caminho nos componentes do rendimento de genótipos de arroz no Rio Grande do Sul. **Pesquisa Agropecuária Brasileira**, Brasília, v. 33, n. 1, p. 43- 48. 1998.