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Selection of rice genotypes with greater seedling vigor under controlled conditions

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ABSTRACT - This study aimed to identify allele sources for seedling vigor in 65 rice genotypes, using the slantboard test in a germination chamber, and to determine the best parameter for evaluating seedling vigor. The experiment was arranged in the randomized block design with three replicate blocks. Root and primary leaf length data were collected from seedlings grown in the dark at 18 °C, 15 days after sowing and at 25 °C, ten days after sowing. The best performing genotypes for seedling vigor were included in Group 2, which contained red rice accessions. The vigor was best evaluated under controlled conditions (grown at 18 °C, 15 days after sowing) through measurements of roots and primary leaves.

Key words: Oryza sativa, Oryza glumaepatula, red rice, genetic parameters, slantboard test.

INTRODUCTION

The trait seedling vigor or the capacity of emerging rapidly from the ground or out of the water (Redoña and Mackill 1996) is desirable to be incorporated into rice cultivars. Field measurements of this trait are however troublesome owing to the strong environmental influence and since they are rather costly and labor-intensive. Jones and Peterson (1976) developed the slantboard test which allows an indirect evaluation of seedling vigor under controlled conditions by measurements of root, coleoptyl, mesocotyl, and primary leaf of seedlings grown at 18 °C, which is the water temperature in irrigated rice plantations in temperate climate. In an evaluation of 20 rice cultivars the same authors identified the length of the first leaf 15 days after germination as the trait with significant correlation with seedling vigor in the field. This methodology has been exploited by several researchers in genetic studies and for the selection of improved lines for greater seedling vigor.

Redoña and Mackill (1996) evaluated 27 rice cultivars and two segregating populations and concluded that the length of the primary leaf measured in the slantboard test was the best and least variable trait for field predictions of seedling vigor, independently of the screening temperature and in strongest correlation with vigor.

In the state of Rio Grande do Sul, low soil temperatures at rice sowing delay the seedling growth. This reduces the competitiveness with weeds, especially in red rice. In the state of Santa Catarina, where the pregerminated system prevails, seedling vigor is important for the establishment of optimal stands in the plantations, since seedlings with this characteristic emerge quickly from the water, thus reducing mortality.

Cultivars with vigorous seeds are required for cultivation areas of upland, irrigated and lowland rice of the tropical region of Brazil, where planting in dry soils is most common. The competition of the rice with weed plants is yet another barrier for the insertion of this crop in sustainable agricultural systems.

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Although red rice is considered a weed, it can be important as parent in the transference of the trait greater seedling vigor to commercial cultivars since it presents high rusticity, high competitiveness for light, water and nutrients in field conditions and produces vigorous plants. *Oryza sative* lines with gene introgression from the wild species *Oryza glumaepatula* (Rangel et al. 2005) can also be a source for this trait.

The objective of this study was to identify genotypes that could be used as sources of high seedling vigor in rice improvement from among red rice accessions and *Oryza sative* lines with gene introgression from the wild species *Oryza glumaepatula* and to establish an appropriate methodology for evaluating this trait for the conditions of rice cultivation in Brazil.

MATERIAL AND METHODS

Sixty-five genotypes derived from three distinct genetics groups were evaluated: a) genetic group 1 (GG1), with 35 lines derived from cross the cultivated species Oryza sativa (line BG 90-2) and the wild species Oryza glumaepatula (accession RS16) (Rangel et al. 2005); b) genetic group two (GG2) comprising 25 red rice accessions, seven from commercial plantations in the state of Rio Grande do Sul, one from Tocantins, three from Venezuela and 14 traditional red rice varieties; and c) genetic group three (GG3) with three commercial cultivars (Formoso, Metica 1 and BR-IRGA 413) and two elite lines (BG 90-2 and CNA 8502) used as controls. The experiment was conducted in the controlled conditions of a germination chamber by the slantboard test, in the experimental design of random blocks with three replications, in procedures described by Jones and Peterson (1976). The seeds of each genotype in evaluation were first put in assay tubes with a commercial 0.5% sodium hypochlorite (NaOCl) solution for 30 minutes. The seeds were then washed with distilled water, placed on Petri dishes with filter paper moistened on the bottom and incubated in a germination chamber model TE 401 (Tecnal) in the dark, for 30 hours, at 32 °C. After this period 30 germinated seeds were randomly collected from each genotype (10 seeds/ replication), and transferred to the slantboard test, which consisted of a tray with distilled water and several acrylic sheets. The germinated seeds were placed under felt paper, fixed with paper towel to the acrylic surface and the sheets set up on edge slantwise in the tray, in contact with the distilled water. The trays were covered with clear plastic wrap and incubated in the dark for 15 days at 18 °C and 10 days at 25 °C. After this period the length of the roots (LRoot18 and LRoot25) and primary leaves (LLeaf18 and LLeaf25) was determined.

Seedling vigor

The rice seedling vigor was estimated by variable *I*, which represents the classical selection index, where the four evaluated traits were considered equally important. Weights of one unit, corresponding to economic values in the methodology of Smith (1936) and Hazel (1943) were attributed to each trait.

The matrices of the phenotypic variance P and genetic variance G were obtained and the multivariate analysis of variance performed by the MANOVA procedure of SAS (SAS Institute 1985), which supplies the matrices with the sum of square and the product for treatment H and for error E, besides the respective degrees of freedom.

The treatments with highest *I* estimates were assumed to have the most vigorous seedlings. To estimate the variance of contrast between the indices of lines *i* and *i'*, Dii' = Ii - Ii', information on the variance of *I* and of *I* i' is required, as well as the covariance between *I* i' and *I*i'.

It can be shown that

a) $\hat{V}(Ii) = \hat{V}(Ii') = \hat{b}' \in \hat{b} / r$, where:

 \hat{b} : estimator of the vector of phenotypic weights obtained by $\hat{b} = P^{-1}Ga$, where:

a: vector of economic weights, assumed to be equal to the unit;

 \in : matrix of residual covariance;

r: number of experimental replications.

b) $C\hat{O}V(Ii,ii')=0$, for any $i'^{1}i$ value, that is, the *I* estimates of the different treatments are independent from each other.

The vigor estimates (index) were compared pairwise by the Tukey test to identify the contrasts that are equal to or surpass the minimum significant difference given by $\Delta = q \left[(1/2) \hat{V} (Dii^{\dagger}) \right]^{1/2}$, according to Pimentel Gomes (1973). The same estimates were subjected to the comparison test of Scott and Knott (1974). The estimate given by $\hat{V}(Ii)$ as "mean square of the error", with replication *r*, equal to one unit and with the number of degrees of freedom of the error of 512, corresponding to the sum of degrees of freedom of the errors of the analyses of variance of each one of the originally evaluated traits was used to adjust to the peculiarities of this test.

Importance of the traits

The relative importance of each one of the evaluated traits for the vigor determination was estimated by two alternative procedures:

a) Correlation between trait *j* and index *I*, r_{Y_jI} $r_{Y_{ij}I} = C \hat{O} V(Y_j, I) / \left[\hat{V}(Y_j) \hat{V}(I) \right]^{1/2}$ where

 $C\hat{o}V(y_j, t)$: estimator of the covariance between trait *j* and index *I*.

 $\hat{v}(y_i)$: estimator of the phenotypic variance of trait j. $\hat{v}(I)$: estimator of the variance of the index, given by $\hat{b} P^{-1}\hat{b}$

It can be demonstrated that the covariance between trait j(Y_j) and index (I)_ can be obtained by: $C\hat{O}V(Y_j, I) = \hat{b} \cdot C_j$ where C_j corresponds to the j^{-th} column of P.

b) Relative efficiency of the reduced index. According to Silva (1980), the methodology of Cunnigham (1969) pinpoints the relative efficiency of the reduced index I_{j}^{*} , obtained by the elimination of trait *j* from index *I*, which is given by $_{Ef}(t_{j}^{*}) = [(\hat{v}(t)) - \hat{b}_{j}^{*2} / W_{u}) / \hat{v}(t)]^{1/2}$, where b_{j} and W_{jj} represent the j^{-th} elements of vector *b* and the diagonal of P^{-1} , respectively.

Furthermore, the genetic and phenotypic correlations between the four traits and their respective coefficients of genetic variation, index of variation and heritability were estimated, according to Vencovsky and Barriga (1992).

RESULTS AND DISCUSSION

The coefficients of experimental variation (Table 1) varied from 7.17% for LLeaf25 to 18.25% for LRoot25, which determined a low to intermediate experimental precision (Pimentel Gomes 1973). Redoña and Mackill (1996) evaluated the primary leaf and root length in seedlings developed at 18 °C and 25 °C and obtained variation coefficients from 6 to 8%.

Apart from LRoot25, with the highest experimental

Table 1. Matrix of phenotypic covariances (P) and coefficient of experimental variation (CV) for four traits in rice

Trait								
Trait	df	LLeaf181	LRoot18 ²	LLeaf25 ³	LRoot254			
LLeaf18		0.73641*	1.02422	0.72854	0.38636			
LRoot18	128	1.02422	5.16309*	0.72228	1.91136			
LLeaf25		0.72854	0.72228	0.88241*	0.33875			
LRoot25		0.38636	1.91136	0.33875	3.05442			
CV(%)		12.69	14.91	7.17	18.25			

¹ LRoot18: length of the roots for 15 days at 18 °C;

²LRoot25: length of the roots for 10 days at 25 °C;

³LLeaf18: length of the primary leaves for 15 days at 18 °C;

⁴LLeaf25: length of the primary leaves for 10 days at 25 °C;

*The estimates of variance, in the diagonal, are significant at 1% probability by the test F

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variation coefficient, the F test showed significant differences between the treatments for the evaluated traits. LRoot25 presented the lowest genetic variation coefficient (Table 2), which indicates that it is little informative as indicator of seedling vigor, opposite to leaf length which presented high coefficients of genetic variation under both temperature regimes, which identifies it as a good indicator of the differences in vigor of the evaluated genotypes.

Assuming that these evaluated traits are sufficient to evaluate the vigor of the study genotypes, a linear combination of the same obtained by the methodology of selection index maximizes the probability of ranking them correctly in respect of the target trait. This allows a better discrimination of the same and, consequently, greater selection efficiency (Silva 1980). For the estimation of this selection index, the vector of phenotypic weights was $b' = [1.8420 \ 0.7737 \ 0.8975 \ 0.0118]$. In this vector the weight of LRoot25 (0.0118) was about 65 times lower than of LRoot18 (0.7737), for instance. This evidences the low importance of this trait for the index, in other words, for the expression of the vigor, reinforcing the information given by the coefficient of genetic variation. The estimates of the matrices of phenotypic covariance P and genetic covariance G, obtained and used to estimate the selection index are displayed in the Tables 1 and 2, respectively.

As judged by the values of index *I* (Table 3), the group of red rice accessions, GG2, is by far the most vigorous while GG3, which represents the group of cultivated varieties/lines, is the least vigorous. GG1, with 35 lines of *Oryza sativa* with gene introgression from the wild species *Oryza glumaepatula*, constituted an intermediate group, closer to GG3, which differs in the mean significantly from the former. Based on these results the conclusion may be drawn that the wild rice (*Oryza glumaepatula*) parent used represents an excellent source of vigor, since with only 12.5% of its genome present in

Table 2. Matrix of genetic covariances (G) and coefficient of genetic variation (CVg) for four traits in rice

Trait						
Trait	LLeaf181	LRoot18	LLeaf25	LRoot25		
LLeaf18	0.67925	0.97999	0.72758	0.42042		
LRoot18	0.97999	3.62908	0.73244	1.21023		
LLeaf25	0.72758	0.73244	0.85559	0.38106		
LRoot25	0.42042	1.21023	0.38106	0.51855		
CVg (%)	25.28	13.25	23.36	4.76		

1 Coded as in Table 1

the interspecific lines of GG1 it attained a significant increase of index *I*. The GG1 lines were derived from the second backcross, with BG 90-2 as recurrent parent. BG 90-2 is classified as one of the treatments with least vigorous seedlings (Table 3), but one of the lines it originated, CNAi 9930, was outstanding. The test of Scott and Knott (1974) identified and classified it in the second most vigorous group. The Tukey test in turn, at 5% probability, did not discriminate it from the second most vigorous treatment, GEN 125, the traditional red rice variety Agulha Dourado from the Ceará region.

The Scott and Knott (1974) test separated the 65 genotypes in four groups. The first consisted of red rice only, with 11 accessions. In the second, containing seven

treatments, there were six red rice accessions and one line with gene introgression from *Oryza glumaepatula*, CNAi 9930. In the third, 74.3% were interspecific lines derived from the second backcross of BG 90-2 with *Oryza glumaepatula*; 20% were red rice and 5.7% cultivated varieties. The fourth contained only one line of red rice, identified as fine long red rice, four of the five controls and eight lines with gene introgression from *O. glumaepatula*. Of the controls, Formoso and Metica 1 were the most vigorous.

LLeaf18 and LLeaf25 were strongly correlated in the phenotypic as well as genetic aspect (Table 4). In the investigation of the association between traits it is fundamental to analyze the components of residual

Table 3. Means for four traits and estimates of the index indicator of seedling vigor, and comparison of these estimates by the tests of Tukey and Scott and Knott (1974) in rice

Treatment		Evaluated trait (cm)				IndexI	Comparison	
Group	Line	LLeaf181	LRoot18	LLeaf25	LRoot25		Tukey ²	SK ³
2	GEN 146	4.97	18.83	5.19	16.03	28.57	а	а
2	GEN 125	4.47	18.80	5.30	19.20	27.75	ab	а
2	GEN 139	5.07	17.30	5.34	15.30	27.69	ab	а
2	GEN 126	4.63	17.77	5.56	17.75	27.48	ac	а
2	GEN 17	4.87	17.40	5.30	13.71	27.34	ac	а
2	GEN 19	4.57	18.30	5.07	17.42	27.32	ac	а
2	GEN 144	4.00	20.23	3.84	15.60	26.65	ad	а
2	GEN 129	4.40	17.37	5.47	15.04	26.63	ad	а
2	GEN 2	4.77	15.43	5.79	15.12	26.10	ae	а
2	GEN 11	4.80	15.40	5.40	14.66	25.77	ae	а
2	GEN 119	4.63	16.30	4.92	15.36	25.74	ae	а
2	GEN 145	4.50	15.80	4.84	15.36	25.03	af	b
2	GEN 5	3.73	16.87	5.08	15.62	24.67	ag	b
2	GEN 118	4.00	14.17	6.31	17.12	24.19	ah	b
2	GEN 752	4.43	13.97	5.33	17.91	23.97	ai	b
2	GEN 128	4.13	14.63	5.05	15.45	23.65	bj	b
1	CNAi 9930	3.63	17.60	3.08	15.49	23.25	bk	b
2	GEN 27	5.07	10.37	6.04	13.86	22.94	ck	b
2	GEN 70	3.57	13.80	5.18	17.80	22.11	d1	с
2	GEN 121	3.70	14.00	4.53	15.61	21.89	e1	с
2	GEN 40	3.90	13.37	4.66	12.04	21.85	e1	с
1	CNAi 9920-88	2.70	17.57	3.42	16.79	21.83	e1	с
1	CNAi 9924-142	3.13	15.93	3.89	13.00	21.74	e1	с
1	CNAi 9924-164	2.83	15.90	3.55	17.41	20.91	fm	с
2	GEN 680	3.63	13.73	3.65	15.06	20.77	fn	с
1	CNAi 9924-117	2.97	15.17	3.71	15.51	20.71	fn	с
1	CNAi 9924-105	2.90	15.03	3.75	14.52	20.51	fn	с
1	CNAi 9920-25	2.73	15.23	3.51	13.91	20.14	gn	с
1	CNAi 9920-60	2.77	15.57	3.12	16.34	20.13	gn	с
1	CNAi 9920-78	2.70	15.47	3.26	16.40	20.06	gn	с

to be continued

Treatment		Evaluated trait (cm)			IndexI	Comparison		
Group	Line	LLeaf18 ¹	LRoot18	LLeaf25	LRoot25		Tukey ²	SK ³
1	CNAi 9924-92	3.03	14.10	3.78	12.69	20.03	hn	с
2	GEN 120	3.50	12.10	4.42	15.20	19.95	hn	с
1	CNAi 9924-3	2.80	14.90	3.33	16.14	19.86	hn	с
1	CNAi 9920-27	2.67	15.40	3.10	16.93	19.80	hn	с
1	CNAi 9924-55	2.67	14.97	3.44	13.97	19.74	hn	с
1	CNAi 9920-92	2.77	14.27	3.63	15.71	19.58	hn	с
1	CNAi 9924-61	2.87	14.30	3.35	14.84	19.52	in	с
1	CNAi 9924-85	2.70	14.40	3.42	15.90	19.37	in	с
1	CNAi 9932	2.70	14.80	3.03	17.00	19.34	in	с
1	CNAi 9924-138	3.13	12.93	3.69	13.25	19.24	jn	с
3	Formoso	2.37	15.40	3.10	13.68	19.22	jn	с
2	GEN 13	3.23	11.80	4.29	12.93	19.09	jn	с
1	CNAi 9924-37	2.63	14.07	3.57	12.77	19.08	jn	с
1	CNAi 9920-40	2.97	13.30	3.49	16.28	19.07	jn	С
1	CNAi 9920-1	2.80	13.37	3.42	17.88	18.78	kn	С
1	CNAi 9920-55	2.63	14.00	3.18	16.33	18.73	kn	С
1	CNAi 9924-15	2.77	13.47	3.35	14.37	18.69	kn	С
1	CNAi 9924-23	2.83	13.20	3.33	13.68	18.58	kn	С
1	CNAi 9924-41	2.77	13.20	3.44	13.94	18.56	kn	С
1	CNAi 9920-74	2.57	13.67	3.30	16.79	18.46	kn	С
2	GEN 9	2.37	14.33	3.13	15.70	18.44	kn	С
1	CNAI 9920-82	2.67	13.47	3.28	12.86	18.43	kn	С
3	Metica 1	2.37	14.30	3.00	15.12	18.29	kn	С
1	CNAi 9920-62	2.83	12.50	3.22	13.23	17.94	1n	D
1	CNAi 9920-89	2.77	12.40	3.24	16.82	17.79	lo	D
3	BG 90-2	2.43	13.47	2.99	16.35	17.77	10	D
1	CNAi 9936	2.63	11.90	3.00	15.55	16.93	mo	D
1	CNAi 9935	2.47	12.20	2.90	13.53	16.75	mo	D
3	BR-IRGA 413	2.47	11.37	3.54	14.67	16.69	mo	D
1	CNAi 9931	2.50	11.47	3.23	13.27	16.53	mo	D
2	GEN 1	2.83	9.30	4.40	12.36	16.51	mo	D
1	CNAi 9934	2.30	12.00	3.08	13.33	16.44	mo	D
1	CNAi 9933	2.60	10.93	3.11	16.23	16.23	no	D
1	CNAi 9937	2.40	11.30	3.21	12.82	16.19	no	D
3	CNA 8502	1.83	9.13	3.02	9.79	13.27	0	D
	Group 1	2.77	14.00	3.35	15.01	19.11	b	-
	Group 2	4.15	15.25	4.96	15.49	24.08	a	-
	Group 3	2.29	12.73	3.13	13.92	17.05	с	-
	Mean	3.26	14.38	3.96	15.11	20.87	-	-

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¹ Coded as in Table 1 ² Estimates of I followed by the same letter did not differ significantly from each other by the Tukey test at 5% probability ³ Estimates of I grouped by the same letter did not differ significantly from each other by the test of Scott and Knott (1974) at 5% probability

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covariance. Two components can be shown: one due to the environmental covariation among, and the other due to the environmental covariation within the plots. When traits are evaluated in different experiments, as in the case of LLeaf18 and LLeaf25, or LRoot18 and LRoot25, one would expect that the component between plots would be zero. However, the component remained within the plot, where the plants of the same treatment share a common environment, causing environmental covariation. This component only disappears when the plot consists of a single individual. It may therefore be expected that the residual covariation between traits of different experiments would be lower than that observed in one and the same experiment.

Genetically, LRoot25 has a weak to intermediate association with the other evaluated traits and presents the greatest differences between the coefficients of

Table 4. Estimates of genetic (r_g) , above the diagonal, and of phenotypic (r_p) correlations, below the diagonal, for four traits in the two rice trials

Correlation	LLeaf181	LRoot18	LLeaf25	LRoot25
LLeaf18	-	0.62	0.95	0.71
LRoot18	0.53	-	0.42	0.88
LLeaf25	0.90	0.34	-	0.57
LRoot25	0.26	0.48	0.21	-
Coded as in Tabl	- 1			

¹Coded as in Table 1

phenotypic and genetic correlation. Other auxiliary parameters for the determination of the importance of the evaluated traits for the study of the vigor of the study genotypes are the variation index, θ and the genetic determination coefficient h^2 (Table 5). According to Vencovsky (1987), θ estimates of more than one unit indicate a favorable condition for selection. The genetic determination coefficient however expresses how much of the phenotypic variation can be ascribed to genetic causes. Consequently, higher h^2 estimates also express greater selection efficiency. The traits that presented the highest θ and h^2 estimates were LLeaf25 and LLeaf18, which were strongly correlated to each other (Table 5). Morais et al. (1997) mentioned the high association between θ and h^2 (Table 5), where the traits of highest h^2 estimates also presented highest θ estimates, and vice-versa. These two statistics also reinforce the lesser importance of LRoot25 for discriminating the studied treatments.

The relative importance of each one of the four study traits for the determination of index I, considered as consolidated indicator of seedling vigor, was examined more in-depth by the $Ef(l_{j}^{*})$ and $r_{Y_{j}l}$ estimates (Table 5). The first statistics corresponds to the ratio between the response to selection by the reduced index, obtained with the elimination of each one of the evaluated traits, and the response that would be obtained, based on the index obtained with all evaluated traits, at the same selection intensity. The estimates obtained for $Ef(I^*)$ did not indicate large reductions in the response to selection with the individual elimination of any one of the evaluated traits, maintaining the other three. The greatest loss of efficiency would be observed if LRoot18 were eliminated. On the other hand, there would be practically no loss of efficiency if LRoot25 were discarded.

Similar information on the relative importance of the traits can be obtained by the second statistics, $r_{Y_{j}I}$, which stands for the correlation between trait Y_j and index *I*. The $r_{Y_{j}I}$ estimates (Table 5) discriminated LRoot25, the least correlated with *I*, better from the other traits and featured LLeaf18 as the most important to determine the index. LRoot18 and LLeaf25 presented estimates of the same magnitude and slightly lower than that of LLeaf25.

Since it is not feasible to conduct the evaluations at two temperature regimes for the determination of the seedling vigor, the obtained results suggest that it would be more convenient to perform these evaluations only at 18°C, measuring leaf and root length 15 days after sowing. LLeaf18 and LLeaf 25 are highly associated and can therefore be considered redundant, while LRoot25 became dispensable by the efficiency of the reduced index obtained

Table 5. Estimates of variation index (θ), coefficient of genetic determination (h^2), efficiency of response to selection with elimination of trait *j*, ($Ef(I^*_{j})$), and the correlation between trait *j* and index *I*, ($r_{y\mu}$)

Trait	θ	h ² (%)	$Ef(I^*)$	r _{yjI}	-
LLeaf181	1.99	0.92	98.7	0.92	
LRoot18	0.88	0.70	93.6	0.81	
LLeaf25	3.26	0.97	99.6	0.81	
LRoot25	0.26	0.17	99.9	0.41	

1 Coded as in Table 1

with its omission, as much as by its low association with index *I* when considering all traits. Estimating the new index *I*', where only LLeaf18 and LRoot18 where taken into consideration, their correlation with the original index was 0.98. Among the 13 best lines identified by the two indices there was a coincidence of 92.3%, that is, only one line of the 13 most vigorous indicated by the two indices (*I* and *I*') was not common.

CONCLUSIONS

1) The red rice accessions GEN 146, GEN 125, GEN 139, GEN 126, GEN 17, GEN 19, GEN 144, GEN 129, GEN 2, GEN 11 and GEN 119 presented high seedling vigor and can be used as source of this trait in genetic rice improvement.

2) Line CNAi 9930, derived from the interspecific cross *Oryza sativa* x *Oryza glumaepatula* presented high plant vigor; it could also be used as donor parent of this trait in genetic rice improvement.

3) Evaluations of vigor under controlled conditions must be performed with seedlings developed in the dark, at 18°C, 15 days after sowing, by measurements of primary leaf and of root length.

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Seleção de genótipos de arroz para maior vigor de plântula em condições controladas

RESUMO - Visando identificar fontes com elevado vigor de plântulas foram avaliados 65 genótipos de arroz em câmara de germinação utilizando a metodologia de "slantboard test", no delineamento experimental de blocos ao acaso com três repetições. Foram coletados dados de comprimento de raiz e de folhas primárias de plântulas, desenvolvidas no escuro, a 18 °C aos 15 dias após a semeadura, e a 25 °C aos 10 dias após a semeadura. Baseando-se nas estimativas de vários parâmetros genéticos, verificou-se que o grupo 2 constituído por acessos de arroz vermelho foi destacadamente o mais vigoroso. Concluiu-se também que a melhor alternativa para avaliação de vigor em condições controladas deve ser feita em plântulas desenvolvidas no escuro, a 18 °C aos 15 dias após a semeadura, medindo-se comprimento de folhas primárias e de raízes.

Palavras-chave: Oryza sativa, Oryza glumaepatula, arroz vermelho, parâmetros genéticos, slantboard test.

REFERENCES

- Cunnigham EP (1969) Animal breeding theory. Landbruksbokhan-delen Universitetsforlaget Vollebekk, Oslo, 272p.
- Hazel LN (1943) The genetic basis for constructing selection indexes. Genetics 28: 476-490.
- Jones DB and Peterson ML (1976) Rice seedling vigor at suboptimal temperatures. Crop Science 16: 102-105.
- Morais OP, Silva JC, Cruz CD, Regazzi AJ and Neves PCF (1997) Estimação dos parâmetros genéticos da população de arroz irrigado CNA-IRAT 4/0/3. Pesquisa Agropecuária Brasileira 32: 421-433.
- Pimentel Gomes F (1973) Curso de estatística experimental. 5th ed., Nobel, Piracicaba, 430p.

- Rangel PHN, Brondani C, Rangel PN, Brondani RPV and Zimmermann FJP (2005) Development of rice lines with gene introgression from the wild *Oryza glumaepatula* by the AB-QTL methodology. **Crop Breeeding and Applied Biotechnology 5**: 10-21.
- Redoña ED and Mackill DJ (1996) Genetic variation for seedling vigor traits in rice. Crop Science 36: 285-290.
- Sas Institute Inc (1985) Sas user's guide: statistics. Version 5, SAS Institute Inc., Cary, 956p.
- Scott AJ and Knott MA. (1974) Cluster analysis method for grouping means in the analysis of variance. Biometrics 30: 507-512.
- Silva MA (1980) Melhoramento animal (índices de seleção). Editora UFV, Viçosa, 65p.
- Smith HF (1936) A discriminant function for plant selection. Annals of Eugenics Volume 7: 240-250.

- Vencovsky R and Barriga P (1992) Genética biométrica no fitomelhoramento. Editora da Sociedade Brasileira de Genética, Ribeirão Preto, 486p.
- Vencovsky R (1987) Herança quantitativa. In: Paterniani E and Viegas GP (eds.) Melhoramento e produção de milho. Vol 1, Fundação Cargil, Campinas, p. 135-214.