

GENETIC BASE OF CUBAN RICE VARIETIES RELEASED BETWEEN 1972 AND 1993

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ABSTRACT. The present work was aimed at studying of the genetic base of Cuban rice breeding program and the genetic relationships among Cuban rice varieties, released during 1972 to 1993. Results showed that the genetic base of this program was composed by 32 landraces, 18 of them contributing to genetic base of the cultivars during all this period, and thus, could be considered as the core group. The genetic base was partially coincident with other foreign rice programs: 45, 49 and 82 % of them also contributed to rice breeding genetic base in the United States, Colombia and Central America, respectively. A UPGMA dendrogram, based on pairwise genealogical distances, separated three varietal groups and two independent varieties, "Perla de Cuba" and "Caribe 1". The genetic information is discussed as a means to assist traditional progeny analysis in the parental selection and to design strategies to widen the present genetic base by introducing new genetic sources.

RESUMEN. En el presente trabajo se estudió la base genética del programa de mejoramiento arrocero en Cuba y el parentesco de las variedades de arroz obtenidas para la producción entre 1972 y 1993. Los resultados mostraron que la base genética del programa proviene de 32 cultivares ancestrales, 18 de estos contribuyeron durante todo este período y por ello se consideraron como el núcleo de la constitución genética del arroz en Cuba. La base genética fue parcialmente coincidente con la de otros programas foráneos: el 45, 49 y 82 % de estos además contribuyeron a la constitución genética de los programas de mejora genética del cultivo en Estados Unidos, Colombia y Centro América, respectivamente. Un análisis de conglomerado basado en las distancias genealógicas pareadas separó tres grupos varietales y dos variedades independientes, Perla de Cuba y Caribe 1. Los resultados son discutidos como una vía para asistir el análisis de progenie tradicional en la selección de progenitores y para desarrollar estrategias dirigidas a ampliar la actual base genética por medio de la introducción de nuevas fuentes genéticas.

Key words: genetic inheritance, rice, *Oryza sativa*, plant breeding, genetic distance

Palabras clave: herencia genética, arroz, *Oryza sativa*, fitomejoramiento, distancia genética

INTRODUCTION

A narrow genetic base, due to the use of a reduced number of ancestors and closely related cultivars as parents, is one of the most important limiting factors of the genetic progress in crop breeding (1). On the other hand, to enhance the breeding genetic base and to use it efficiently, a reliable genetic diversity estimate is required (2).

The coefficient of parentage (3), defined as the probability that a random gene from one individual is identical by descent with a random gene from another

individual, has been traditionally used to assess genetic diversity in crop species. An important number of works have been conducted to improve the precision of genetic relationship estimates (4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17).

Genetic diversity analysis in rice crop was primarily developed in 1979 (18). These authors showed the prevalence of a unique cytoplasm source in cultivars planted in Asian countries. Another author (9), studying 140 varieties from the United States rice germplasm, demonstrated that only 22 and 23 Asiatic ancestors contributed to the genetic base of cultivated varieties in the southern and western regions of this country. More recently, it has been reported that 14 ancient cultivars contributed nearly to 70 % of the genes present in irrigated rice in Latin America and the Caribbean (11).

Commercial rice germplasm in Cuba is composed by varieties introduced from the United States, the Philippines, Thailand, Colombia and Peru, additionally to those obtained *in situ*. The present study is aimed to determine the genetic base composition and relationships among Cuban rice varieties, released by the Rice Research Institute (IIA) during 1972 to 1993.

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MATERIALS AND METHODS

Twenty-six varieties, released during 1972 to 1993 by the breeding program conducted at IIA, were studied (Table I).

Pedigrees of each variety were obtained from hybridization programs reports at IIA, the International Center of Tropical Agriculture (CIAT) and other sources (18, 19, 20).

To determine the core group of the genetic base, it was calculated for each ancestor using the following indexes: percentage of participation, percentage of genetic contribution and average participation frequency (11). Four periods were considered: from 1972 to 1982, characterized by the exploitation of varieties selected in Cuba from segregants obtained in other countries (ex: the Philippines, Colombia, Thailand and Peru); from 1982 to 1987 and 1988 to 1993, corresponding to the release of cycle Cuban varieties with one exception, "Perla de Cuba", and the total period from 1972 to 1993.

The percentage of participation was calculated as the number of cultivars where the ancestor was present expressed as percentage. The genetic contribution was calculated, for each pair of ancestors and cultivars, as the total probability of two common alleles being identical by descent, considering the number of generations (n) between them and 50 % of gene transmission in each generation ($\frac{1}{2}^{n-1}$). The percentage of genetic contribution of each ancestor was estimated, averaging its individual contribution to the varieties considered in a period.

Ancestors with increased indexes in successive periods were considered as a member of core group.

The genetic relationship between all possible pairs of cultivars was estimated by the coefficient of parentage (3).

$$r_{ij} = \frac{\sum \left(\frac{1}{2}\right)^{n_1+n_2} \times (1 + F_A)}{\sqrt{(1 + F_i)} \times \sqrt{(1 + F_j)}}$$

where: r_{ij} is the coefficient of parentage between individuals i and j ; n_1 and n_2 are the path numbers from ancestor to individuals i and j ; F_A , F_i and F_j are the coefficients of ancestry of ancestor, individuals i and j , respectively.

Coefficient of parentage (r_{ij}) was calculated assuming the following: *i*) all ancestors, cultivars, and parental lines were homozygous and homogeneous; *ii*) a cultivar derived from a single cross; half of its genes obtained from each parent ($r_{ij} = 0.50$); *iii*) the ancestors were unrelated to each other ($r_{ij} = 0$); *iv*) the r value between a selection from a cultivar and the cultivar equaled 0.75; and *v*) the r value between two selections from the same cultivar was $r_{ij} = (0.75)^2 = 0.56$ (21).

Genealogical distances between all possible genotype pairs were calculated (22). As the differences of magnitudes of the genealogical distance estimates, expressed as complement of r_{ij} , were small, they were transformed as: $GD_{ij} = e^{(1-r_{ij})} - 1$. A cluster analysis was performed based on the matrix of distance estimates using the computer package NTSYS-pc (23) with the unweighed pair group arithmetic mean (UPGMA) method.

Table I. Rice varieties developed by Cuban rice breeding program at IIA during 1972 to 1993

No	Varieties	Nomination year	Parents	Origin
1	IR-880C9	1972	IR-8 ³ /IR-749	Philippines
2	IR-1529ECIA	1979	IR-305/IR-24	Philippines
3	P-723	1980	IR-930-2/IR-882-432	Colombia
4	Jucarito-104	1981	IR-480-5-9-2 / IR-930-16-1	Peru
5	Caribe 1	1981	Selection from unknown variety	Thailand
6	Caribe 7	1981	IR-8/CEB29	Peru
7	CP1-C8	1983	Cica-4 / IR-24	Cuba
8	Amistad-82	1984	IR-1529ECIA / VNIIR3223	Cuba
9	CP3-C2	1985	IR-880C9 / IR-1529ECIA	Cuba
10	ECIA31-2005	1985	IR-1529ECIA / IR-759-54-2-2	Cuba
11	ECIA24	1987	IR-1529ECIA / VNIIR3223	Cuba
12	ECIA31-2006	1991	IR-1529ECIA / IR-759-54-2-2	Cuba
13	Perla de Cuba	1991	Selection from unknown variety	Unknown
14	IACuba-14	1991	CP1-C8 / ECIA-22-8-163	Cuba
15	IACuba-15	1991	CP3-C2/ECIA-13-31 // CP1-C8/CE4-10-1	Cuba
16	IACuba-16	1991	PNA46-110 / CP1-C8	Cuba
17	IACuba-17	1992	Jucarito-104 / Century Patna	Cuba
18	IACuba-18	1992	IRA13/ECIA31-104-2-1-2 // Amistad-82	Cuba
19	IACuba-19	1992	Jucarito-104 // Jucarito-104/Cica8	Cuba
20	IACuba-20	1993	ICA-10 / ECIA-31-104-2-1-2	Cuba
21	IACuba-21	1993	Mutant line derived from Jucarito-104	Cuba
22	IACuba-22	1993	Mutant line derived from Jucarito-104	Cuba
23	IACuba-23	1993	Mutant line derived from Jucarito-104	Cuba
24	IACuba-24	1993	Jucarito-104/ICA-10 // Jucarito-104/Siguaraya	Cuba
25	IACuba-25	1993	Somaclone from Amistad-82	Cuba
26	IACuba-26	1993	Somaclone from Jucarito-104	Cuba

RESULTS AND DISCUSSION

A combined genealogical tree of 24 varieties developed by Cuban rice breeding program during 1972 to 1993 is shown in Figure 1. This tree evidenced that 52 varieties or breeding lines and 32 landraces compose the genetic base of this program. 29 landraces provided 90 % of the total genetic constitution of the released varieties and were originated in 15 countries. Three landraces of unknown origin provided the remaining 10 % (Table II).

The extension of the Cuban rice genetic base is similar to the one of the Colombian programs (19), and it is slightly greater than those of the rice breeding programs in the United States and Central America. Some authors (9) found that 22 and 23 landraces contributed to the genetic constitution of released varieties in the South (Arkansas, Louisiana, Mississippi, Missouri, and Texas) and West

(California) of the United States, respectively. Others (20) found that the number of landraces that contributed to the genetic base of rice breeding programs in Central America was variable. Thus, 11, 12, 18, 27, 28 and 29 landraces contributed to release cultivars in Costa Rica, Nicaragua, Honduras, El Salvador, Panamá and Guatemala, respectively.

Many landraces presented in Table II were also ancestors contributing to rice breeding programs of Nicaragua (73 %), Costa Rica (73 %), Guatemala (72 %), El Salvador (67 %), Panamá and Honduras (61 %). On the contrary, only 50 % of these landraces were ancestors of Colombia varieties, whereas 44 and 38 % were also ancestors of the varieties released in the South and West of the United States, respectively. These results point to the convenience of varietal interchange from Colombia and USA to widen the genetic base of Cuban rice germplasm.

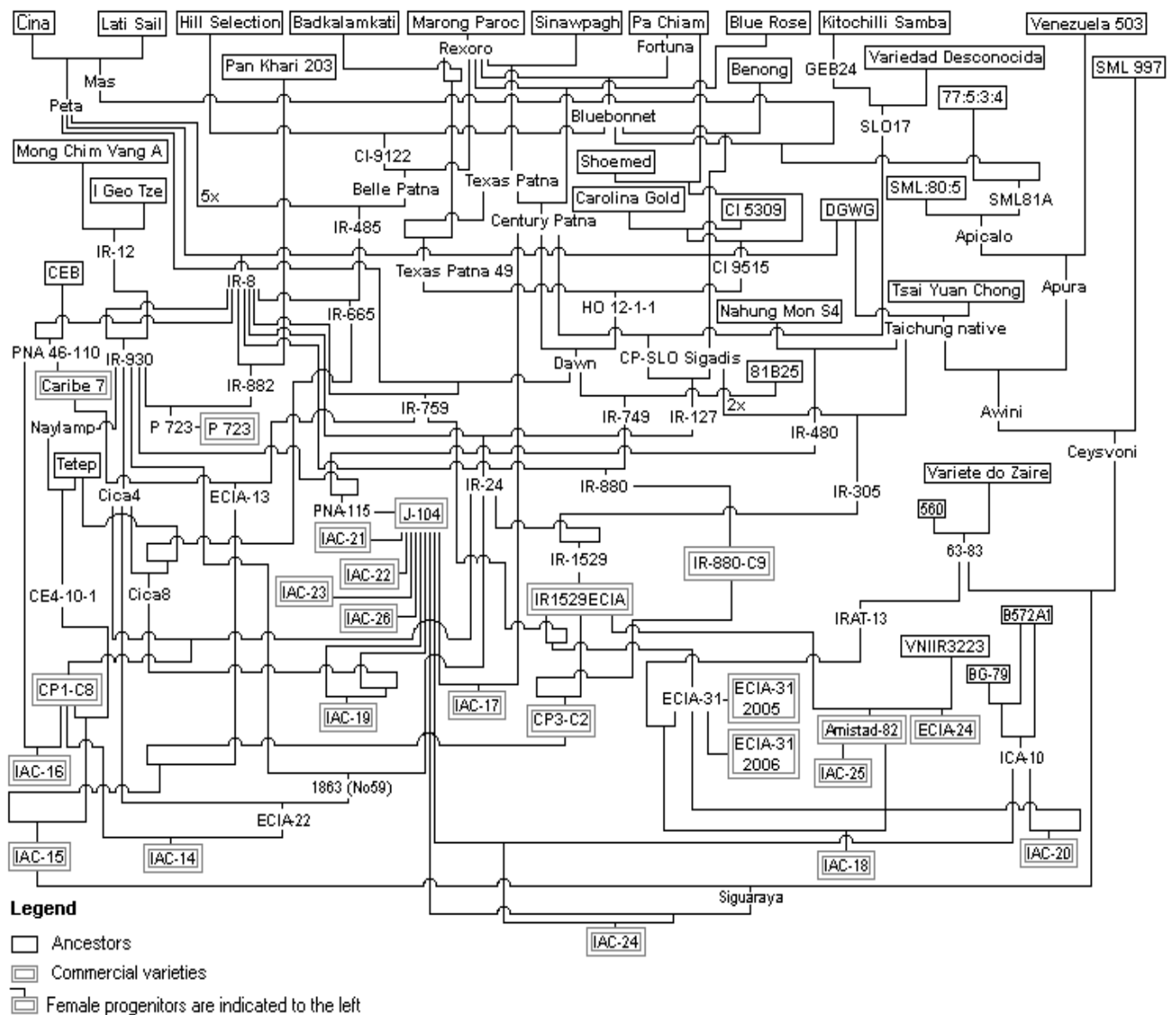


Figure 1. Combined genealogical tree of the 24 varieties released by the rice breeding program of IIA between 1972-1993

Table II. Participation indexes of landraces composing the genetic base of Cuban rice

Landraces	Origin	Percentage of genetic contribution ^a	Percentage of participation ^b
Dee Geo Woo Gen	China	21.01	100
Cina	China	9.20	100
Lati Sail	India	9.20	100
VNIIR3223	Russia	6.58	16
Marong Paroc	Philippines	6.45	84
Benong	Indonesia	5.04	68
Mon Chim Vang A	Vietnam	4.81	47
I Geo Tze	China	4.81	47
Tsai Yuan Chong	Philippines	4.65	68
CEB	Unknown	4.32	21
Nahug Mon S4	Thailand	3.62	21
B572A1-6-3P	Unknown	2.96	10
Pa Chiam	China	2.81	79
81B25	Unknown	2.16	21
Sinawpagh	Philippines	1.99	79
Blue Rose	Unites States	1.73	79
Pan Khari 203	India	1.31	5
Kitchilli Samba	India	1.11	74
Unknown variety	India	1.11	74
Tetep	Vietnam	1.07	16
BG-79	Sri-Lanka	0.99	10
560	Liberia	0.82	10
Variete do Zaire	Zaire	0.82	10
CI5309	China	0.26	42
Carolina Gold	Madagascar	0.26	42
Shoemed	Philippines	0.26	37
Badkalamkati	Bangladesh	0.26	37
SML997	Surinam	0.16	5
Venezuela 503	Venezuela	0.04	5
Hill Selection	Unites States	0.02	5
SML80:5	Surinam	0.02	5
77:5:3:4	Surinam	0.01	5

a: assuming 50 % contribution of each parent in a single cross
b: Somaclones, mutants, “Caribe-1” and “Perla de Cuba” varieties were excluded from this analysis. Then, percentages were calculated considering a total number of 19 varieties

A group of 18 landraces, from eight countries were present in at least one cultivar released along the three periods considered (Table III), and their participation indexes increased in successive periods (Figure 2).

Supported by these results, it was considered the core group of Cuban rice breeding (11), which provided 77 % of the total genetic constitution of the released varieties, mainly conferring genes for the adaptation to general rice growing conditions, grain quality and blast resistance. Landraces as Dee Geo Woo Gen, Cina, Lati Sail, Marong Paroc, Benong, Mon Chim Vang A, I Geo Tze and Tsai Yuan Chong, particularly the first three ones, were the most important. Dee Geo Woo Gen and Cina provided the dwarfing gene and cytoplasm to IRRI-varieties (18), respectively. It has also indicated that Marong Paroc and Pa Chiam provided the genes for grain

quality to Latin America rice germplasm (11) and, probably, to Cuban cultivars.

Additionally, 15 landraces originated from eleven countries contributed to release cultivars in specific periods (Table IV). The overall contribution of these landraces was relatively smaller. This group provided 23 % of the total genetic constitution of the released varieties. However, the contribution of some landraces for specific cultivars reached up to 50 % of their genetic constitution. It is the case of the contribution of VNIIR3223 to varieties Amistad-82 and ECIA-24, and CEB to variety Caribe 7.

The most important landraces of this group were those conferring resistance genes to diseases. Tetep and IRAT-13 were commonly used in Latin American rice breeding programs, including Cuban program, as blast resistance sources. Dawn variety has been used in Cuban program to introduce blast resistance gene from CI-5309 landrace (see Table III). Any source of resistance to “Hoja Blanca” virus is present in the genetic base of Cuban breeding program, which indicates the necessity to introduce and study genetic sources for this character.

The coefficient of parentage pairwise estimates are presented in Table V. Considering the lower limit of inbreeding as $r_{ij}=0.125$ (24), Cuban commercial germplasm has a high level of inbreeding as estimates ranged from 0 to 0.82 with a mean value of 0.22; 68 % of pair combinations were closely related ($0.125 < r_{ij} < 0.81$), and the remaining 32 % showed a distant relationship ($0 < r_{ij} < 0.125$).

It was also found (20) that average of r_{ij} for Central America is 0.28; this value is very similar to others reported for Latin American germplasm (11). These results indicate that the genetic diversity of Cuban rice varieties is similar to those disposed by other breeding programs in the region.

Cluster analysis results based on genealogical distance estimates are presented in Figure 3. Three varietal groups (I-III) and two independent varieties “Perla de Cuba” and “Caribe-1” could be considered. Average distance among groups are: I-II 0.77; I-III 0.81; and II-III, 0.89. The presence of these groups denoted genetic diversity among Cuban varieties. This information could be useful to assist phenotypic and progeny evaluations to select parents for breeding purposes.

Present results also confirmed the use of a limited number of female cytoplasm sources and of a reduced number of parents as the main causes of consanguinity in Cuban rice germplasm. Increased or decreased genetic diversity is not *per se* an objective for plant breeders, but a by-product of crossing and selection according to selection criteria. In rice breeding, the maintenance of crop quality have tended to decrease diversity. It has been also a trend in Latin American rice breeding programs (11). Although genes for yield components in wild related species (25) have been identified, breeders are reluctant to use them, as long-lasting introgression programs are required to obtain improved parents for the breeding program.

Table III. Landraces contributing to genetic constitution of Cuban rice varieties, during the periods considered. Core group

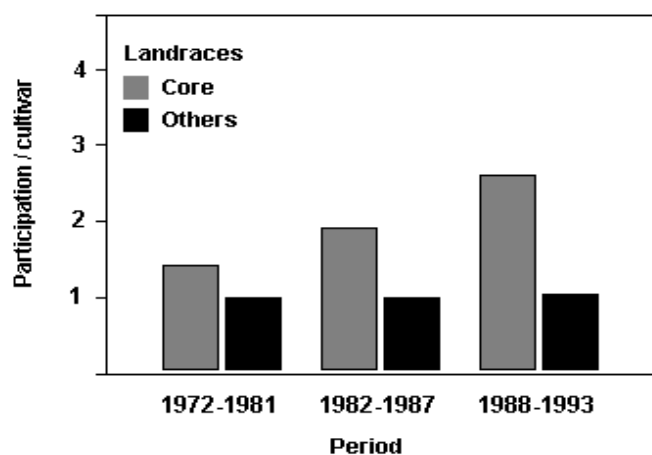
Landraces	Period from 1972-1981		Period from 1982-1987		Period from 1988-1993		Period from 1972-1993	
	% Particip. [†]	% Contrib.*	% Particip. [†]	% Contrib.*	% Particip. [†]	Contrib.*	Particip. [†]	Contrib.*
Dee Geo Woo Gen	100	25.0	100	20.0	100	19.35	100	21.01
Cina	100	10.0	100	8.75	100	9.01	100	9.20
Lati Sail	100	10.0	100	8.75	100	9.01	100	9.20
Marong Paroc	40	4.06	100	8.11	100	6.87	84	6.45
Benong	20	3.75	100	8.75	78	3.69	68	5.04
Mon Chim Vang A	40	5.00	20	2.50	67	5.99	47	4.81
I Geo Tze	40	5.00	20	2.50	67	5.99	47	4.81
Tsai Yuang Chong	40	5.00	80	5.00	78	4.27	68	4.65
Pa Chiam	40	2.19	100	4.68	89	2.11	79	2.81
81B25	20	5.00	20	2.50	22	0.39	21	2.16
Sinawpagh	40	1.25	100	1.87	89	2.47	79	1.79
Blue Rose	40	0.94	100	1.56	89	2.27	79	1.73
Kitchilli Samba	20	0.62	100	1.87	78	0.97	74	1.11
Unknown variety	20	0.62	100	1.87	78	0.97	74	1.11
CI5309	20	0.31	40	0.31	55	0.20	42	0.26
Carolina Gold	20	0.31	40	0.31	55	0.20	42	0.26
Shoemed	20	0.31	40	0.31	55	0.20	37	0.26
Badkalamkati	20	0.31	40	0.31	55	0.20	37	0.26
Total	-	79.67	-	79.95	-	74.16	-	76.93

Table IV. Landraces contributing to genetic constitution of Cuban varieties in specific periods of Cuban rice breeding program

Landraces	Period from 1972-1981		Period from 1982-1987		Period from 1988-1993		Period from 1972-1993	
	% Particip. [†]	% Contrib.*	% Particip. [†]	% Contrib.*	% Particip. [†]	Contrib.*	Particip. [†]	Contrib.*
VNIIR3223	-	-	40	20.0	11	2.77	16	6.58
CEB	20	10.0	-	-	33	3.56	21	4.31
Nahung Mon S4	20	5.00	-	-	33	4.86	21	3.62
B572A1	-	-	-	-	22	6.25	10	2.96
Pan Khari 203	20	5.00	-	-	-	-	5	1.31
Tetep	-	-	-	-	33	2.26	16	1.07
BG-79	-	-	-	-	22	2.08	10	0.99
560	-	-	-	-	22	1.73	10	0.82
Variete do Zaire	-	-	-	-	22	1.73	10	0.82
SML 997	-	-	-	-	11	0.35	5	0.16
Venezuela 503	-	-	-	-	11	0.09	5	0.04
Hill Selection	-	-	-	-	11	0.04	5	0.02
SML 80:5	-	-	-	-	11	0.04	5	0.02
77:5:3:4	-	-	-	-	11	0.02	5	0.01
Total	-	20.00	-	20.00	-	25.78	-	22.73

(†) Percentage of the total number of cultivars (19) that had the corresponding landraces as an ancestor

(*) Average percentage of genetic contribution of genes from the corresponding landraces to each cultivar for which it was an ancestor

**Figure 2. Participation frequency of landraces in the parentage of Cuban varieties**

Data presented here show the need to widen the genetic base of Cuban rice cultivars. The introduction of new cytoplasm sources and landraces could be the obligated strategy for genetic diversification. On this regard, the use of mutation breeding using ionizing radiation can also be an adequate approach. We have previously shown that these techniques are effective to diversify this crop for specific traits (26, 27).

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Table V. Coefficient of parentage estimates between combination pairs of varieties released during 1972 to 1993

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	
1. IR880-C9																							
2. IR1529ECIA	0.18																						
3. P-723	0.25	0.16																					
4. Jucarito-104	0.16	0.16	0.34																				
5. Caribe 1	0.00	0.00	0.00	0.00																			
6. Caribe 7	0.25	0.16	0.25	0.16	0.00																		
7. CP1-C8	0.26	0.38	0.44	0.34	0.00	0.25																	
8. Amistad-82	0.09	0.50	0.08	0.08	0.00	0.08	0.22																
9. CP3-C2	0.59	0.59	0.20	0.16	0.00	0.20	0.32	0.29															
10. ECIA31-2005	0.28	0.60	0.23	0.17	0.00	0.23	0.35	0.30	0.37														
11. ECIA31-2006	0.28	0.60	0.23	0.17	0.00	0.23	0.35	0.30	0.37	0.50													
12. ECIA-24	0.09	0.50	0.08	0.08	0.00	0.08	0.22	0.50	0.29	0.30	0.30												
13. Perla de Cuba	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00											
14. IA Cuba-14	0.26	0.24	0.41	0.37	0.00	0.25	0.81	0.12	0.29	0.32	0.32	0.12	0.00										
15. IACuba-15	0.32	0.17	0.28	0.23	0.00	0.21	0.50	0.08	0.27	0.32	0.32	0.08	0.00	0.41									
16. IACuba-16	0.26	0.26	0.34	0.26	0.00	0.62	0.62	0.13	0.26	0.25	0.25	0.13	0.00	0.44	0.33								
17. IACuba-17	0.17	0.13	0.17	0.50	0.00	0.08	0.21	0.07	0.14	0.15	0.15	0.07	0.00	0.22	0.15	0.14							
18. IACuba-18	0.11	0.40	0.08	0.08	0.00	0.09	0.16	0.20	0.24	0.37	0.37	0.20	0.00	0.14	0.12	0.13	0.09						
19. IACuba-19	0.16	0.15	0.36	0.82	0.00	0.17	0.31	0.07	0.16	0.17	0.17	0.07	0.00	0.40	0.25	0.22	0.41	0.07					
20. IACuba-20	0.14	0.30	0.11	0.09	0.00	0.12	0.17	0.15	0.19	0.50	0.50	0.15	0.00	0.16	0.16	0.12	0.07	0.20	0.08				
21. IACuba-21	0.16	0.16	0.34	0.75	0.00	0.16	0.34	0.08	0.16	0.17	0.17	0.08	0.00	0.37	0.23	0.26	0.50	0.08	0.82	0.09			
22. IACuba-22	0.16	0.16	0.34	0.75	0.00	0.16	0.34	0.08	0.16	0.17	0.17	0.08	0.00	0.37	0.23	0.26	0.50	0.08	0.82	0.09	0.56		
23. IACuba-23	0.16	0.16	0.34	0.75	0.00	0.16	0.34	0.08	0.16	0.17	0.17	0.08	0.00	0.37	0.23	0.26	0.50	0.08	0.82	0.09	0.56	0.5	
24. IACuba-24	0.12	0.12	0.19	0.53	0.00	0.08	0.23	0.06	0.13	0.13	0.13	0.06	0.00	0.25	0.26	0.14	0.27	0.07	0.42	0.18	0.53	0.5	
25. IACuba-25	0.09	0.50	0.08	0.08	0.00	0.08	0.22	0.75	0.29	0.30	0.30	0.50	0.00	0.12	0.08	0.13	0.07	0.20	0.07	0.15	0.08	0.0	
26. IACuba-26	0.16	0.16	0.34	0.75	0.00	0.16	0.34	0.08	0.16	0.17	0.17	0.08	0.00	0.37	0.23	0.26	0.50	0.08	0.82	0.09	0.56	0.5	

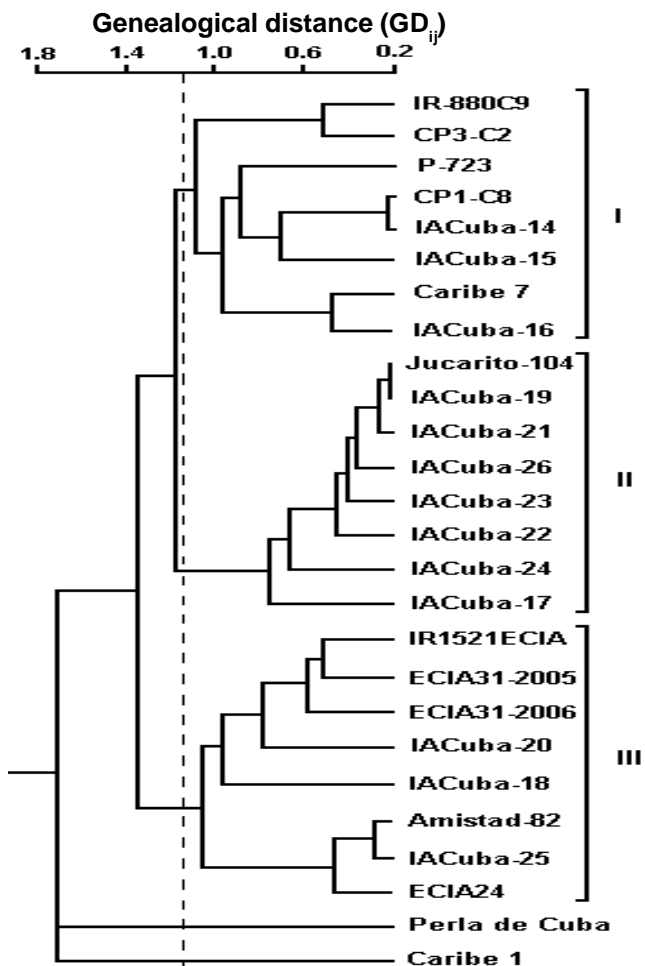


Figure 3. Dendrogram from Cuban varieties based on the estimate of genealogical distance (GD_{ij})

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