

RELATIONSHIP OF YIELD WITH THE OTHER CHARACTERS IN RICE TRADITIONAL CULTIVARS COLLECTED IN PINAR DEL RÍO

Relación del rendimiento con otros caracteres en cultivares tradicionales de arroz colectados en Pinar del Río

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ABSTRACT. The research was conducted with the objective of finding a relationship among the yield, their components and other characters and providing, to specialists in rice crop, useful information for breeding programs. Eleven traditional cultivars collected in Pinar del Río province were studied, as well as commercial cultivar INCA LP-5 that have very good acceptance among growers and they were evaluated seven morphoagronomics characters during the full season crop: cycle, full and vain grains per panicle, panicle length, panicle m², 1000 grains weight and yield. The quantitative data matrix obtained (genotypes x variables) is processed by statistical multivariate techniques of Principal Components and Multiple Linear Regression, through Statgraphics Plus v.5. The analysis revealed the existence of differences among the cultivars, constituting an important genetic source to be used in the Rice Breeding Program. The equation proposed by the multiple linear regression analysis allows, through the estimated coefficients, expressing the prospective change of the dependent variable yield for each unit of change of the studied independent variables.

Key words: plant breeding, *Oryza sativa* L., multivariate technical

RESUMEN. La investigación se desarrolló con el objetivo de encontrar una relación entre el rendimiento, sus componentes y otros caracteres y proporcionar a especialistas del cultivo del arroz, información útil para los programas de mejoramiento genético. Se estudiaron once cultivares tradicionales colectados en la provincia Pinar del Río, así como, el cultivar comercial INCA LP-5 que tiene muy buena aceptación entre los productores y fueron evaluados siete caracteres morfoagronómicos durante el ciclo de desarrollo del cultivo: ciclo, granos llenos por panícula, granos vanos por panícula, longitud de la panícula, panícula por m², masa de 1000 granos y rendimiento. La matriz de datos cuantitativos obtenidos (genotipos x variables) fue procesada por las técnicas multivariadas de Componentes Principales y Regresión Lineal Múltiple mediante el Statgraphics Plus v.5. El análisis reveló la existencia de diferencias entre los cultivares, constituyendo una importante fuente genética para ser utilizadas en el Programa de Mejoramiento de Arroz. El modelo propuesto por el análisis de regresión lineal múltiple permite, a través de los coeficientes estimados, expresar el cambio esperado de la variable dependiente rendimiento para cada unidad de cambio de las variables independientes estudiadas.

Palabras clave: mejoramiento genético de plantas, *Oryza sativa* L., técnicas multivariadas

INTRODUCTION

The only important cereal that is used almost exclusively in human food is rice. It is considered one of the main sources of food in the world and sustenance for more than half of the global population. It is one of the oldest domesticated grains and is closely associated with lifestyles and culture (1,2).

Genetic diversity is the basis for the progress of plant genetic improvement and genetic resources comprise the diversity contained in the primitive, traditional, wild and improved cultivars that can be used now and in the future for agriculture and food. Plant genetic resources that are of vital importance are seriously threatened. Worldwide, traditional rice cultivars as well as wild rice species are being lost due to genetic erosion.

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Farmers often adopt new rice cultivars, which produce more grain in less time and do not sow the traditional ones they had grown for generations. The seeds of the ancient cultivars are often forgotten and many of these traditional ones are lost. However, in the future, breeders will need the genetic variation of traditional cultivars and related wild genera to cope with the many adverse factors, both biotic and abiotic, that put rice production at risk for this generation and the future ones (3).

Through various strategies, Rice Genetic Improvement Programs strive to respond to the need to constantly increase the yield potential of rice. The main limitations are related to the narrow genetic base because the pace and magnitude of genetic improvement generally depend on the amount of genetic diversity present in the germplasm (4).

The cooperative and peasant sector in Cuba includes the traditional ones within the wide range of cultivars that it sows. The aspiration of rice breeders to increase the existing national genotype is the collection of these local cultivars that farmers have traditionally planted and conserved. The selection that the producers themselves have made in a rudimentary and almost unconscious way has generated the existence of many of them that are exploited in this sector and that possess appropriate genes for the different biotic and abiotic conditions (5).

Based on the previous approaches, this work aims to find a relationship between yield, its components and other characters in traditional cultivars and provide specialists with useful information for breeding programs in rice cultivation.

MATERIALS AND METHODS

In the Scientific Technological Unit of Base (UCTB) "Los Palacios", belonging to the National Institute of Agricultural Sciences (INCA), this trial was carried out on a Gley Nodular Petroferric soil (6).

The plant material studied consists of a total of 12 genotypes, of which 11 traditional rice cultivars (*Oryza sativa* L.) collected in farms of producers from three locations in Pinar del Río province and, in addition, an improved cultivar obtained in the scientific institution where the study was carried out (Table 1).

Table 1. List of cultivars studied and their provenance

No	Cultivars	Origin
1	¾ Pulla	Mantua
2	Pulla	Mantua
3	Caracol Dima	Mantua
4	Caracol	Mantua
5	Estrella Roja Especial	Mantua
6	Agustín 1	La Palma
7	Agustín 2	La Palma
8	220	La Palma
9	Andrés	La Palma
10	Frances	San Juan y Martínez
11	Bluebonnet	San Juan y Martínez
12	INCA LP-5	UCTB Los Palacios

A completely randomized design with five replications was used and the cultivars constituted the treatments. They were planted in the field directly to drill, in plots 2 x 1,5 m (3 m²) at a distance of 15 cm between rows and 50 cm between plots. The agrotechnical tasks (land preparation, sowing, fertilization, irrigation and phytosanitary treatments) were carried out during the crop cycle, according to what is established in the Technical Instruction for Rice Cultivation (7). During the culture development cycle, seven quantitative characteristics were evaluated, using the methodologies: Standard Evaluation System for Rice, CIAT Varietal Descriptors and Varietal Description Form for Rice.

- ◆ Cycle at 50 % flowering, C (days).
- ◆ Grains filled by panicle, Gil.
- ◆ Vain grains per panicle, Gv.
- ◆ Length of the panicle, LP (cm).
- ◆ Panicle per m², Pm².
- ◆ Mass of 1000 grains, Mg (g).
- ◆ Agricultural yield, R (t ha⁻¹).

The observations were made in 10 randomly selected plants in each plot. For the qualitative variables, the value of the fashion was taken and for the variables of quantitative type they were assigned the value of the average of the measurements made. The panicles per square meter were also sampled once per plot, in a frame of 0,1 m².

The remaining components (filled grains/panicle and mass of 1000 grains) were determined in 20 central panicles taken at random and the agricultural yield of the crop was calculated in an area of 1 m². The matrix of quantitative data obtained (genotypes under study x analyzed variables) was processed by Multivariate Analysis of Principal Components (using the Euclidean distance squared), Multiple Linear Regression (considering performance as the dependent variable and the rest as independent) and Pearson's correlations, all with the help of the statistical package Statgraphics Plus v.5.

RESULTS AND DISCUSSION

Table 2 shows the phenotypic correlations (Pearson correlations) existing among the variables analyzed.

Table 2. Matrix of phenotypic correlations

	Gll	Gv	LP	Mg	Pm ²	R
C	-0,2274 0,4772	-0,0290 0,9288	0,0177 0,9564	0,0553 0,8645	0,0162 0,9602	-0,0445 0,8908
Gll		-0,5206 0,0827	0,2576 0,4188	0,5585 0,0591	0,3900 0,2101	0,7434 0,0056**
Gv			-0,1233 0,7026	-0,4921 0,1041	-0,5385 0,0708	-0,7076** 0,0100
LP				0,0945 0,7702	-0,3363 0,2851	0,1253 0,6980
Mg					0,6213* 0,0310	0,8195** 0,0011
Pm ²						0,8156** 0,0012

Cell content: Pearson correlation, P value
 * Correlation is significant at the 0,05 level
 ** Correlation is significant at the 0,01 level

The yield correlated strongly and positively with its components (panicle per square meter, filled grains per panicle and mass of 1000 grains) and negatively with the empty grains per panicle, other authors have obtained similar results (8-10). The performance character and those related to it are regulated by multiple genes, which are significantly influenced by the environment (11,12).

Strong and positive, it is also the correlation between the panicles per square meter and the mass of 1000 grains. Other authors have suggested that the mass of 1000 grains is typical of the variety, although they highlight some intracultivar variability and point out that an increase in yield can be achieved by selecting materials of greater weight in the grain (13).

Table 3 shows the results obtained from the Principal Component Analysis and the selection of the new variables for this technique was carried out based on the Cliff Criterion, which indicates that components whose own values explain 70 % or more, must be considered acceptable more than the total variance.

Table 3. Result of the Principal Component Analysis for the variables studied

	C1	C2
Proper values	3,52047	1,29409
% contribution	50,292	28,487
% accumulated	50,292	78,779
C	0,0288	-0,2309
Gll	-0,4124	0,3281
Gv	0,4127	-0,0440
LP	-0,0482	0,7977
Mg	-0,4483	-0,0235
Pm ²	-0,4254	-0,4473
R	-0,5238	0,0041

An accumulated variance of 78,77 % was detected in the first two components. The variables that best explained the variance in the first component (50,3 %) were the yield, the number of filled and empty beans per panicle and the mass of 1,000 grains, which were related to each other in a negative way; while the second component extracted a variance of 28,48 %, which was explained by the characters length of the panicle (positively) and panicles per m², negatively.

The Figure shows a great dispersion in the location of the genotypes, which could be given by the diversity of these materials, not allowing the realization of any type of grouping.

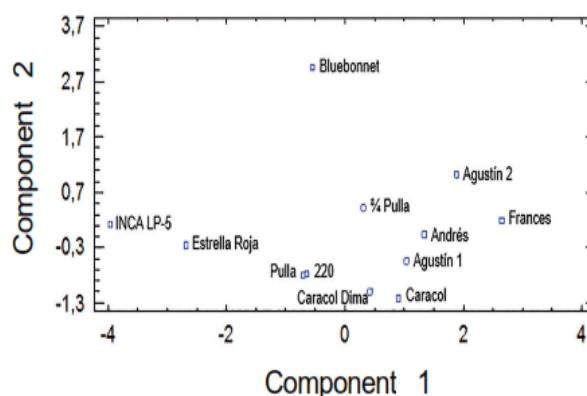


Figure 1. Distribution of the genotypes studied for the first two components

According to the distribution of the cultivars, in the extreme left of component 1 where the individuals with higher values in terms of yield, mass of 1000 grains and full grains per panicle are found and also have less amount of empty grains per panicle they are the cultivate INCALP-5 and Estrella Roja. On the contrary, the genotypes found at the other end reached the highest values for the variable vain grains per panicle.

The variability in yields was wide, with values between 1,70 and 6,10 t ha⁻¹, for the cultivars Frances and INCALP-5 respectively. Likewise, the cultivars Estrella Roja, Pulla and 220 showed good behavior, the rest presented low values for this character. This could be due to the diversity of its genetic constitution. In addition, climatic conditions such as precipitation, temperature, solar brightness, specifically at the time of flowering, can decrease yields of rice varieties (5). Bluebonnet, away from the rest at the upper end of component 2, has the longest panicles. The length of the panicle presented an average of 22.19 cm, the minimum and maximum were 18,57 and 32,35.

The number of full grains fluctuated between 53 and 81, with INCALP-5 having the best performance. This component is considered very important to obtain good yields and the climatic conditions can be the causes of which a greater number of them are formed (5).

The cultivars Frances, Agustín 2, Andrés and Agustín 1 had the highest amount of empty beans per panicle. Several causes are known that affect the roaming of rice grains, among which are those related to plant health (different causal agents, use of hormonal herbicides in the stage of fertilization and grain filling), but also agrochemicals (insufficiency or nitrogen excess, deficit of micronutrients), genetic (not

full emersion of the panicles and fertilization capacity) and climate (relative humidity, strong and dry winds, drought and temperature).

INCALP-5 and Estrella Roja exhibited the highest number of panicles per square meter, greater than 300. This performance component is the most variable and has been the main cause that has limited it in Cuban conditions. Its values are closely related to the quality of soil preparation and sowing, the sowing norm, the tillering capacity of cultivars, water management and nitrogen fertilization.

Regarding the cycle, the average was 145 days; the shortest period was INCALP-5 and Andrés, differing from the rest.

Table 4 shows the results of the multiple linear regression analysis, where the yield is the dependent variable and the cycle, the height of the plant, the filled grains per panicle, the length of the panicle, the mass of 1000 grains and the number of panicles per square meter were the independent variables, as these were the ones that showed the highest correlation with the dependent character.

The model proposed by the multiple linear regression analysis allows, through the estimated coefficients, to express the expected change of the dependent variable yield for each unit of change of the independent variables studied. 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 variable "cycle" of the plant presents p-value of 0,8841 the highest in the independent variables, thus being the least information that contributes to the model.

Table 4. Results of Multiple Linear Regression Analysis where performance is the dependent variable

Parameter	Estimation	Standard error	Statistical T	P-Value	
Constant	-4,78126	2,02686	-2,35895	0,0648	
C	-0,00137155	0,00894442	-0,153341	0,8841	
GII	0,0391833	0,01567	2,50053	0,0545	
Gv	-0,0228881	0,0201331	-1,13684	0,3071	
LP	0,0703946	0,0325113	2,16523	0,0826	
Mg	0,10714	0,0517588	2,06998	0,0932	
Pm ²	0,00845627	0,00188705	4,48121	0,0065	
Variance analysis					
Source	Square sum	GL	Mean square	F	P-Value
Model	16,5516	6	2,75859	27,58	0,0011
Residual	0,500105	5	0,100021		
Total	17,0517	11			
R ²	97,0671				

The R_2 statistic indicates that the model explains 97,06 % of the variability in performance, determining that the linear combination of independent variables, for studies under similar conditions, is an optimal predictor of performance. In different investigations other authors have used this analysis with good results (14).

In characterizations of genotypes made in Japan (15), Bluebonnet expresses values that suggest that it is the same cultivar found in Pinar del Río. During the 50s the predominant rice cultivars were of the American type and among the most cultivated were Bluebonnet 50, Bluebelle, Century Patna, among others. Similar researches have been developed by other authors, confirming the existence of great genetic diversity (16,17).

The prediction equation of the model is:

$$R = -4,78126 - 0,00137155 * C + 0,0391833 * GII - 0,0228881 * Gv + 0,0703946 * LP + 0,10714 * Mg + 0,00845627 * Pm^2$$

Native and traditional cultivars have been cultivated for long periods of time by farmers and have developed adaptive capacities to local conditions, which is why several authors have agreed on the importance of this type of study for breeders and farmers, since it allows identifying and selecting beneficial genes for crop improvement. The large-scale extension of modern high-yielding cultivars has replaced traditional cultivars in irrigated rice, reducing their genetic base and increasing their vulnerability (5,18).

CONCLUSIONS

- ◆ The results revealed the existence of differences between the cultivars, constituting an important genetic source to be used in the Rice Improvement Program, especially the cultivars Andres, Bluebonnet, Estrella Roja and Caracol that show interesting characters such as precocity and length of the panicle, used as parents could contribute to obtain progress in offspring. Estrella Roja genotype had greater similarities with the improved cultivar INCA LP-5 included in the study.
- ◆ It is recommended to use the traditional rice cultivars in the Program of Improvement to increase the diverse sources of parents and the variability in the improved genotypes and incorporate them into the Germplasm Bank to guarantee their conservation and future employment.

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