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Original article

Genotypic diversity of Cuban rice cultivars obtained by INCA in the 1984-2020 period

Diversidad genotípica de cultivares cubanos de arroz obtenidos por el INCA en el período 1984-2020

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ABSTRACT: Genetic diversity can be seen as a source of options to grow diverse and nutritious foods with fewer resources, adapted to more hostile environments and making crops less susceptible to pests. In this sense, the present work was carried out with the objective of determining the genetic diversity, based on their genealogy, of the 20 rice cultivars released by the National Institute of Agricultural Sciences of Cuba in the 1984-2020 period. Through the CROPDIVER V. 01.20.19 program, the combined genealogical tree of all cultivars was elaborated, their parentage coefficients, the percentage of participation and the contribution of each ancestor in the cultivars obtained were calculated, in addition the dendrogram was constructed using parentage coefficient as genetic similarity estimate. The results showed that the genealogical tree, of the 20 cultivars obtained, is made up of 28 Ancestors and 65 cultivars or improved lines, the highest level of contribution falls on four ancestors and 12 contribute the genes present in the cytoplasm, through the maternal way. Although, as a whole, the obtained germplasm is consanguineous, the grouping carried out differentiated three groups of cultivars that allow establishing genetic similarities between them and making recommendations for their use in Cuban rice production.

Key words: *Oryza sativa*, consanguinity, parentage coefficient.

RESUMEN: La diversidad genética puede verse como una fuente de opciones para cultivar alimentos diversos y nutritivos con menos recursos, adaptados a ambientes más hostiles y haciendo a los cultivos menos susceptibles a plagas; en este sentido, se llevó a cabo el presente trabajo que tuvo como objetivo determinar la diversidad genética, en base a su genealogía, de los 20 cultivares de arroz liberados por el Instituto Nacional de Ciencias Agrícolas de Cuba en el período 1984-2020. Mediante el programa CROPDIVER V. 20.01.19 fue elaborado el árbol genealógico combinado de todos los cultivares, fueron calculados sus coeficientes de parentesco, el porcentaje de participación y la contribución de cada ancestro en los cultivares obtenidos; además, se construyó el dendrograma utilizando el coeficiente de parentesco como estimado de similitud genética. Los resultados mostraron que el árbol genealógico de los 20 cultivares obtenidos lo forman 28 ancestros y 65 cultivares o líneas mejoradas, el mayor nivel de contribución recae sobre cuatro ancestros y 12 aportan los genes presentes en el citoplasma, por vía materna. Aunque, en su conjunto, el germoplasma obtenido es consanguíneo, el agrupamiento realizado diferenció tres grupos de cultivares que permiten establecer las similitudes genéticas entre ellos y hacer recomendaciones para su utilización en la producción arrocera cubana.

Palabras clave: *Oryza sativa*, consanguinidad, coeficiente de parentesco.

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INTRODUCTION

Around 10,000 years ago, different cultures in the Americas, Asia and Africa invented agriculture independently of each other, giving way to sedentary, stratified human settlements capable of sustaining ever-growing populations: How to feed a growing human population with a quality diet in a context of climate change, biodiversity loss, finite natural resources, human migrations and the negative effects of industrialized agriculture and, moreover, how to do so without losing the biocultural legacy of peoples and further degrading the Earth's remaining natural ecosystems (1).

Rice is one of the most versatile of staple crops grown in tropical and subtropical zones, and it is considered one of the main sources of food in the world, providing sustenance for more than half of the global population (2,3). It is one of the oldest domesticated grains and is closely associated with lifestyles and culture (4,5).

Given the need to achieve food self-sufficiency in order to dispense with dependence on foreign markets, which are so variable and increasingly insecure, Cuba is committed to increasing national grain production and the Rice Genetic Breeding Program seeks, through various strategies, to constantly increase the crop's yield; however, there are limitations related to the existing narrow genetic base, which is believed to have reached a supposed ceiling (6).

Genetic diversity can be seen as a source of options to grow diverse and nutritious foods with fewer resources, adapted to more hostile environments and making crops less susceptible to pests (1). Therefore, knowledge of genetic diversity among cultivars for a region is important for planning breeding strategies and reducing genetic vulnerability (7-9).

This work was conceived with the objective of determining the genetic diversity, according to the analysis of pedigree based on the parentage coefficient, of the rice varieties released by the Rice Breeding Group of the National Institute of Agricultural Sciences of Cuba in the period 1984-2020.

MATERIALS AND METHODS

For the development of this work, 20 rice cultivars were used (Table 1) (10), obtained through the breeding program developed by researchers of the National Institute of Agricultural Sciences (INCA) of Cuba, in 1984-2020. The sample includes 11 cultivars obtained through hybridization, four by *in vitro* cultivation of anthers, four by *in vitro* cultivation of seeds and one in which two breeding techniques were combined, since seeds irradiated with protons were cultivated *in vitro* (10).

Using the Cropdiver V. 20.01.19 program (11), the combined genealogical tree of the 20 cultivars was elaborated and kinship coefficients, the participation percentage and the genetic contribution percentage of each ancestor were calculated.

Cropdiver program has a database from the genetic breeding programs of the Cuban crop, in which the Grain Research Institute (IIG) and the National Institute of Agricultural Sciences (INCA) participate, as well as from the International Center for Tropical Agriculture (CIAT) of Colombia and the International Rice Information System (IRIS, www.iris.irri.org) (12). For the present work, this database was updated with information on the new cultivars obtained by INCA.

Mediante el programa Cropdiver V. 20.01.19 (11) fue elaborado el árbol genealógico combinado de los 20 cultivares y calculados los coeficientes de parentesco, el porcentaje de participación y el porcentaje de contribución genética de cada ancestro.

The genetic relationship between cultivars was estimated by means of parentage coefficients (r_{ij}), which were calculated according to the formula (13):

$$\mathrm{rij} = \frac{\sum(\frac{1}{2})^{n1+n2} \quad \mathrm{x}(1+\mathrm{FA})}{\sqrt{(1+Fi)} \quad x \quad \sqrt{(1+Fj)}}$$

where:

r_{ij}- coefficient of relatedness between individuals i and j.

n_1 and n_2- number of generations between the ancestors and the individuals

F_i and F_j- coefficients of inbreeding of the individuals

F_A- inbreeding coefficient of the common ancestor (A)

The contribution of each ancestor in the cultivars obtained was estimated by means of the participation percentage and the genetic contribution percentage, the former was obtained by the sum of the number of cultivars where the ancestor was present divided by the total number of crosses and expressed as a percentage, while the genetic contribution was expressed as the sum of the individual contribution of the kinship coefficient of the ancestors with their descendant cultivars.

Finally, the dendrogram was constructed, in which the parentage coefficient was used as an estimate of genetic similarity of all the cultivars that make up the family tree and the materials were grouped by the uncorrected pairwise method, using arithmetic averages (UPMGA) and the NTSYSpc program.

RESULTS AND DISCUSSION

The combined genealogical tree of the 20 rice cultivars (Figure 1) is formed by 28 ancestors and 65 cultivars or breeded lines. These ancestors provide 94.6 % of its genetic constitution, one of them (2.2 %) of unknown origin, 5 % comes from the American continent, from two countries, the United States and Brazil, and the rest, mostly from the Asian continent, for 82.8 % (Table 2).

The predominance of Asian germplasm is probably the result of selection for irrigated rice conditions and consumption preferences that are oriented towards long grain rice with high amylose; in addition, the primary and secondary centers of rice diversity are located in these regions (7).

The highest level of contribution falls on four ancestors (Cina, Dee Geo Woo Gen, Marong Paroc, and Lati Sail) with 43.2 % in total and similar values among them,

Table 1. Cuban rice cultivars obtained by INCA in 1984-2020 period

	Cultivars	Breeding methods	Progenitors
1	Amistad´82	Hybridizations	IR 1529-430/VNIIR 3223
2	INCA LP-1	Hybridizations	J-104/Amistad´82
3	INCA LP-2	Hybridizations	IR 759-54-2-2/6066
4	INCA LP-3	Hybridizations	Cica 8/CP$_1$C$_8$
5	INCA LP-4	Hybridizations	6066/IR 759-54-2-2
6	INCA LP-5	Hybridizations	2077/CP$_1$C$_8$
7	INCA LP-6	Hybridizations	2077/CP$_1$C$_8$
8	INCA LP-7	*In vitro* seed culture	Amistad´82
9	INCA LP-8	*In vitro* seed culture	Amistad´82
10	INCA LP-9	*In vitro* seed culture	Amistad´82
11	INCA LP-10	*In vitro* seed culture	Amistad´82
12	INCA LP-11	Hybridizations	IR 1529-430/IR 759-54-2-2
13	Anays LP-14	*In vitro* culture of anthers	Amistad´82/IR 759-54-2-2
14	Roana LP-15	Hybridizations	8073//IR 759-54-2-2/J-104
15	Ginés LP-18	*In vitro* proton irradiated seed culture	J-104
16	Guillemar LP-19	Hybridizations	Amistad´82/INCA LP-7
17	José LP-20	Hybridizations	Amistad´82/J-112
18	Eduar LP-21	*In vitro* culture of anthers	INCA LP-10/C4 153
19	INCA LP-22	*In vitro* culture of anthers	Amistad´82/2077
20	INCA LP-23	*In vitro* culture of anthers	INCA LP-1/Tetep

followed by Pa chiam, VNIIR3223, Benong, Tsai Yuag Chong, I Geo Tze, Mang Chim Vang A, whose values are between 5.82 and 2.97 %.

Sixteen ancestors are used only as male parents (CI5309, Takao Iku 18, Badkalamkati, Sinawpagh, Blue Rose, Lati Sali, Khao Dawk Mali 105, C46-15, Tetep, I Geo Tze, Tadukan, Benong, Tsai Yuag Chong, VNIIR3223, C4153 and an unknown ancestor), five as female parents only (Mang Chim Vang A, Hill Selection, Carolina Gold, Nahung Mon S4 and Bayang), three as female parents and male parents (Cina, Dee Geo Woo Gen, Pa chiam) and four are material from which lines or cultivars were selected (Marong Paroc, Kitchilli Samba, Guinosgar, Dourado Agulha).

This means that, out of 28 ancestors present in the genealogical tree, 12 contribute the extranuclear genes of mitochondria and chloroplasts, present in the cytoplasm, through the maternal route. This result shows an advance with respect to what was found in previous works developed in Cuba (14), where it was reported that Cina contributed the cytoplasm of the cultivars released by the IRRI breeding program, which constituted the initial source of the progenitors of the genetic breeding program of rice in Cuba during the period 1972-1993.

In this sense, there are known advantages provided by genes present in the cytoplasm, among them, the sequencing of chloroplast DNA has revealed that there are about 100 genes in land plants that are involved in photosynthetic carbon fixation, but depend on the nuclear genome for the determination of many of their functions. Also, in many of the male sterile lines used in the commercial production of rice hybrids, fertility is controlled by the interaction of genes present in the cytoplasm and recessive genes present in the nucleus (15).

According to the literature consulted prior to 2003, regarding the number of ancestors that contribute, the genetic constitution of the 20 cultivars developed by INCA is broader than that of the United States (which had only 23), Costa Rica (11), Nicaragua (12) and Honduras (18); similar to that of El Salvador (27), Panama (28) and Guatemala (29) and inferior to that of Colombia (32,14).

Recent results (7), from a work carried out with 51 rice cultivars released between the years 2003 - 2014, in 13 member countries of the Latin American Fund for Irrigated Rice (FLAR), concluded that an expansion of the genetic base has been obtained, that diversity was represented by 120 ancestors and that 33 of these contributed 83.9 % of their genes.

Since pedigree analysis does not require morphological, molecular or isoenzyme observations between the genotypes to be studied and is not influenced by the environment, it is a useful and economical methodology that provides preliminary information about the interrelationships between groups of genotypes. These results constitute an approximation to the analysis of the genetic diversity existing in rice varieties released in the thirteen countries of the region (7).

Regarding the important genes present in the ancestors, it is known that Marong Paroc and Pa Chiam contribute genes for grain quality, as well as Tetep and CI5309 resistance to the fungus *Magnaporthe grisea* Barr (*Pyricularia grisea* Sacc) that causes *Piriculariosis* (14). Prior to the development of cultivar IR8, the Dee Geo Woo Gen ancestor was used to provide the semi-dwarfing trait gene and is also moderately resistant to Piriculariosis (3).

On the other hand, Peta, a cultivar present in the genealogical tree and coming from the cross between the ancestors Cina and Lati Sail, is resistant to tungro virus

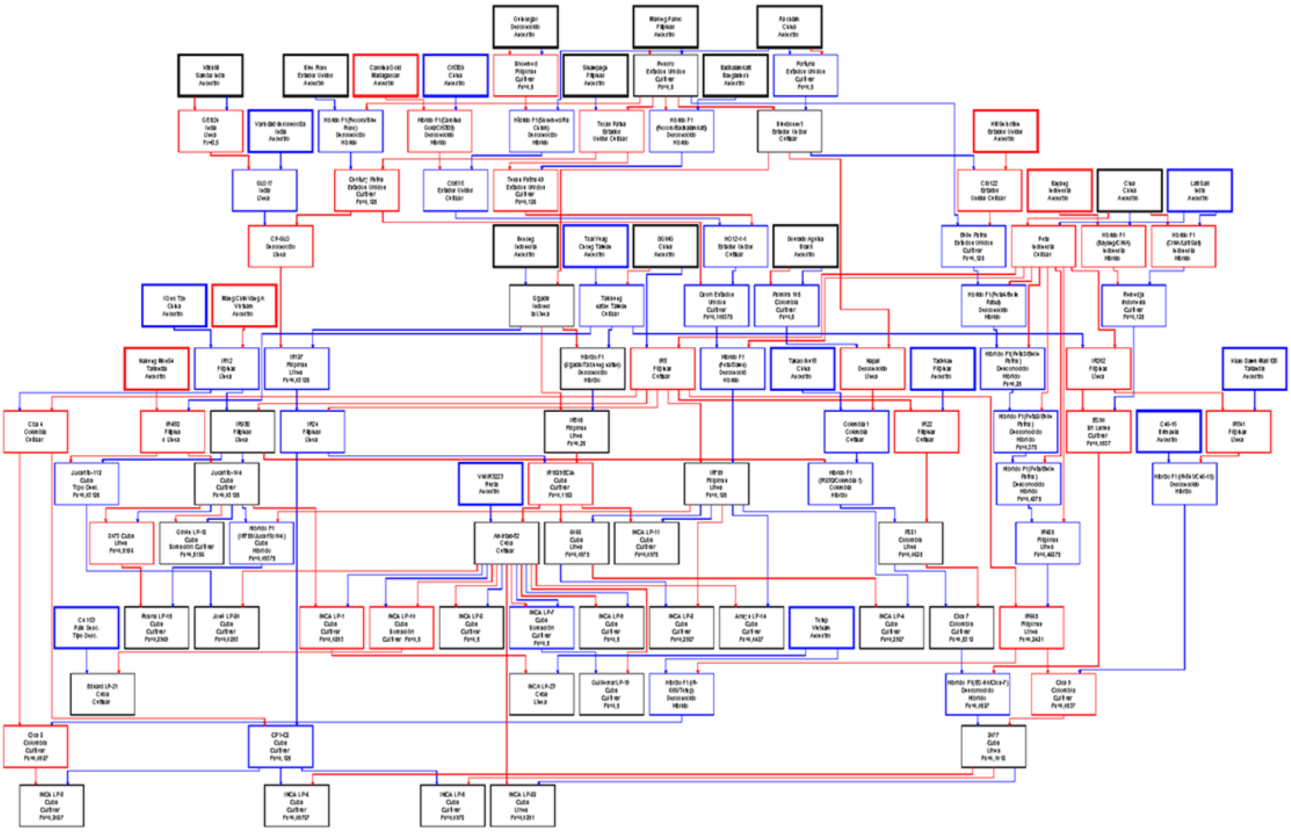

Figure 1. Combined genealogical tree of the 20 rice cultivars obtained by INCA in the period 1984-2020

(*Rice tungro bacilliform virus*), moderately resistant to Piricularіosis and tolerant to salinity (3).

In previous works, the absence of ancestors and cultivars that provide resistance to the white leaf virus is raised (12,14), this is a task still to be solved since the genetic improvement program of rice in Cuba has cultivars resistant to Sogata (*Tagosodes oryzicolus* Muir), insect that transmits it and confers certain protection in the field, but there are no cultivars resistant to the virus.

The 190 pairs of possible combinations corresponding to the estimated inbreeding values (Table 3), among the 20 cultivars studied, showed values ranging from 0 to 0.82, with an average value of 0.27.

If we consider a minimum limit of 0.125, the absolute inbreeding of ten cultivars (Amistad'82, INCA LP-1, INCA LP-5, INCA LP-6, INCA LP-11, Anays LP-14, Jose LP-20, Eduard LP-21, INCA LP-22 and INCA LP-23) is lower than that value, but 75 % of the pairs of combinations among the 20 cultivars were closely related with values greater than 0.125 and the remaining 25 % showed distant kinship ties, with values less than 0.125, so we can posit that as a whole the germplasm is inbred.

In this regard, it should be noted that four cultivars come from the somatic culture of Amistad'82 (INCA LP-7, INCA LP-8, INCA LP-9, INCA LP-10), that is, their genes come from the same source, and five others (Anays LP-14, Guillemar LP-19, José LP-20, INCA LP-22 and INCA LP-1) include it in their progenitors, the first four as female, and in the breeding of INCA LP-10, the first four as female.

female and in the obtaining of INCA LP-1 it is used as male, so theoretically 50 % of its genes have the same origin.

By definition, a genotype has a kinship coefficient of 1.00 with itself, in progenies of complete siblings is equal to 0.50, in progenies of half siblings 0.25 and in individuals that do not share parents is 0.00 (7).

The results obtained with Cuban germplasm obtained by the IIG, up to 2002, showed an average value of the kinship coefficient of 0.24, 68 % of the pairs of combinations were closely related ($0.125 \leq r_{ij} \leq 0.81$), only the remaining 32 % showed distant kinship ties ($0 \leq r_{ij} < 0.125$) and the authors concluded that the germplasm was clearly inbred (14).

Work on 51 rice cultivars released between 2003 - 2014, in 13 FLAR member countries, reported that the relatedness coefficient ranged from 0.03 to 0.99, with an average value of 0.19 and only 54 pairs of combinations (4.2 %), out of 1275 possible, were highly related. The authors conclude that the genetic base of cultivars released by FLAR is less narrow than that of Latin America and broader than that of irrigated rice in Brazil (7).

Estimating the diversity that exists among a group of materials by means of the parentage coefficient makes it possible to discriminate pairs of genotypes carrying identical alleles, by descent, which has been widespread among self-pollinated species, such as soybean, wheat,

Table 2. Participation rates and genetic contribution (%) of ancestors that compose the genetic base of Cuban rice cultivars obtained by INCA, during the period 1984-2020

No.	Ancestors	Origin	Genetic contribution	Participation
1	Cina	China	11.31	67
2	Dee Geo Woo Gen	China	10.91	60
3	Marong Paroc	Philippines	10.84	69
4	Lati Sail	India	10.14	65
5	Pa chiam	China	5.82	64
6	VNIIR3223	Russia	4.59	14
7	Benong	Indonesia	3.72	31
8	Tsai Yuag Chong	Philippines	3.54	43
9	I Geo Tze	China	2.97	27
10	Mang Chim Vang A	Vietnam	2.97	27
11	Kitchilli Samba	India	2.38	31
12	Nahung Mon S4	Thailand	2.34	12
13	Sinawpagh	Philippines	2.27	39
14	Dourado Agulha	Brazil	2.20	13
15	Guinosgar	Unknown	2.18	17
16	Blue Rose	United States	1.65	37
17	Tetep	Vietnam	1.59	5
18	Tadukan	Philippines	1.43	10
19	Unknown ancestor	India	1.42	30
20	Takao Iku 18	China	1.30	11
21	C46-15	Burma	1.23	7
22	Carolina Gold	Madagascar	1.22	15
23	CI5309	China	1.22	15
24	Badkalamkati	Bangladesh	1.20	15
25	Khao Dawk Mali 105	Thailand	1.20	8
26	Bayang	Indonesia	1.17	10
27	Hill Selection	Estados Unidos	1.15	19
28	C4 153	Korea	0.59	1

barley and rice. In maize, it has been shown that the correlation between estimating genetic diversity measured by this coefficient and by molecular markers (RFLP) is high (r=93%), so it was concluded that using the kinship coefficient is simpler, faster and cheaper than any of the other methods recommended to study genetic diversity among potential parents (7).

If we analyze the parentage of some cultivars in particular, with the rest of those studied, we can appreciate that Ginés LP-18, coming from the *in vitro* culture of Jucarito 104 seeds irradiated with protons, has distant parentage links with 12 cultivars (coefficient less than 0.125) and for the remaining seven the values were in the range of 0.125 - 0.568. Also, the sister lines INCA LP-5 and INCA LP-6, coming from the same cross, as well as Roana LP-15, in their relationship with the rest present eight distant cultivars.

The existing relationship between INCA LP-5 and INCA LP-7 cultivars, with a very low parentage coefficient, 0.096 and a cytoplasmic source of different ancestors, Cina for INCA LP-5 and Marong Paroc for INCA LP-7, represents some progress in the results of crop improvement present in the rice production of the country in the period after 2000, so we can say that some recommendations of previous works have been taken into account.

Among these recommendations was the possibility of exploiting through genetic crosses the greatest diversity of commercial varieties of importance in Cuba, such as: Jucarito-104 and Amistad'82, the incorporation of new cytoplasmatic sources and the use of mutation induction as a useful tool, which has proved to be an effective way to diversify the crop (14).

Figure 2 shows the cluster analysis performed on the basis of the parentage coefficient matrix of all Cuban rice cultivars obtained by INCA in the period 1984-2020.

The theoretical genetic diversity and the interrelationships among all the cultivars, taking as a reference a similarity value of 0.20, allowed the formation of three groups. In the first one: Amistad'82, together with its somaclones INCA LP-7, INCA LP-8, INCA LP-9 and INCA LP-10, four cultivars (Anays LP-14, Guillemar LP-19, José LP-20 and INCA LP-22), in which Amistad'82 is present as a parent and Eduard LP-21 whose female parent is INCA LP-10. All of them, due to their origin, have similar genetic information; however, phenotypically, differences have been observed in terms of qualitative and quantitative characters evaluated (10), as well as in their resistance to the mite (*Steneotarsonemus spinki* Smiley), Piriculariosis and tolerance to salinity and drought.

Table 3. Absolute inbreeding values and parentage coefficients of Cuban rice cultivars obtained by INCA, in the period 1984-2020

Fx	Cultivars	Amistad'82	INCA LP-10	INCA LP-7	INCA LP-8	INCA LP-9	INCA LP-1	INCA LP-3	INCA LP-5	INCA LP-6	José LP-20	INCA LP-11	INCA LP-2	Roana LP-15	Anays LP-14	Eduard LP-21	Ginés LP-18	Guillemar LP-19	INCA LP-22	INCA LP-23
0.000	Amistad'82																			
0.500	INCA LP-10	0.816																		
0.500	INCA LP-7	0.816	0.667																	
0.500	INCA LP-8	0.816	0.667	0.667																
0.500	INCA LP-9	0.816	0.667	0.667	0.667															
0.029	INCA LP-1	0.522	0.426	0.426	0.426	0.426														
0.203	INCA LP-3	0.114	0.093	0.093	0.093	0.093	0.149													
0.098	INCA LP-5	0.118	0.096	0.096	0.096	0.096	0.146	0.394												
0.098	INCA LP-6	0.118	0.096	0.096	0.096	0.096	0.146	0.394	0.545											
0.029	José LP-20	0.522	0.426	0.426	0.426	0.426	0.400	0.149	0.146	0.146										
0.098	INCA LP-11	0.285	0.233	0.233	0.233	0.233	0.212	0.244	0.251	0.251	0.212									
0.299	INCA LP-2	0.174	0.142	0.142	0.142	0.142	0.159	0.236	0.242	0.242	0.159	0.500								
0.297	Roana LP-15	0.060	0.049	0.049	0.049	0.049	0.374	0.186	0.181	0.181	0.222	0.221	0.252							
0.049	Anays LP-14	0.536	0.438	0.438	0.438	0.438	0.323	0.194	0.199	0.199	0.323	0.418	0.427	0.197						
0.000	Eduard LP-21	0.500	0.408	0.408	0.408	0.408	0.261	0.057	0.059	0.059	0.261	0.143	0.087	0.030	0.268					
0.516	Ginés LP-18	0.048	0.039	0.039	0.039	0.039	0.424	0.153	0.144	0.144	0.236	0.118	0.121	0.568	0.098	0.024				
0.500	Guillemar LP-19	0.816	0.667	0.667	0.667	0.667	0.426	0.093	0.096	0.096	0.426	0.233	0.142	0.049	0.438	0.408	0.039			
0.029	INCA LP-22	0.522	0.426	0.426	0.426	0.426	0.309	0.147	0.339	0.339	0.309	0.234	0.189	0.110	0.346	0.261	0.085	0.426		
0.000	INCA LP-23	0.265	0.216	0.216	0.216	0.216	0.493	0.133	0.074	0.074	0.203	0.108	0.081	0.190	0.164	0.132	0.215	0.216	0.157	
0.299	INCA LP-4	0.174	0.142	0.142	0.142	0.142	0.159	0.236	0.242	0.242	0.159	0.500	0.615	0.252	0.427	0.087	0.121	0.142	0.189	0.081

Fx- Absolute Consanguinity

Amistad'82, of short cycle, was incorporated to rice production in Cuba for several years, while INCA LP-7, of medium cycle, has been planted since 2000 with excellent performance, both in waterlogged conditions and in soils with certain saline content, and has also shown resistance to mite.

The second group is formed by the cultivars INCA LP-1, Roana LP-15, Ginés LP-18 and INCA LP-23, which share genetic information from the commercial cultivar Jucarito 104, which remained in production in Cuba for more than 20 years, due to its excellent agricultural yield, but with negative traits such as poor industrial quality and susceptibility to Piriculariosis and mite.

INCA LP-1, of medium cycle, was incorporated into rice production in Cuba and Colombia (16) and Ginés LP-18 since 2019 began its generalization in the country, where it has shown excellent behavior both in waterlogged conditions and in soils with certain saline tenors.

The third group is formed by the six remaining cultivars, which are results of the genetic improvement program for resistance to Piriculariosis, hence the presence of IR 759-54-2-2 and 2077 among their parents, with genes from the ancestors Cina and Lati Sail, parents of the cultivar Peta, with known resistance to the disease. The cultivars IR 759-54-2-2 and 2077 have shown resistance in evaluations in infection beds in 'hot spot' zones, of high incidence of the disease in Cuba (17).

Among them, the cultivar 'INCA LP-5', obtained from a simple cross, is characterized for being very vigorous, its green leaves maintain a slow senescence, stands out for its short vegetative cycle, excellent agricultural and industrial yield and resistance to Sogata (17). From great acceptance by the grain producers, it has been present for 20 years in the production in Cuba.

The main objective in the breeding of a given species should be to incorporate genetic diversity for resistance to pathogens e insects, and combine it with agronomic and morphological characters that confer high yields, adaptability and stability, in this way, the resistance genes coming from diverse progenitors introgressed in the elite cultivars, could offer greater protection against unexpected appearances of plagues (7).

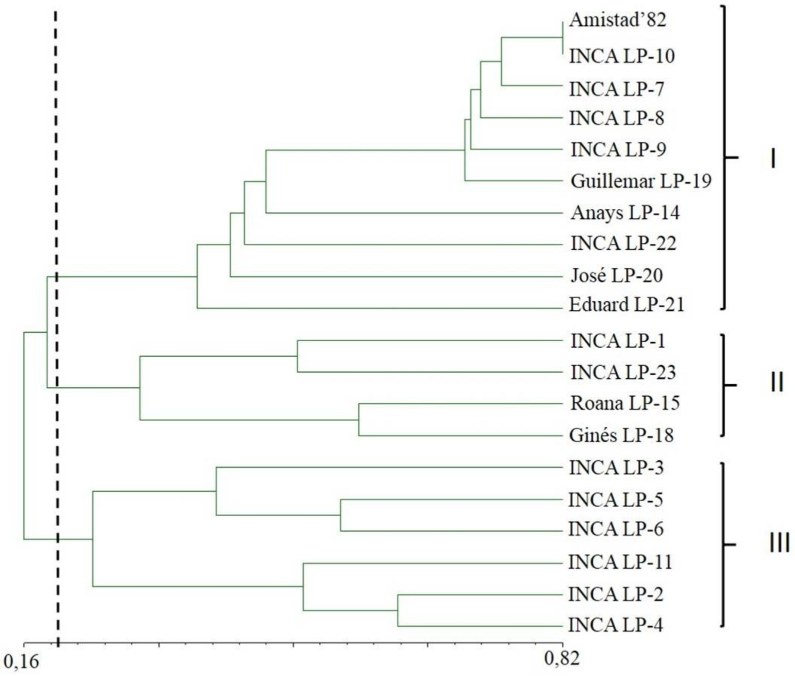

Figure 2. Dendrogram for all Cuban rice cultivars obtained by INCA in the period 1984-2020, according to the Cluster Analysis, based on the kinship coefficient matrix

CONCLUSIONS

The genealogical tree of the 20 cultivars obtained by INCA in the period 1984-2020 is formed by 28 ancestors and 65 cultivars or improved lines, although the highest level of contribution falls on four ancestors and 12 of them contribute the extranuclear genes of mitochondria and chloroplasts, present in the cytoplasm, through the maternal route.

Although, as a whole, the germplasm obtained is inbred, the grouping carried out differentiated three groups of cultivars, which constitutes a tool for defining varietal policy, when selecting cultivars from each diversity group identified, as well as for the selection of parents in breeding programs.

In this sense, a joint analysis of the cultivars obtained by INCA with those developed by the Cuban Grain Research Institute would be useful to visualize in a more general way the most genetically distant groups of interest for the genetic improvement program of the crop in the country and, in this way, achieve an adequate genetic diversity in the field.

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