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Genetic base of Brazilian irrigated rice cultivars

Hudson de Oliveira Rabelo[1*], João Filipi Rodrigues Guimarães[2], José Baldin Pinheiro[3] and Edson Ferreira da Silva[4]

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Abstract – *The aim of this study was to estimate the genetic base of Brazilian irrigated rice cultivars released in the period from 1965 to 2012. The genealogies of the cultivars were obtained based on information from marketing folders, websites, crossings records, and scientific articles. The following factors were calculated: relative genetic contribution (RGC), accumulated genetic contribution (AGC), frequency (in percentage) of each ancestor in the genealogy (FAG), number of ancestors that constitute each cultivar (NAC), number of ancestors responsible for 60%, 70%, 80% and 90% of the genetic base (NAGB), and average number of ancestor per cultivar (ANAC). The cultivars were also grouped based on the period of release (1965-1980, 1981-1990, 1991-2000 and 2001-2012). For each grouping, the previously described factors were also estimated. A total of 110 cultivars were studied and it was concluded that the genetic base of Brazilian irrigated rice cultivars is narrow.*

Key words: Oryza sativa*, relative genetic contribution, accumulated genetic contribution, genealogies, genetic vulnerability.*

INTRODUCTION

Rice is considered to be the cereal crop of greatest socioeconomic importance since it is one of the staple food components and the main dietary energy source for the human population. Brazil is the eighth largest producer of this grain, and Brazilian production in the 2010/2011crop season was estimated at 9.45 million tons (CEPA 2011). The high productivity rates obtained in the country are mostly due to the activity of research institutes, mainly through development of new cultivars and crop techniques.

The first rice genetic breeding activities in Brazil began in 1936, at the Instituto Agronômico de Campinas (IAC), when the first competitive tests were carried out. After that, in 1938, the first hybridizations were carried out between varieties introduced from other countries and local breeds (Viegas et al. 1945). In the same year, the Instituto Rio Grandense de Arroz (IRGA) began its irrigated rice breeding program (Soares et al. 2004a). Up to the 1970s, rice breeding in Brazil was carried out basically through the activities of IAC and IRGA. As of 1970, other programs were established at federal and state level. The development of domestic cultivars spurred Brazilian rice growing, making it competitive and profitable in view of yield increases in the order of 30% registered in the middle of the 1980s (Morais and Rangel 1997).

The Brazilian irrigated rice cultivars were developed from lines and cultivars coming from international research institutes, such as the *International Rice Research Institute* (IRRI) in the Philippines (Morais et al. 2004), the *International Center for Tropical Agriculture* (CIAT), and the *Institute for Research in Tropical Agriculture* (IRAT), currently called the *Centre de Coopération Internationale en Recherche Agronomique pour le Développement* (CIRAD), headquartered in France. These genotypes were introduced in Brazil by domestic breeding programs, and they represent most of the genetic base of Brazilian irrigated rice cultivars. The genetic base is defined by Cui et al. (2000) as the entire set of genes that contribute toward the development of cultivars of a determined species.

Since they originate from a restricted group of ancestors, from crosses with kinship relations, and for having been developed by breeding methods that do not allow broad recombination, such as genealogical, populational and backcrossing methods (Cordeiro 2008), Brazilian cultivars

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[1] Universidade Federal Rural de Pernambuco (UFRPE), Departamento de Agronomia, Rua Dom Manoel de Medeiros, s/n, 52.171-900, Recife, PE, Brazil. *E-mail: hudsonorabelo@gmail.com

[2] Universidade Federal de Viçosa (UFV), Departamento de Biologia Geral, Av. P.H. Rolfs, s/n, 36.571-900, Viçosa, MG, Brazil

[3] Escola Superior de Agricultura Luiz de Queiroz (ESALQ), Departamento de Genética, Av. Pádua Dias, 11, 13.418-900, Piracicaba, SP, Brazil

[4] UFRPE, Departamento de Biologia

have a narrow genetic base (Rangel et al. 1996).

Narrowing of the genetic base is considered one of the main drawbacks of modern agriculture since it causes genetic vulnerability of cultivars to biotic and abiotic stresses, which may result in yield reduction in the rice crop (Rangel et al. 1996). For genetic breeding purposes, narrow genetic base results in low variability, which may limit possibilities for recombination and genetic segregation, and hinder achievement of gains from selection. Knowledge regarding the magnitude of the genetic base of Brazilian irrigated rice cultivars may help in the choice of divergent parents in breeding programs, contributing to the broadening of the genetic base of cultivars and cultivated species.

In order to provide assistance to genetic breeding programs, the aim of this study was to estimate the genetic base of Brazilian irrigated rice cultivars released in the commercial market in Brazil in the period from 1965 to 2012, except for the cultivars developed by private companies, since their genealogical records are not disclosed.

MATERIAL AND METHODS

Irrigated rice cultivars released for commercial use in the period from 1965 to 2012 were studied. The purpose was to construct the genealogy of each cultivar for the identification of divergent ancestors. During the preparation of the genealogies, it was considered information obtained from marketing folders of varieties, websites, genealogical records of research institutes, such as the IRRI (1985, 1998) and CIAT (2005), and scientific articles (Dilday 1990, Rangel et al. 1996, Montalván et al. 1998, Silva et al. 1999, Châteal and Guimarães 2002, Cutrim and Rangel 2002, Soares

Table 1. Relative genetic contribution (RGC%), accumulated genetic contribution (AGC%) and frequency of the ancestors in the genealogy (FAG%) of Brazilian cultivars of rice released on the commercial market in the period from 1965 to 2012

Ancestors	RGC (%)	AGC (%)	FAG (%)	Ancestors	RGC (%)	AGC (%)	FAG (%)
Dee Geo Woo Gen	14.6351	14.6351	89.0909	IAC 1104	0.4545	86.2407	0.9091
Latsail	12.7504	27.3855	84.5455	Kaohsiung Sen 12	0.4545	86.6953	0.9091
Cina	12.6349	40.0204	84.5455	Pazudofuzu	0.4545	87.1498	0.9091
MarongParoc	5.1153	45.1356	84.5455	NSW	0.4545	87.6044	0.9091
MCVA	4.8242	49.9599	70.9091	Taichung 24	0.4545	88.0589	0.9091
I Geo Tze	4.8242	54.7841	70.9091	Arborio	0.4545	88.5134	0.9091
KhaoDawk Mali 105	3.6475	58.4315	42.7273	IRGA 1598	0.4545	88.9680	0.9091
Tadukan	3.2704	61.7019	49.0909	SCS 151	0.4545	89.4225	0.9091
Tetep	2.4960	64.1979	40.0000	Pisari	0.4545	89.8771	0.9091
Pa Chiam	2.3705	66.5685	84.5455	Huan-Sem-Go	0.4545	90.3316	0.9091
Blue Rose	1.7348	68.3033	31.8182	95 Ay 222	0.4545	90.7862	0.9091
TakauIko 18	1.4968	69.8001	41.8182	Campeche A80	0.4545	91.2407	2.7273
HO 12	1.4347	71.2347	13.6364	CNA 6183	0.4545	91.6953	1.8182
Tsai Yuan Chung	1.2146	72.4494	64.5455	CNA 1394	0.4545	92.1498	0.9091
C 74	1.0409	73.4903	34.5455	Nam-Sa-Gui	0.4261	92.5759	9.0909
Hill Sel	1.0242	74.5144	67.2727	Gam Pai	0.4217	92.9976	15.4545
IRGA 407	1.0227	75.5372	3.6364	Sinawpagh	0.3720	93.3696	31.8182
Costa Rica	0.9091	76.4463	6.3636	Remalta	0.2273	93.5969	0.9091
17719	0.9091	77.3554	1.8182	Moroberekan	0.2273	93.8241	1.8182
BRS Taim	0.7955	78.1508	0.9091	63-105	0.2273	94.0514	1.8182
Nanhang Mon 54	0.7670	78.9179	4.5455	MIF B 3322-1	0.2273	94.2787	0.9091
Palmira 105	0.7484	79.6663	41.8182	MRC 5720	0.2273	94.5060	0.9091
Benong	0.7393	80.4055	20.9091	Tangkai Rotan	0.1989	94.7048	8.1818
Kitchili Samba	0.7342	81.1398	22.7273	Thekkan	0.1909	94.8957	13.6364
DissiHatif	0.6889	81.8287	11.8182	Eravapandi	0.1909	95.0866	13.6364
Nanicão	0.6818	82.5105	2.7273	Caloro	0.1882	95.2748	0.9091
AS 3510	0.6818	83.1923	3.6364	SML 1010	0.1705	95.4452	6.3636
Batatais	0.6250	83.8173	7.2727	DouradoPrecoce	0.1705	95.6157	0.9091
Vellaikar	0.6016	84.4190	19.0909	10-7	0.1705	95.7861	0.9091
Zenith	0.4581	84.8771	1.8182	LU 1-29	0.1527	95.9388	5.4545
Big Tang Chien	0.4545	85.3316	0.9091	SML 997	0.1420	96.0809	1.8182
T 7	0.4545	85.7862	0.9091	M 312	0.1420	96.2229	1.8182

To be continued …

et al. 2005, Rangel et al. 2007, Cordeiro and Medeiros 2010a). Hybrid cultivars and a large part of the cultivars developed by private companies were not evaluated since their genealogical records are not disclosed.

The relative genetic contribution (RGC) of each ancestor was estimated considering that there is no degree of kinship between the ancestors, and that the theoretical proportion of genes transferred from a parent to its offspring is 50% (Delannay et al. 1983). This is estimated from the sum of the individual contributions of each ancestor in all the cultivars, according to the methodology used by Rangel et al. (1996), Montalván et al. (1998) and Silva et al. (1999). The ancestors were classified in decreasing order of the RGC values, and the Accumulated Genetic Contribution (AGC) was estimated from the successive sum of the RGC of each ancestor.

The frequency (in percentage) of each ancestor in the genealogy (FAG) was estimated considering the number of cultivars that had a certain ancestor in their genealogy in relation to the total number of cultivars analyzed. For each cultivar, it was estimated the number of ancestors that constitute them (NAC).

The cultivars were also grouped according to the year of commercial release, establishing four periods delimited by the years 1965-1980, 1981-1990, 1991-2000 and 2001-2012. For each grouping it was determined: number of ancestors responsible for 60%, 70%, 80% and 90% of the genetic base (NAGB), number of ancestors and cultivar (NA and NC, respectively), ratio between the number of ancestors and number of cultivars (NA/NC), and average number of ancestors per cultivar (ANAC). The latter corresponds to the sum of each NAC divided by the total number of cultivars.

RESULTS AND DISCUSSION

The genealogical information from 110 Brazilian irrigated rice cultivars was obtained, which were developed from 123 different ancestors (Table 1). The cultivars IAC 600, IAS 12-9 Formosa and BR 3 Caeté were not included

Ancestors	**RGC** (%)	**AGC** (%)	**FAG** (%)	**Ancestors**	**RGC** (%)	**AGC** (%)	**FAG** (%)
Unknown	0.1326	96.3555	19.0909	Palgweng	0.0568	99.3001	1.8182
Oryza nivara	0.1324	96.4879	16.3636	FB 24	0.0568	99.3569	0.9091
Venezuela 503	0.1232	96.6111	14.5455	Lung Shengi	0.0568	99.4137	0.9091
Bayang	0.1155	96.7266	27.2727	63-104	0.0568	99.4706	0.9091
Hayayuki	0.1136	96.8403	0.9091	Tox 1525	0.0568	99.5274	0.9091
Asominori	0.1136	96.9539	1.8182	Tox 939	0.0568	99.5842	0.9091
HR 21	0.1136	97.0675	0.9091	CNA 5278	0.0568	99.6410	0.9091
URN-ISID-IRRI-ORG-1-Germplasm-2608-1	0.1136	97.1812	0.9091	Kiryouyoshi	0.0462	99.6872	2.7273
Matão	0.1136	97.2948	0.9091	B 589 A	0.0393	99.7265	9.0909
Pérola	0.1136	97.4084	0.9091	419 C-57	0.0284	99.7549	6.3636
Jaguari	0.1136	97.5221	0.9091	Della - X2	0.0284	99.7833	0.9091
Yola	0.1136	97.6357	0.9091	SeraupaBesar 15	0.0262	99.8095	11.8182
Lambayeque Mo1	0.1136	97.7494	0.9091	Kameji	0.0213	99.8308	1.8182
Siam 29	0.1136	97.8630	2.7273	Olvan Chu	0.0213	99.8521	1.8182
Tox 1010	0.1136	97.9766	0.9091	BB	0.0183	99.8704	2.7273
Balila	0.1136	98.0903	0.9091	TchenTchou Ai	0.0142	99.8846	0.9091
Agostano	0.1136	98.2039	0.9091	Joshyu	0.0142	99.8988	0.9091
Cesariot	0.1136	98.3175	0.9091	Pankari 203	0.0142	99.9130	0.9091
Oro	0.1136	98.4312	0.9091	283 A7	0.0142	99.9272	1.8182
Jojutla	0.0959	98.5271	3.6364	Smooth 4	0.0142	99.9414	0.9091
Mudgo	0.0852	98.6123	1.8182	Aikoku	0.0107	99.9521	1.8182
Makalioka	0.0852	98.6975	1.8182	Colusa	0.0071	99.9592	0.9091
Variety From Zaire	0.0852	98.7827	0.9091	Shoemed	0.0071	99.9663	0.9091
560	0.0852	98.8680	0.9091	OS 6	0.0071	99.9734	0.9091
S 12-30	0.0710	98.9390	1.8182	D 85-42	0.0071	99.9805	0.9091
Lady Wright	0.0675	99.0065	0.9091	Machique	0.0071	99.9876	0.9091
SML 80-5	0.0616	99.0680	14.5455	D 52-37	0.0071	99.9947	0.9091
SML 81-A	0.0616	99.1296	14.5455	Mira	0.0036	99.9982	0.9091
Basmati 370	0.0568	99.1865	2.7273	RB 2	0.0018	100.0000	0.9091
Carreon	0.0568	99.2433	2.7273				

in the evaluations since they were derived from direct selection of the ancestors Wang Xue Ren, Kashiung 21 and Pisari, respectively. Fourteen cultivars produced by private companies were not considered due to the lack of genealogical information. The relative genetic contributions (RGC) ranged from 0.0018 to 14.6351%. The highest values are in reference to the ancestors Dee Gee Woo Gen, Latisail and Cina, which contributed to approximately 40% of the genes of the 110 cultivars, with RGC of 14.6351, 12.7504 and 12.6349%, respectively (Table 1).

The average number of ancestors per cultivar (ANAC) was 14.37, with values ranging from 2 to 41 (Table 2). Cultivars Bluebonnet, Bluebonnet 50 and BRS Sinuelo CL presented the lowest number of ancestors per cultivar (NAC= 2); Bluebonnet and Bluebonnet 50 are derived from the crossing between Rexoro and Fortuna cultivars. BRS Sinuelo CL was obtained by three cycles of backcrossing between BRS7 Taim and the genotype AS 3510; the latter contains a gene, which confers tolerance to imidazolinone-based herbicides used mainly for red rice control in commercial crops (Magalhães Júnior et al. 2010). Nevertheless, since the parents of BRS 7 Taim are not known, it is possible that BRS Sinuelo CL has a broader genetic base than it has

Table 2. Number of ancestors per cultivar (NAC) of 110 Brazilian irrigated rice cultivars released on the commercial market in the period from 1965 to 2012

Cultivar	NAC	Cultivar	NAC	Cultivar	NAC
Aliança	11	Curumim	9	IAC 400	17
Belle Patna	3	Dawn	6	IRGA 419	16
Bluebelle	5	Diamante	11	IRGA 420	16
Bluebonnet	2	EEA 406	12	IRGA 421	10
Bluebonnet 50	2	El Paso 144	8	IRGA 422 CL	26
BR IPA Moxotó	8	EMPASC 100	5	IRGA 423	20
BR IRGA 409	8	EMPASC 101	8	IRGA 424	20
BR IRGA 410	8	EMPASC 102	6	IRGA 425	36
BR IRGA 411	7	EMPASC 103	8	Javaé	30
BR IRGA 412	8	EMPASC 104	5	Jequitibá	11
BR IRGA 413	8	EMPASC 105	11	Le Bonnet	6
BR IRGA 414	8	EPAGRI 106	30	Metica 1	15
BR/MS 1	11	EPAGRI 107	12	MG 1	15
BR/MS 2	5	EPAGRI 108	35	MG 2	7
BRS 6 Chuí	8	EPAGRI 109	35	Mucuri	17
BRS Alvorada	16	EPEAL 101	8	Oryzica 1	16
BRS Atalanta	14	EPEAL 102	17	Pericumã	12
BRS Biguá	6	Franciscano	14	PESAGRO 101	18
BRS Firmeza	10	IAC 100	18	PESAGRO 102	14
BRS Formoso	29	IAC 101	18	PESAGRO 103	6
BRS Fronteira	21	IAC 104	9	PESAGRO 104	10
BRS Jaburu	27	IAC 105	16	PESAGRO 105	5
BRS Jaçanã	21	IAC 106	18	PESAGRO 106	12
BRS Ligeirinho	8	IAC 1278	14	PESAGRO 107	18
BRS Ourominas	20	IAC 238	20	Qualimax 13	11
BRS Pampa	41	IAC 242	20	Rio Grande	17
BRS Pelota	8	IAC 300	6	Roraima	25
BRS Sinuelo	2	IAC 4440	9	Samburá	17
BRS Tropical	30	IAC 500	10	Sapucaí	16
BRSGO Guará	16	IAC 899	6	SCS 112	12
BRSMG Predileta	17	IAPAR 58	10	SCS 114 Andosan	5
BRSMG Seleta	39	Inca	19	SCS 115 CL	36
Capivari	26	IR 8	3	SCS 117 CL	36
Cica 4	5	IRGA 408	5	SCS BRS 111	21
Cica 7	10	IRGA 416	10	SCS Pantaneira	36
Cica 8	9	IRGA 417	25	Urucuia	17
Cica 9	9	IRGA 418	11	-	-

been reported. Genetic contributions of AS 3510 are also observed in the cultivars SCS 115 CL, SCS 117 CL and BR IRGA 422 CL.

The greatest NAC are attributed to BRS Pampa (NAC= 41) and BRSMG Seleta (NAC= 39). Both of them have two sources of resistance to rice blast (*Pyricularia grisea*) coming from the ancestors Tetep and Tadukan (Rangel et al. 1996). According to Magalhães Júnior (2011), BRS Pampa has intermediate to moderate resistance to rice blast and according to Soares et al. (2004b), BRSMG Seleta is resistant.

The 17 cultivars released commercially in the period from 1965 to 1980 have a narrow genetic base, and they were developed from 32 ancestors (Table 3), with eight cultivars being introduced from other countries (Belle Patna, Bluebelle, Bluebonnet, Bluebonnet 50, Cica 4, Cica 7, Dawn and Le Bonnet). Eight of these ancestors represented approximately 70% of the genealogy, and Marong Paroc, Dee Geo Woo Gen, Cina and Latisail ancestors together contributed to 45% of the genealogy (Table 4). The narrowing of the genetic base in this period from 1965 to 1980 is more accentuated, for around 90% of the genes are represented by 15 ancestors, and the cultivars consist of an average of 1.88 ancestors (Table 3).

In the period of 1981-1990, twenty-five new ancestors were incorporated in the genetic base of the Brazilian irrigated rice cultivars. In numerical terms, there was no alteration of the genetic base, since approximately 70% of the gene pool originate from eight ancestors, just as in the previous period (Table 3). In the period of 1991 – 2000 it began what was considered as an increase in the genetic base, since around 70% of the genealogy of the 36 cultivars released commercially in this period originate from 11 ancestors (Table 3). Nevertheless, just as in the previous period, a preference was seen for the use of more adapted genotypes in the development of the cultivars, since Dee Geo Woo Gen, Cina, Latisail and MCVA are responsible for around 50% of the gene pool. The genetic base with the greatest number of ancestors was observed for the 26 cultivars released commercially from 2001 to 2012. In this period, ninety-two ancestors were used, thirty-nine of them being new, and approximately 60% of the genetic base is represented by 14 ancestors, practically double the average of the previous periods (Table 3). The greatest values of ANAC (20.19) and NA/NC (3.53) are also attributed to this period, which highlight the cultivars broad genetic base.

In spite of the large number of ancestors, the genetic base of Brazilian upland rice cultivars is considered to be narrow, since around 70% of the gene pool studied is derived from 13 ancestors. Cuevas-Pérez et al. (1992) obtained similar results for irrigated rice cultivars recommended from 1971 to 1989 for the regions of Latin America and the Caribbean. Similar to the present study, it was observed that 14 ancestors represented 70% of the genetic base, and that Cina, Latisail and Dee Geo Woo Gen were the most used ancestors. Montalván et al. (1998) report a similar narrowing for upland rice cultivars released for commercial use from 1971 to 1993; it was observed that approximately 70% of the genetic base is derived from the Brazilian ancestors Dourado Precoce, Pérola and Pratão.

When ancestors with RGC of less than 2% are disregarded, the genetic base becomes even narrower, being restricted to ten ancestors, which represent 66% of the entire gene pool (Table 1). Rangel et al. (1996) report greater narrowing of the genetic base of irrigated rice cultivars recommended for Brazil in the 1992/93 crop season, also obtaining an effective size (N_e) of ten ancestors, when considering only those with RGC above 2%. The same ten ancestors contributed to 68% of the genes of the cultivars used in the period from 1980 to1992.

The average number of ancestors per cultivar (ANAC) was estimated at 14.37 (Table 3). This parameter should be used with restriction in the study of genetic base, since it does not represent the amplitude of contributions from parents for the cultivars. In addition, within each cultivar, the genetic contributions of the ancestors vary in magnitude, such as the cultivar IRGA 425, which, in spite of being

Table 3. Number of cultivars (NC), number of ancestors (NA), average number of ancestor per cultivar (ANAC), number of ancestors responsible for 60%, 70%, 80% and 90% of the genetic base (NAGB), number of new ancestors added to the genetic base for each reporting period and ratio between the number of ancestors and the number of cultivars (NA/NC) of Brazilian irrigated rice cultivars released on the commercial market in the period from 1965 to 2012

Period	NC	NA	ANAC	NAGB (%)				NA/NC	Previous ancestors	New ancestors
				60	70	80	90			
1965-1980	17	32	5.88	6	8	11	15	1.88	-	32
1981-1990	31	43	10.87	6	8	13	20	1.39	18	25
1991-2000	36	59	17.27	7	11	16	25	1.64	32	27
2001-2012	26	92	20.19	14	19	26	38	3.53	53	39
1965-2012	110	123	14.37	8	13	23	43	1.12	-	-

composed of 36 ancestors, 50% of its genes come from the ancestor IRGA 1598.

The ratio between the number of ancestors and the number of cultivars (NA/NC) was 1.12, and it is considered low, comparing with values of other studies in which the genetic base was considered narrow. Cuevas-Pérez et al. (1992) obtained a value of 1.25 for the irrigated rice cultivars recommended for Latin America and the Caribbean from 1971 to 1989, and Montalván et al. (1998) obtained a value of 1.29 for Brazilian upland rice cultivars. Therefore, the value of NA/NC obtained in this study may be one more indication of the narrow genetic base of Brazilian irrigated rice.

The low value of NA/NC is brought about by the use of the same ancestors in the composition of various cultivars due to the preference of breeding programs in using the most adapted genotypes as parents in different crossings.

In relation to the use of genotypes from breeding programs in crossings, Nass and Parteniani (2000) emphasize that wild accessions, or those that are not a result of breeding programs, have been left aside by breeders since the use of new sources of variability requires prior work for characterization and more selection cycles for obtaining superior genotypes.

The ancestor Dee Geo Woo Gen is involved in the formation of 89.19% of the cultivars evaluated. According to Soares et al. (2004a), this genotype, as well as I Geo Tze, is Chinese cultivar that bear a recessive allele which confers low height, and, exclusively in these cultivars, the dwarf allele does not affect the stretching out of spikelets and panicles. Therefore, the use of these ancestors seeks to obtain semi-dwarf size cultivars, a trait that is desirable for modern rice cultivars.

The ancestors Cina and Latisail were likewise used in 83.78% of the cultivars. The high frequency of these genotypes in the genealogy is due in part to the fact of being the genitors of Peta cultivar - which, for its part, is the female parent of IR 8, with Dee Geo Woo Gen being the male parent. Released by the IRRI in 1966, IR 8 has semi-dwarf height, insensitivity to photoperiod, high tillering and high yield. IR 8 is considered as the first cultivar of the Indica group, which is highly productive and adapted to tropical climates (Soares et al. 2004a). Since it aggregates various agronomic traits favorable to the climatic conditions of Brazil, IR 8 was widely used in the development of Brazilian cultivars.

Table 4. Relative genetic contribution (RGC%), accumulated genetic contribution (AGC%) and frequency of the ancestors in the genealogy (FAG%) of the principal ancestors of Brazilian cultivars of rice released on the commercial market in the four reporting periods (1965-1980, 1981-1990, 1991-2000, 2001-2012)

Ancestors	**RGC** (%)	**AGC** (%)	**FAG** (%)
Period 1965-1980			
MarongParoc	16.2799	16.2799	58.8235
Dee Geo Woo Gen	12.5000	28.7799	52.9412
Cina	8.5938	37.3736	52.9412
Latisail	8.5938	45.9674	52.9412
Pa Chiam	7.8699	53.8373	58.8235
MCVA	6.2500	60.0873	41.1765
Period 1981-1990			
Dee Geo Woo Gen	17.0961	17.0961	96.7742
Latisail	15.0194	32.1155	90.3226
Cina	14.9501	47.0656	90.3226
MCVA	5.4435	52.5091	64.5161
I Geo Tze	5.4435	57.9527	64.5161
Tetep	4.9395	62.8922	32.2581
Period 1991-2000			
Dee Geo Woo Gen	15.9901	15.9901	100.0000
Latisail	15.1166	31.1067	94.4444
Cina	14.8935	46.0003	94.4444
MCVA	4.8665	50.8668	88.8889
I Geo Tze	4.8665	55.7333	88.8889
KhaoDawk Mali 105	3.7272	59.4606	61.1111
MarongParoc	3.1445	62.6051	97.2222
Period 2001-2012			
Dee Geo Woo Gen	11.2208	11.2208	88.4615
Latsail	9.4865	20.7072	84.6154
Cina	9.3893	30.0965	84.6154
MarongParoc	3.8840	33.9805	84.6154
KhaoDawk Mali 105	3.8105	37.791	50.0000
BRS Taim	3.3654	41.1564	3.8462
MCVA	3.0950	44.2514	73.0769
I Geo Tze	3.0950	47.3463	73.0769
AS 3510	2.8846	50.2309	15.3846
Tadukan	2.6433	52.8742	73.0769
IRGA 407	1.9231	54.7973	7.6923
17719	1.9231	56.7204	3.8462
Arborio	1.9231	58.6434	3.8462
IRGA 1598	1.9231	60.5665	3.8462

The narrowing of the genetic base in the period from 1965 to 1980 is more accentuated, for around 90% of the genes are represented by 15 ancestors, and the cultivars consist of an average of 1.88 ancestors (Table 3). In the period from 1981 to 1990, 70% of the gene pool came from eight ancestors, just like on the previous period. However, it can be considered that there was genetic narrowing, since the ancestors Dee Geo Woo Gen, Latisail, Cina and MCVA represented 52% of the total genealogy, and Dee Geo Woo Gen was the one that stood out (Table 4)

All the cultivars released commercially in the period from 1991 to 2000 have some degree of kinship, since 100% of them have genes from Dee Geo Woo Gen (Table 4). In the period from 2001 to 2012 it was observed some widening in genetic base for the 26 cultivars released commercially. In this period, 92 ancestors were used, 39 of them being new and approximately 60% of the genetic base is represented by 14 ancestors, practically double the average of the previous periods (Table 3). This may be due to disclosure of the genealogies and studies on the genetic base of Brazilian cultivars in the 1990's.

The greatest values of ANAC (20.19) and NA/NC (3.53) are also attributed to this period, which highlight the broad genetic base of the cultivars. Nevertheless, the genetic base may be considered as unbalanced, for only 38 ancestors represent around 90% of the genealogy, and the remaining 50 contribute to less than 10%. Just as in most of the previous periods, Dee Geo Woo Gen, Cina and Latisail were the most used ancestors. This practice restricts the possibilities for recombination in breeding programs and increases the genetic uniformity of the nucleus and cytoplasm, which may result in vulnerability of the cultivars to biotic and abiotic stresses and restriction of gains from selection, especially for quantitative traits (Vello et al. 1988, Rangel et al. 1996, 2000).

Aiming at expanding the genetic base, Rangel et al. (1996) suggest some alternatives. One of them would be the crossing of divergent parents originating from other breeding programs for the desired agronomic traits. Another option would be the use of multiple crossings between accessions of exotic germplasm and non-kin elite genotypes, or genotypes with a small degree of kinship. A third strategy consists of using recurrent selection for composition of populations with a broad genetic base; nevertheless, the high cost of implementation of this method impedes its adoption in breeding programs (Canci et al. 1997).

The use of male-sterile lines may make the use of recurrent selection viable, since it reduces operational costs, and favors natural recombination (Coimbra et al. 2008). However, the use of male-sterility is restricted due to the complexity of handling and maintenance of the genotypes bearing the sterility genes.

Rangel et al. (1996) also indicate the use of wild rice species as another alternative for expansion of the genetic base. In this context, the use of *O. glumaepatula* in hybridizations with *O. sativa* is an efficient alternative for increasing the genetic base of rice, as well as providing the attainment of genotypes with high yield and desirable agronomic traits, which are able to be used as parents in new crosses (Cordeiro and Medeiros 2010b).

It may be seen that the narrow total genetic base of Brazilian irrigated rice cultivars is due to the fact that the genetic breeding programs for Brazilian rice began from a reduced number of genotypes, nearly all of them coming from other countries. Over the years, there was incorporation of new sources of variability, which contributed to expansion of the genetic base. This may have arisen from awareness on the part of breeders in regard to the risks of genetic base narrowing. Nevertheless, the use of new genotypes appraisable by genetic breeding and better utilization of currently available genetic resources are necessary since many of the ancestors of the genetic base of Brazilian irrigated rice are little used.

CONCLUSIONS

The genetic base of Brazilian irrigated rice cultivars in the period from 1965 to 2012 is narrow.

The narrowing of the genetic base is mainly brought about by the use of the same genotypes as parents of various crossing.

The genetic base of cultivars released commercially in the period from 2001 to 2012 is the broadest among the periods evaluated. Nevertheless, many of the ancestors used in this period contribute in small proportion to the genetic base.

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Base genética das cultivares brasileiras de arroz irrigado

Resumo – *O presente trabalho teve por objetivo estimar a base genética de cultivares brasileiras de arroz irrigado liberadas comercialmente no período de 1965 a 2012. As genealogias das cultivares foram obtidas com base em informações de folders de divulgação de cultivares, sites de internet, livros de registros de cruzamentos e artigos científicos. Os seguintes fatores foram calculados: contribuição genética relativa (RGC), contribuição genética acumulada (AGC), frequência (em porcentagem) de cada ancestral na genealogia (FAG), número de ancestrais que constitui cada cultivar (NAC), número de ancestrais responsáveis por 60%, 70%, 80% e 90% da base genética (NAGB) e número médio de ancestrais por cultivar (ANAC). As cultivares foram também agrupadas baseando-se no período de lançamento (1965-1980, 1981-1990, 1991-2000 e 2001-2012); para cada agrupamento, os fatores previamente citados também foram estimados. Um total de 110 cultivares foi estudado. Concluiu-se que a base genética das cultivares brasileiras de arroz irrigado é estreita.*

Palavras-chave: Oryza sativa*, contribuição genética relativa, contribuição genética acumulada, genealogias, vulnerabilidade genética.*

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