



BEHAVIOR AND SELECTION OF RICE ADVANCED LINES (*Oryza sativa* L.) OBTAINED BY BREEDING PROGRAM IN LOS PALACIOS

Comportamiento y selección de líneas avanzadas de arroz (*Oryza sativa* L.) obtenidas por el Programa de Mejoramiento en Los Palacios

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ABSTRACT. Low yields, climate change effects and heterogeneous culture conditions are some reasons for the development of new rice cultivars. This trial was developed with the objective of studying the behavior of sixteen advanced lines of rice under flooded conditions and to select the best for moving on to a higher stage. A Completely Randomized Design with three replications was used, the genotypes constituted the treatments and four commercial control were used. The available information was processed statistically by the combination of univariate and multivariate analysis. Results showed correlation of the yield with all their components, the cluster analysis detected that the maximum genetic diversity between types V and VI and the minimum was detected between types I and II and the regression indicated that the model had a good adjustment (93.5 %). The combination of statistical analyses used allowed to select five more promissory lines and to propose its validation.

Key words: rice, cultivars, correlations, plant breeding, yield performance

RESUMEN. Los bajos rendimientos, los efectos del cambio climático y las heterogéneas condiciones de cultivo son algunas de las razones que justifican la obtención de nuevos cultivares de arroz. Este ensayo se desarrolló con el objetivo de estudiar el comportamiento de dieciséis líneas avanzadas de arroz en condiciones de aniego y seleccionar las mejores para pasar a una fase superior. Se utilizó un Diseño Completamente Aleatorizado con tres repeticiones, los genotipos constituyeron los tratamientos y se utilizaron cuatro testigos comerciales. La información disponible fue procesada mediante la combinación de análisis univariados y multivariados. Los resultados mostraron correlación del rendimiento con todos sus componentes, el análisis de conglomerado detectó que la máxima diversidad genética se presentó entre las clases V y VI y la mínima fue detectada entre las clases I y II y la regresión indicó que el modelo tuvo un buen ajuste (93.5 %). La combinación de los análisis estadísticos utilizados permitió seleccionar las cinco líneas más promisorias y proponer su validación.

Palabras clave: arroz, cultivares, correlaciones, fitomejoramiento, rendimiento

INTRODUCTION

Rice is one of the main sources of food in the world where growing demand is awaiting production in many parts of Asia, Africa and Latin America (1). It is one of the earliest domesticated grains and is closely associated with lifestyles and culture (2). This crop covers 9 % of arable land, provides 21 % of the global human energy per capita and provides 15 % per capita protein.

Rice Genetic Improvement Programs strive and research for through diverse strategies to respond to the need to constantly increase rice yield potential. However, there have been no major advances in rice yields since 1990 (3). The limitations are related to the narrow genetic base because the rate and magnitude of genetic improvement generally depends on the amount of genetic diversity present in the germplasm (4).

Given the need to achieve food self-sufficiency in order to avoid dependence on foreign markets, which are so variable and increasingly insecure,

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Cuba is committed to increasing national production of grains and to this end diversify the production forms and stimulate small and medium scale, as well as giving land in usufruct to devote to these crops in order to substitute imports. Rising prices and increasing frequency of adverse climatic events oblige national policies to contribute to food self-sufficiency in the production of rice, beans, maize and other grains. Cuban science has a leading role in this endeavor and scientific institutions are taxed to achieve that goal. It is necessary to liberate new cultivars, more resistant and productive, establish mechanisms of defense against adverse biotic and abiotic factors and implement production systems more efficient, sustainable and non-aggressive to the environment (5).

In the country, progress has been made in recent years related to obtaining and registering rice cultivars of high yields for different conditions, resulting from the Genetic Improvement Program, which have benefited the varietal structure in the country. However, it is still insufficient for which it is necessary to strengthen the capacities and to increase the actions aimed at the obtaining of superior cultivars that possess diverse genetic sources and able to adapt to the heterogeneous conditions of culture. Based on the foregoing background, this research aims to evaluate the behavior of 16 advanced rice lines compared to four commercial controls, under the conditions of analysis and to select the ones with the best possibilities to advance to a higher phase.

MATERIALS AND METHODS

The experiment was carried out during the low rainy period 2013-2014 at Basic Scientific and Technological Unit1 Los Palacios (UCTB according its acronyms in Spanish), belonging to the National Institute of Agricultural Sciences, under flooding conditions and on a Gley Nodular Petroferric Hydromorphic soil (6). In the same, 16 advanced rice lines were studied, resulting from INCA's program of improvement of this crop, as well as four commercial controls, including INCA LP-5 and INCA LP-7 obtained from the institution where the study was carried out, as well as IACuba-31 and IACuba-32 obtained from the Grain Research Institute. These were selected taking into account their good characteristics and the high percentage of area that these cultivars occupy at the national level.

A completely randomized design with three replicates was used and the lines/cultivars constituted the treatments. The sowing was made in the field directly to trickle, in plots of 6 m², at a distance of 15 cm between rows and 50 cm between plots.

The cultural work carried out during the rice cycle (preparation of the land, planting, fertilization, irrigation and phytosanitary treatments) was carried out, according to the Technical Instructions on Rice Cultivation (7).

Taking into account the International Rice Research Institute's Standard Rice Evaluation System (IRRI) and the Varietal Description Form for Rice of the Ministry of Agriculture of Cuba, the following quantitative characteristics were evaluated prior to harvest:

- ◆ Height of plant: HP (cm)
- ◆ Number of fertile tiller: NH
- ◆ Flag leaf length: FLL (cm)
- ◆ Flag leaf blade width: FLBW (cm)
- ◆ Panicle length: PL (cm)
- ◆ Number of filled grains per panicle: GF
- ◆ Number of vain grains per panicle: GV
- ◆ 1000 paddy grain mass: Mg (g)
- ◆ Number of panicles per m²: Pm²
- ◆ Yield: R (t ha⁻¹)
- ◆ Cycle at 50 % flowering: C (days)

The panicles per square meter were also sampled once per plot, within a frame of 0,25 m². The remaining components (full grains/panicle and mass of 1000 grains) as well as the panicles were determined in 20 central panicles taken at random. The agricultural yield of the crop at 14 % moisture was calculated in an area of 1 m² and the rest of the characters were evaluated in 10 plants selected at random in each plot.

Available information was processed using Simple Classification Variance Analysis for fixed effects and the means were doped by Duncan Multiple Rank Tests. The data matrix (genotype x variable) was processed using the multivariate cluster analysis technique (using squared Euclidean distance), Pearson correlations and a multiple regression, to evaluate the magnitude and direction of the yield relationship (variable Dependent) with the remaining variables, using the Minitab version 15.0 statistical package in all cases.

RESULTS AND DISCUSSION

Statistical analysis (ANOVA) showed significant differences between genotypes evaluated for all traits (Table I). Similar results were obtained by other authors when evaluating the variability in rice germplasm (8).

Table I. Results of Analysis of Variance (ANOVA) for each of the evaluated variables

No.	Genotypes	A	NH	LHB	AHB	LP	GII	Gv	Mg	Pm ²	R	C
1	66	92,8 g	12,2 bcdef	29,1 hij	1,03 abcde	27,6 defg	101,1 fgh	23,0 b	30,8 bcd	356,0 gh	6,06 h	109,00 cd
2	83	101,9 f	14,9 a	28,5 ijk	1,20 ab	29,5 bc	109,7 defg	18,5 bcdef	29,0 k	337,3 hi	6,20 gh	108,33 d
3	90-2	114,3 b	12,2 bcdef	38,2 bc	1,04 abcde	32,1 a	154,1 a	12,0 g	31,6 a	381,3 fgh	8,16 b	112,67 b
4	105-1	110,2 cd	13,5 b	34,0 def	1,22 a	27,2 efg	105,3 fg	22,7 b	30,8 bcd	350,7 gh	6,53 defgh	110,33 bcd
5	117 a	109,8 cd	12,8 bcde	28,3 ijk	0,85 e	24,3 h	94,9 gh	18,3 bcdef	29,0 jk	364,0 gh	6,41 fgh	109,00 cd
6	S 74	107,8 de	13,0 bcd	27,3 jk	0,84 e	29,1 bcd	150,0 a	15,0 efg	30,5 cdefg	378,7 fgh	7,11 cd	111,67 bc
7	S 76	104,6 ef	12,5 bcdef	29,4 ghij	0,96 cde	29,2 bcd	107,7 efg	19,0 bcde	30,0 efghi	473,3 bc	7,06 cde	111,00 bcd
8	S 88-1	105,4 ef	11,7 cdef	30,8 fghi	0,95 cde	29,6 b	156,0 a	13,0 g	30,1 defgh	296,0 ij	6,80 cdefg	111,67 bc
9	S 81 a	110,7 bcd	11,6 def	32,4 efgh	1,03 abcde	29,5 bc	115,9 cdef	13,5 fg	29,6 hijk	445,3 bcd	7,95 b	110,67 bcd
10	S 80- 1a	107,3 de	11,8 cdef	31,6 efghi	1,02 abcde	23,9 h	109,3 defg	14,7 efg	29,3 ijk	456,0 bcd	7,15 cd	113,00 b
11	S 91 - 3	106,8 de	11,1 f	32,1 efgh	0,96 cde	27,9 bcdef	122,4 cd	13,6 fg	29,1 jk	452,0 bcd	6,48 efgh	112,33 b
12	S 99 - 2	109,9 cd	13,1 bc	34,3 de	0,92 de	29,4 bc	120,3 cde	16,7 cdefg	29,9 fghi	444,0 bcd	7,98 b	113,00 b
13	SDB	112,5 bc	13,1 bc	32,2 efgh	1,15 abc	28,4 bcde	136,6 b	12,8 g	30,9 abc	552,0 a	8,93 a	112,67 b
14	S 112	114,5 b	11,4 ef	25,7 k	1,09 abcd	28,3 bcde	127,9 bc	14,7 efg	31,4 ab	293,3 ij	6,68 cdefg	108,33 d
15	S 110-2	94,4 g	12,3 bcdef	39,8 ab	1,00 abcde	26,4 fg	69,6 j	28,8 a	27,3 l	445,3 bcd	4,95 i	99,33 e
16	S 110	127,4 a	12,8 bcde	42,0 a	0,94 cde	27,8 cdef	79,3 ij	21,7 bc	26,4 m	282,7 j	3,73 j	98,67 e
17	INCALP-5*	75,9 i	12,7 bcde	35,7 cd	1,15 abc	26,0 g	105,7 fg	15,7 defg	29,8 ghij	492,0 b	7,18 c	111,33 bcd
18	INCALP-7*	85,9 h	12,9 bcde	32,8 defg	1,12 abcd	28,6 bcde	127,0 bc	12,4 g	30,2 cdefgh	496,0 b	7,96 b	121,00 a
19	IACuba-31*	96,1 g	12,1 bcdef	29,0 hij	1,00 bcde	28,6 bcde	107,7 efg	16,0 defg	30,5 cdef	421,3 cde	7,02 cdef	110,33 bcd
20	IACuba-32*	102,4 f	11,9 cdef	30,5 ghij	1,11 abcd	24,1 h	89,8 hi	20,6 bcd	30,6 cde	405,3 efg	6,70 cdefg	112,67 b
	Media General	104,5	12,48	32,20	1,02	27,88	114,51	17,11	29,82	406,13	6,85	110,35
	Error Estándar	1,4518	0,1382	0,5692	0,0180	0,2846	3,0544	0,6461	0,1680	9,9219	0,1495	0,6301

Means with equal letters do not differ from each other (p<0,05) * Control

It can be seen that the best performance genotypes were lines 13, 3, 9, 12 and the INCA control LP-7, with significant differences between line 13 and the others, which did not differ between them. These five genotypes also showed good characteristics for the panicle performance components per square meter and 1000 grain mass and are among the highest cycle along with the other controls included in the test. The use of improved cultivars of high yield potential is an important way to reduce hunger and food insecurity in developing countries (9). Today, about 80 super-varieties of rice have been released and some of them show high grain yields of 12-21 t ha⁻¹ in 1 m² in field experiments. The main reasons for the high yields of the super varieties of rice, compared to those of the conventional cultivars, are related to more spikelets per cob and greater number of spikelets per square meter; Leaf area index, green leaf duration, photosynthesis rate, bedding resistance, accumulation of dry matter before the panicle stage, remobilization of previously stored carbohydrates from stems and leaves to grains during the period of filling grain; as well as a larger root system and better root activity (10).

They also have the highest values for final plant height, except line 12 and INCA LP-7, which are among the smaller sizes; have the widest leaves in turn, except line 12; have the highest number of fertile offspring, except lines 3 and 9 and the lowest values for the vain grain per panicle, except line 12.

The lowest yield characterized the line 16, which showed significant differences with all the others, in turn turned out to be the genotype higher and of greater length of leaf flag

The lowest yield characterized the line 16, which showed significant differences with all the others, in turn turned out to be the genotype higher and of greater length of leaf flag. As for height of the plant the range was between 85,9-124,4 cm and a mean of 104,5 cm. Only five genotypes classified as dwarfs with less than 100 cm and among them three of the controls, the rest are semen type (100-130 cm). This suggests that the selection made for this character has been successful. In analysis of variability of rice germplasm in another context they detected a wide range of variation (73-190 cm) and more than 50 % of the accessions turned out to be tall plants in the range of 131-150 cm, very few accessions classified as semi dwarf (11). A study on the biology of plant height revealed that the last internode was the most determinant in stem height, those of high height have the internodes in ascending order in length and that the dwarf plants turned out to be very low especially for mechanized harvesting (2).

In the case of panicle length, the mean value was 27,88 cm and the lowest and highest value for this character turned out to be 23,9 and 32,1 cm respectively. In one trial in China they detected a wide genetic variation for this character and ranged from 14,0 cm to over 41,0 cm (12). It is also argued that this variable contributes, but it is not the only one responsible for high yields in rice and report a range of values of 19-34 cm and a mean of 27,13 cm in length (11).

It is important to note that for the number of panicles the variation was between 12 and 29, most of the genotypes (70 %) were below 15 % of emptiness, which is the acceptable value for Indica cultivars. Only six lines and the IACuba-32 control had higher percentages. However, it should be noted that in the last sowing campaigns carried out at the Grain Agroindustrial Company Los Palacios, rice production has been affected by a higher incidence of pathogens that damage the quality of the grains and that it is contemplated that this could be related to climatic variability, among other factors.

The correlation matrix between each pair of characters is presented in Table II. In the same it can be seen that in this case the characters, height of the plant, number of fertile tiller, as well as length and width of the flag leaf did not show correlations with any other character evaluated. In a study of isogenic rice line characterization, neither was the width of the flag leaf correlated with any other character^A, although other authors have reported correlations of this variable with performance (12).

The length of the panicle appears strongly and positively correlated with the panic full grains. While the panicle-filled grains showed a strong and direct correlation with the 1000 grain mass, coinciding with what was found in studies of the same type where correlation and conglomerate analyzes were performed on twenty rice cultivars (13). Likewise, this variable correlated strongly but indirectly with the vain grains.

Strong and positive correlations showed performance with its components (panicle filled grains, mass of 1000 grains and panicles per square meter), similar results have been obtained by other authors when analyzing the correlations between performance and its components (14, 15). He also expressed a strong, but inverse relationship with panic-free grains.

^APérez, N. *Obtención de cultivares de arroz (Oryza sativa L.) resistentes a Pyricularia grisea Sacc. con buen comportamiento agronómico*. Tesis de Doctorado, Instituto Nacional de Ciencias Agrícolas, 2012, Mayabeque, Cuba, 118

Table II. Matrix of phenotypic correlations of the variables

	A	NH	LHB	AHB	LP	GII	Gv	Mg	Pm ²	R
NH	-0,061 0,797									
LHB	0,099 0,679	0,045 0,850								
AHB	-0,303 0,194	0,325 0,162	0,047 0,844							
LP	0,214 0,364	0,123 0,605	0,063 0,793	-0,041 0,864						
GII	0,137 0,563	-0,106 0,657	-0,310 0,184	-0,081 0,734	0,634 0,003					
Gv	-0,079 0,741	0,233 0,324	0,287 0,220	0,036 0,879	-0,402 0,079	-0,813 0,000				
Mg	-0,123 0,607	-0,132 0,580	-0,536 0,015	0,283 0,226	0,288 0,218	0,642 0,002	-0,482 0,031			
Pm ²	-0,438 0,053	-0,027 0,911	0,103 0,665	0,170 0,474	-0,113 0,635	0,010 0,968	-0,232 0,324	0,104 0,662		
R	-0,143 0,548	-0,036 0,880	-0,304 0,192	0,190 0,422	0,317 0,174	0,672 0,001	-0,725 0,000	0,728 0,000	0,588 0,006	
C	-0,316 0,175	-0,058 0,810	-0,411 0,072	0,185 0,436	0,138 0,562	0,606 0,005	-0,702 0,001	0,681 0,001	0,456 0,044	0,819 0,000

Cell Content: Pearson Correlation / P-Value

Another character that correlated significantly and directly was the cycle with the yield and its components, just as it did with the grains, but indirectly.

In similar investigations, other authors have reported that neither the number of fertile children showed correlations with the characters, plant height, panicle length, panicle grains and the weight or mass of 1000 grains. Also, the cycle was not correlated with the height of the plant and the length of the panicle (13).

To carry out a general study we used a Conglomerate Analysis with the data matrix conformed by means of each one of the genotypes for each variable studied. The corresponding dendrogram appears in the Figure and the means and distribution of the genotypes by classes are presented in Table III.

The twenty cultivars were grouped in six classes and the analysis revealed that the maximum genetic diversity was presented between classes V and VI and the minimum genetic diversity was detected between classes I and II. This type of assessment has been reported in related research (13).

Classes II and V concentrate the three lines with the most outstanding characteristics of the studied material (3, 6, 14), superior to the class III where the four witnesses were located in terms of the performance and its components, except in panicles per square meter in the case of lines 3 and 6.

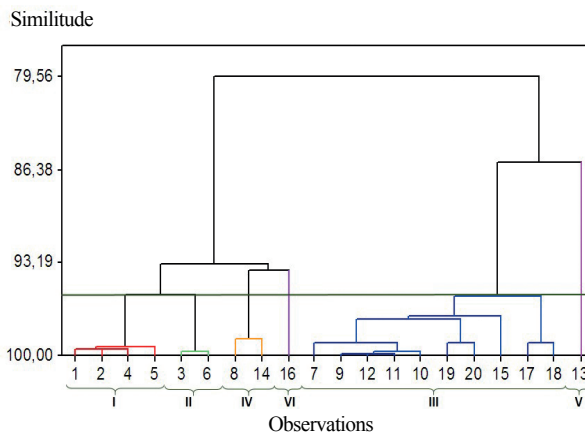


Figure. Dendrogram obtained according to the Analysis of Clusters

In addition, they were the ones with the highest cycle, with the lowest values in the vain grain category and the highest plants, only surpassed by line 16, located in class IV. It is considered that the components that determine the yield are the number of panicles per unit area, the number of grains per panicle and the weight of 1000 grains (16). Also, some authors report that rice yield and rice-related characteristics are regulated by multiple genes, which are significantly influenced by the environment (17, 18).

In addition to the controls (INCALP-5, INCALP-7, IACuba-31 and IACuba-32), lines 7,9,10,11,12,15 are found in class III with excellent performance and its components, vain grains and also show the smallest height. This latter character is related to rice bedding and some authors suggest that height reduction may improve tolerance and decrease performance losses associated with this character (11).

Class VI, integrated by line 16, presented the worst behavior in relation to the characters performance and its components, also it was turned out to have the greater height and quantity of vain grains.

Several authors have used the analysis of conglomerates in rice with different objectives and excellent results (4, 13, 19, 21).

Table III. Distribution of genotypes in effectives and means by classes, according to the Cluster Analysis

CLASSES	A	NH	LHB	AHB	LP	GII	Gv	Mg	Pm ²	R	C
I	103,68	13,38	29,98	1,07	27,15	102,74	20,61	29,88	352,00	6,30	109,17
II	111,07	12,58	32,74	0,94	30,61	152,05	13,50	31,03	380,00	7,64	112,17
III	99,41	12,19	32,78	1,03	27,36	107,54	17,09	29,62	453,07	7,04	111,47
IV	109,95	11,53	28,25	1,02	28,97	141,93	13,83	30,74	294,67	6,74	110,00
V	112,47	13,13	32,24	1,15	28,40	136,62	12,83	30,89	552,00	8,93	112,67
VI	127,40	12,80	42,05	0,94	27,85	79,33	21,67	26,40	282,67	3,73	98,67
CLASSES	LINES		EFFECTIVES								
I	1,2,4,5		4								
II	3,6		2								
III	7,9,10,11,12,15,17,18,19,20		10								
IV	8,14		2								
V	13		1								
VI	16		1								

Table IV. Results of Multiple Linear Regression Analysis where yield is the dependent variable

Parameters	Estimation	Standard error	Statistic T	P-Value	
Constant	-14,571	5,850	-2,49	0,034	
A	0,01166	0,01123	1,04	0,326	
NH	0,1887	0,1453	1,30	0,226	
LHB	0,00914	0,03310	0,28	0,789	
AHB	-0,558	1,267	-0,44	0,670	
LP	0,01268	0,07246	0,18	0,865	
GII	0,00154	0,01174	0,13	0,899	
Gv	-0,07971	0,05473	-1,46	0,179	
Mg	0,4661	0,1702	2,74	0,023	
Pm ²	0,007593	0,001812	4,19	0,002	
C	0,01792	0,04723	0,38	0,713	
Analysis of variance					
Source	Sum of squares	GL	Mean square	F	P-Value
Model	23,3214	10	2,3321	12,89	0,0000
Residue	1,6278	9	0,1809		
Total	24,9492	19			
R ²	93,5 %				

Table IV shows the results of the multiple linear regression analysis, where the yield is the dependent variable and cycle, plant height, full grains per panicle, panicle length, mass of 1000 grains and amount of panicles per meter Square were the independent variables, because these were the ones that showed the highest correlation with the dependent character.

The regression equation is:

$$R = -14,6 + 0,0117 A + 0,189 NH + 0,0091 LHB - 0,56 AHB + 0,0127 LP + 0,0015 GII - 0,0797 Gv + 0,466 Mg + 0,00759 Pm^2 + 0,0179 C$$

Since the p-value in the analysis of variance is less than 0.01; There is a statistically significant relationship between the variables for a confidence level of 99 %. The regression coefficient (R²) indicates that the model accounts for 93,5 % of the variability in yield, determining that the linear combination of the independent variables, for studies under similar conditions, is an optimal predictor of yield.

The combination of the uni and multivariate analysis facilitated the identification of the most promising lines, so it is suggested to select 3, 6 and 13 that were placed in the best classes according to the conglomerate; and to consider the results of the analysis of variance to include lines 9 and 12 that also had excellent behavior in terms of performance and some of its components. These surpass three of the witnesses included in the study, so it is proposed to pass these five lines to the validation phase. The results show the effectiveness of the Program for Improvement, the use of genetic variability and the selection technique used allowed the production of new rice lines with high productive potential.

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