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Assessment of the Genetic Diversity and Genetic Structure of Rice Core Parent Guichao 2, its Parents and Derivatives

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ABSTRACT

The concept of a "core parent" was proposed by breeders to describe elite lines with both good field performance and high potential for breeding superior new lines. Guichao 2 is one of the most important rice core parents in China. In the present study, Simple Sequence Repeat marker (SSR) based genome-wide screening was performed for Guichao 2, its parents and derivatives to study the genetic diversity and structure of them. A total of 348 polymorphic markers and 833 polymorphic alleles were detected. The Polymorphic Information Content (PIC) value ranged from 0.15 to 0.95 and averaged 0.39. Genetic similarity among the ten varieties varied from 0.751 to 0.926 with an average of 0.842, indicating that the genetic diversity is not abundant. At the whole genome level, Chaoyangzao 18 (30.4%) contributed many more genetic components to Guichao 2 than Guiyangai 49 (16.3%) did. The amount of genetic material transmitted by Guichao 2 to its derivatives varied from 49.7% (Qingliuai) to 59.5% (Fengqingai), with an average of 54.7%. In addition, 78 genomic regions of Guichao 2 were identified as stably inherited by these derivatives, with contribution ratios ranging from 14.29 to 85.71%, with an average of 47.25%. Ten of these regions with the same contribution ratio of 85.1% (RM3412-RM140, RM1339-RM1068, RM6997-RM6172, RM3524-RM3042, RM1388-RM1136, RM1353-RM1243, RM5508-RM3753, RM3395-RM3662, RM3662-RM44 and RM6643-RM2915) were found to be significantly important in the derivative cultivars.

Key words: Core parent, Guichao 2, derivative, genetic diversity, genetic structure, genetic contribution, SSR, PIC

INTRODUCTION

Rice is a staple food for nearly half of the world's population and it is likely the most important grain with regards to human nutrition and caloric intake, providing almost one-quarter of the global dietary energy supply per capita (Miura *et al*., 2010). China is a traditional country of rice planting and consumption and scientists and breeders here have concentrated their efforts on developing rice cultivars for decades. According information from China Rice Dada Centre, there are 6564 rice cultivars that have been released from 1949 to 2010. However, rice production in China has encountered a yield ceiling caused by a decrease in available arable land (Cheng *et al*., 2007). Consequently, it is still a challenge for rice scientists and breeders to develop high yield, high quality and disease-resistant rice varieties.

One of the most important events of human history is the domestication of cultivated plant species which allowing early human populations access to plentiful and stable food resources (Londo *et al*., 2006). As only a subset of wild plants is selectively propagated, the process of most crops' domestication associated with strong selection and genetic bottlenecks, resulted for in a precipitous loss of the genetic diversity. Rice is no exception; during domestication genetic diversity of cultivated rice was reduced up to 80% from the wild ancestor (Pusadee *et al*., 2009). While much of the world's rice harvest is based on modern high-yield varieties, it is essential and meaningful for breeders to reveal variations of genetic structure between parents and its derivatives for understanding the effects of core parent on its derivatives and using in future breeding programs.

Core parents are summarized according to breeding practices and pedigree analysis and core parents are characterized by many excellent agronomic qualities and high inherited ability. During a certain period, a core parent and its derivatives were widely used in crop production and breeding programs; certain features of many new cultivars might be found to come from them (Zhao *et al*., 2006). Guichao 2 which was derived from a cross between Guiyangai 49 and Chaoyangzao 18, is one of the most important parents in China. In the present study, a genome-wide scan of Guichao 2, its parents and derivatives was performed by using SSR markers to learn genetic diversity among these cultivars, the genetic structure of core parent and transfer patterns of genetic components to derivatives.

MATERIALS AND METHODS

Plant materials: Ten rice varieties were used in this study, including 8 derivatives of Guichao 2 and its parents, Chaoyangzao 18 and Guiyangai 49. All materials were supplied by the Rice Research Institution, Sichuan Agricultural University. Figure 1 displays the pedigree information of these varieties.

Microsatellite analysis: Total genomic DNA for microsatellite analysis was extracted from the leaves of field-planted seedlings using a modified Cetyltrimethyl Ammonium Bromide extraction (CTAB) method. A total of 2,092 SSR primer pairs covering all of the rice chromosomes were synthesized for the genome-wide scan.

Oligonucleotide primers were synthesized by Shanghai Sangon Biological Engineering Technology and Services Co. PCR amplifications were carried out in 20 μL reactions volumes containing 10×buffer (with $MgCl_2$) 2.0 μL, 2.0 μL dNTP (2.5 μmol L^{-1}), 0.3 μL Taq polymerase (5U μL^{-1}), 2.5 μL template DNA (50 ng μL^{-1}), 2.0 μL primers (50 pmol) and 11.2 μL ddH_2O. The reactions were performed using an M.J. PTC-220 DNA Engine Dyrad Cycler and the amplification conditions were as follows: 5 min at 94°C, 35 cycles of 45 s at 94°C, 45 s at 55°C, 45 s at 72°C and a final extension at 72°C for 10 min. Amplification products were electrophoresed on a 3.5% agarose gel containing Gelview (Bioteke Corporation).

Data analysis: Amplified fragment length polymorphism profiles were scored for the presence or absence of bands and similar size bands were assumed to be homologous. The data served as a tool for calculating the polymorphism information content of the markers being studied. For marker i, the Polymorphism Information Content (PIC) was calculated by using the simplified formula of (Anderson *et al*., 1993).

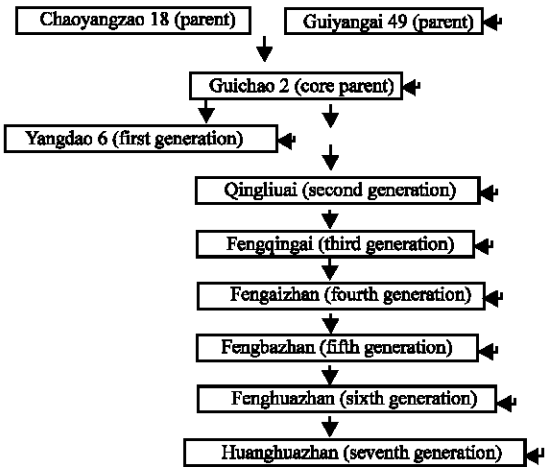

Fig. 1: Pedigree of core parent Guichao 2

$$PIC_i = 1 - \sum_{j=1}^{n} p_{ij}^2$$

where, taking into account not only the number of alleles per microsatellite locus but also their relative frequencies in the population studied, the PIC value provides an estimate of the discriminatory power of a microsatellite locus (Ribeiro-Carvalho *et al*., 2004).

DNA segments at polymorphic loci were scored as presence (1) or absence (0) of an allele and used to construct a binary matrix which was then transformed to genetic similarity matrix using Dice similarity coefficient. Genetic Similarities (GS) between pairs of accessions were measured as GS = 2a/(2a+b+c) where a is the number of positive matches (presence of an allele in both accessions) and b+c is the number of mismatches (presence of an allele either in one of the accessions but absent in the other accession) (Kuleung *et al*., 2006). Genotypes were grouped by cluster analysis according to their relationship, using the average linkage between groups fusion method UPGMA (unweighted pair group method with arithmetic average) in NTsys 2.10e[8] (Ribeiro-Carvalho *et al*., 2004).

The genetic contributions of Guichao 2 or its parents were countered by the method described by HAN (Jun *et al*., 2009).

RESULTS

SSR and genetic diversity analysis: Out of 2,092 SSR primer pairs, 348 markers (29.57%) indicated amplification polymorphisms among all the 10 rice varieties. Detailed information for these primers is shown in Table 1. A total of 833 polymorphic alleles were obtained in the 10 rice varieties. The number of alleles detected by a single marker ranged from 2 to 6 with an average of 2.39 alleles. The markers on chromosome 9 had the highest average allelic number, 2.61±0.14, while those on chromosome 4 had the lowest number: 2.21±0.09 (Fig. 2). The Polymorphic Information Content (PIC) value was calculated for each marker and each chromosome (Table 2). The PIC value ranged from 0.15 to 0.95 and averaged 0.39 for each marker. The highest mean PIC was 0.42±0.03 on chromosomes 10 and 12 and the lowest mean PIC was 0.33±0.03 on chromosome 4. On the other hand, RM3520, a marker located on chromosome 1, had the highest PIC value

Table 1: Information of microsatellite markers

Chromosomes	Marker amount	Polymorphic markers	Polymorphism rate (%)	Average physical distance (Kb)
1	100	27	27.00	435.81
2	110	20	18.18	326.59
3	113	35	30.97	321.64
4	104	28	26.92	338.88
5	124	35	28.23	240.86
6	73	17	23.29	427.84
7	116	40	34.48	255.71
8	110	41	37.27	257.35
9	79	33	41.77	290.37
10	82	25	30.49	278.99
11	85	28	32.94	334.84
12	81	19	23.46	339.46
Total	1177	348		

Marker amount: No. of markers on a chromosome, Polymorphic markers: No. of polymorphic markers on a chromosome, Average physical distance: Average physical distance between two neighbour markers

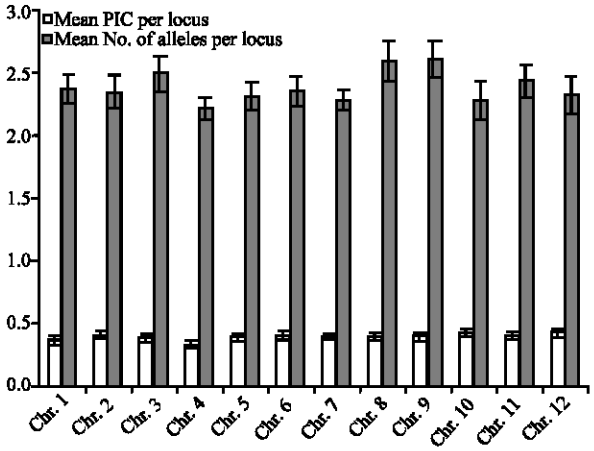

Fig. 2: Polymorphism information content for chromosomes

(0.95); RM1068 and RM3631 which were located on chromosome 1 and 5, respectively, shared the lowest PIC value (0.15). Furthermore, aside from RM3520, there were other nine markers that had PIC values higher than 0.70 which were RM2421 (Chr.3), RM4501 (Chr.5), RM1959 (Chr.8), RM1384 (Chr.8), RM8057 (Chr.8), RM3025 (Chr.9), RM2504 (Chr.10), RM 1355 (Chr.11) and RM2596 (Chr.11). For all 348 markers, 88 of them had PIC values below 0.25, 183 of them ranged from 0.25 to 0.5 and 77 of them had PIC values falling between 0.5 and 1.0.

Genetic similarity among the ten varieties varied from 0.751 to 0.926 with an average of 0.842. And these varieties could be divided into two clusters when the coefficient is 0.78, cluster I contains 4 varieties and the rest 6 formed cluseter II (Fig. 3). Just as we expected, all derivatives were grouped in cluster II except Yandao 6. While, cluster I consisted of Guichao 2, its parent and a first generation Yangdao 6. In accordance with previous analysis results, genetic constituent of Guichao 2 is more similar to Chaoyangzao 18 than Guiyangai 49. Otherwise, from results of cluster II, we find the two varieties with direct genetic relationship always be grouped into a same cluster. It indicated results of cluster analysis via SSR markers were corresponded with the Pedigree which was credible and reliable.

Table 2: PIC values of SSR markers

Markers	Chr.	PIC	Markers	Chr.	PIC	Markers	Chr.	PIC	Markers	Chr.	PIC	Markers	Chr.	PIC
RM495	1	0.18	RM426	3	0.58	RM7081	5	0.18	RM1376	8	0.42	RM6833	10	0.50
RM3148	1	0.54	RM6329	3	0.42	RM3631	5	0.15	RM1148	8	0.58	RM4455	10	0.46
RM6324	1	0.32	RM3525	3	0.58	RM87	5	0.32	RM3572	8	0.18	RM3283	10	0.48
RM3652	1	0.34	RM8269	3	0.32	RM7653	5	0.48	RM5432	8	0.18	RM6142	10	0.18
RM3425	1	0.32	RM5801	3	0.32	RM3170	5	0.58	RM1111	8	0.54	RM5758	10	0.58
RM151	1	0.18	RM3719	3	0.34	RM8121	6	0.18	RM8019	8	0.32	RM5689	10	0.32
RM490	1	0.42	RM1230	3	0.18	RM8059	6	0.18	RM6429	8	0.34	RM1937	10	0.48
RM243	1	0.18	RM5612	3	0.18	RM170	6	0.32	RM3214	8	0.34	RM6704	10	0.42
RM1287	1	0.54	RM6363	3	0.18	RM7639	6	0.32	RM6010	8	0.18	RM6737	10	0.18
RM3412	1	0.32	RM422	3	0.48	RM190	6	0.48	RM3395	8	0.18	RM6100	10	0.42
RM140	1	0.18	RM442	3	0.18	RM6263	6	0.32	RM3662	8	0.18	RM3510	10	0.48
RM6681	1	0.48	RM148	3	0.48	RM1163	6	0.42	RM44	8	0.18	RM304	10	0.42
RM5964	1	0.18	RM200	4	0.48	RM6176	6	0.48	RM1384	8	0.78	RM6745	10	0.18
RM5422	1	0.34	RM8213	4	0.46	RM5754	6	0.34	RM3409	8	0.18	RM1146	10	0.42
RM7192	1	0.34	RM3658	4	0.18	RM2615	6	0.46	RM6382	8	0.32	RM5841	10	0.42
RM5718	1	0.56	RM3471	4	0.62	RM3330	6	0.42	RM2910	8	0.32	RM3773	10	0.48
RM5	1	0.54	RM6659	4	0.5	RM3827	6	0.18	RM7285	8	0.18	RM4477	10	0.64
RM488	1	0.54	RM1155	4	0.18	RM7579	6	0.46	RM1309	8	0.58	RM5471	10	0.32
RM5931	1	0.18	RM5635	4	0.46	RM6202	6	0.48	RM3689	8	0.58	RM3750	10	0.42
RM3324	1	0.18	RM6997	4	0.32	RM7309	6	0.56	RM342	8	0.32	RM1162	10	0.32
RM8002	1	0.64	RM6172	4	0.18	RM3430	6	0.58	RM5808	8	0.32	RM7093	10	0.42
RM1339	1	0.18	RM3524	4	0.18	RM5509	6	0.58	RM7356	8	0.34	RM1248	11	0.48
RM1068	1	0.15	RM3042	4	0.46	RM3831	7	0.46	RM210	8	0.48	RM181	11	0.42
RM7246	1	0.32	RM3866	4	0.50	RM5711	7	0.32	RM8057	8	0.8	RM1182	11	0.42
RM3520	1	0.95	RM3839	4	0.18	RM1353	7	0.18	RM3361	8	0.18	RM6327	11	0.18
RM104	1	0.32	RM7051	4	0.18	RM1243	7	0.18	RM419	8	0.48	RM3863	11	0.74
RM8136	1	0.32	RM138	84	0.18	RM1134	7	0.46	RM1345	8	0.18	RM1812	11	0.42
RM7451	2	0.66	RM1136	4	0.18	RM8006	7	0.18	RM3895	8	0.48	RM5918	11	0.18
RM110	2	0.50	RM1354	4	0.18	RM3583	7	0.42	RM447	8	0.42	RM1124	11	0.18
RM236	2	0.42	RM5714	4	0.18	RM3859	7	0.32	RM3754	8	0.32	RM5704	11	0.46
RM7082	2	0.46	RM5320	4	0.42	RM1186	7	0.32	RM3761	8	0.42	RM7283	11	0.18
RM5897	2	0.48	RM2441	4	0.42	RM3635	7	0.48	RM3120	8	0.58	RM3185	11	0.48
RM3680	2	0.18	RM6365	4	0.18	RM7184	7	0.56	RM3840	8	0.18	RM1206	11	0.42
RM1081	2	0.32	RM5511	4	0.18	RM2878	7	0.48	RM3609	9	0.18	RM7391	11	0.48
RM1234	2	0.18	RM5473	4	0.50	RM3755	7	0.32	RM8219	9	0.18	RM4862	11	0.46
RM424	2	0.46	RM3335	4	0.18	RM7338	7	0.48	RM5688	9	0.66	RM6272	11	0.18
RM7426	2	0.18	RM5506	4	0.42	RM5543	7	0.56	RM5799	9	0.18	RM287	11	0.32
RM5101	2	0.54	RM131	4	0.42	RM5481	7	0.32	RM4348	9	0.46	RM1355	11	0.70
RM5578	2	0.50	RM127	4	0.48	RM7110	7	0.42	RM6920	9	0.34	RM6680	11	0.58
RM3858	2	0.50	RM2431	4	0.48	RM5603	7	0.32	RM5515	9	0.34	RM5349	11	0.32
RM1694	2	0.48	RM1248	5	0.18	RM5793	7	0.48	RM5526	9	0.34	RM2596	11	0.70
RM332	2	0.66	RM153	5	0.18	RM6835	7	0.56	RM7364	9	0.32	RM3605	11	0.18
RM5427	2	0.34	RM5816	5	0.48	RM418	7	0.48	RM296	9	0.42	RM206	11	0.54
RM3874	2	0.48	RM4777	5	0.58	RM6394	7	0.18	RM3769	9	0.58	RM6105	11	0.18
RM6366	2	0.32	RM6300	5	0.18	RM432	7	0.58	RM1896	9	0.66	RM4112	11	0.50
RM1092	2	0.42	RM3334	5	0.46	RM3691	7	0.32	RM105	9	0.18	RM2778	11	0.50
RM3535	2	0.18	RM1200	5	0.18	RM3404	7	0.42	RM88	9	0.18	RM2064	11	0.34
RM4108	3	0.32	RM5579	5	0.34	RM3826	7	0.46	RM6771	9	0.32	RM4844	11	0.34

Table 2: Continued

Markers	Chr.	PIC	Markers	Chr.	PIC	Markers	Chr.	PIC	Markers	Chr.	PIC	Markers	Chr.	PIC
RM5761	3	0.34	RM3853	5	0.32	RM182	7	0.32	RM5122	9	0.32	RM5926	11	0.18
RM6829	3	0.18	RM3777	5	0.48	RM5495	7	0.18	RM3700	9	0.18	RM1880	12	0.42
RM6849	3	0.42	RM3328	5	0.32	RM70	7	0.50	RM3025	9	0.78	RM2851	12	0.18
RM2421	3	0.80	RM7118	5	0.46	RM5508	7	0.18	RM3492	9	0.46	RM20	12	0.48
RM3126	3	0.54	RM2998	5	0.66	RM3753	7	0.32	RM7175	9	0.42	RM6371	12	0.42
RM35	3	0.32	RM3381	5	0.48	RM5397	7	0.42	RM410	9	0.66	RM3472	12	0.66
RM5347	3	0.32	RM3437	5	0.42	RM8023	7	0.18	RM2190	9	0.50	RM7003	12	0.42
RM6058	3	0.18	RM7363	5	0.48	RM6420	7	0.18	RM5535	9	0.58	RM3103	12	0.42
RM1002	3	0.42	RM1237	5	0.50	RM3552	7	0.54	RM3919	9	0.58	RM3246	12	0.48
RM7	3	0.42	RM5948	5	0.32	RM1209	7	0.48	RM3249	9	0.32	RM7195	12	0.42
RM282	3	0.18	RM163	5	0.48	RM3555	7	0.56	RM3787	9	0.58	RM5939	12	0.34
RM338	3	0.18	RM164	5	0.18	RM1357	7	0.62	RM201	9	0.18	RM1047	12	0.42
RM3291	3	0.32	RM3638	5	0.50	RM1362	7	0.32	RM1553	9	0.34	RM1337	12	0.32
RM3400	3	0.54	RM3663	5	0.32	RM1306	7	0.42	RM6643	9	0.18	RM7102	12	0.42
RM1334	3	0.46	RM3575	5	0.48	RM5911	8	0.48	RM2915	9	0.34	RM1261	12	0.18
RM5684	3	0.32	RM3800	5	0.42	RM6369	8	0.48	RM6294	9	0.48	RM1986	12	0.64
RM7431	3	0.54	RM4501	5	0.74	RM1019	8	0.58	RM2482	9	0.46	RM3813	12	0.48
RM2453	3	0.62	RM5401	5	0.32	RM1959	8	0.72	RM7586	9	0.18	RM3331	12	0.18
RM7395	3	0.46	RM3295	5	0.32	RM3702	8	0.32	RM7492	10	0.48	RM12	12	0.48
RM6832	3	0.46	RM3870	5	0.32	RM1235	8	0.58	RM2504	10	0.74	RM1296	12	0.58
RM5626	3	0.32	RM5311	5	0.58	RM4955	8	0.48	RM5348	10	0.32			
RM2614	3	0.32	RM3673	5	0.18	RM3819	8	0.18	RM3311	10	0.32			

Note: PIC values of 348 Polymorphic markers on all twelve chromosomes

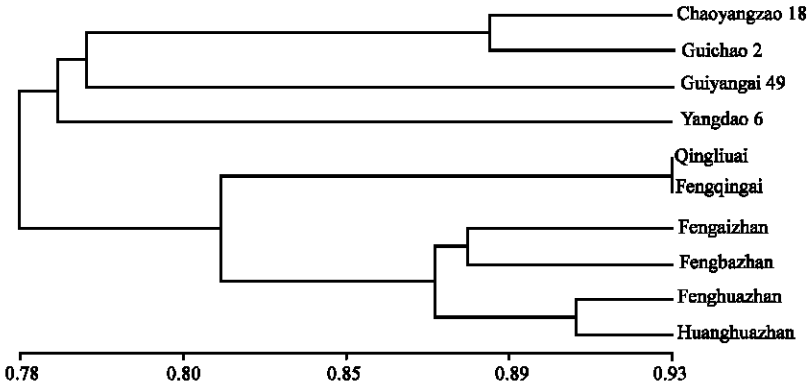

Fig. 3: Genetic similarity of Guichao 2, its parents and derivatives

Genetic structure of Guichao 2 and its genetic contribution to derivatives: Based on the results of SSR analysis, we found that Chaoyangzao 18 contributed more genetic components (30.4%) to Guichao 2 than Guiyangai 49 (16.3%) on the whole genome level. Figure 4 indicated genomic contributions of Chaoyangzao 18 and Guiyangai 49 to Guichao 2. As far as single chromosome, the contributions of Chaoyangzao 18 varied from 6.9% (Chr.11) to 56.0% (Chr.10); while those of Guiyangai 49 ranged from 10.0% (Chr. 1 and Chr.7) to 42.9% (Chr.4). Otherwise, for most chromosomes, Chaoyangzao 18 contributed more genomic components than Guiyangai 49, especially for chromosome 12, Guiyangai 49 contributed none genomic regions to Guichao 2.

Figure 5 shows the genetic contribution of Guichao 2 to its derivatives. The lowest contribution was 10.5%, to Fengaizhan which came from chromosome 12 and the highest contribution was

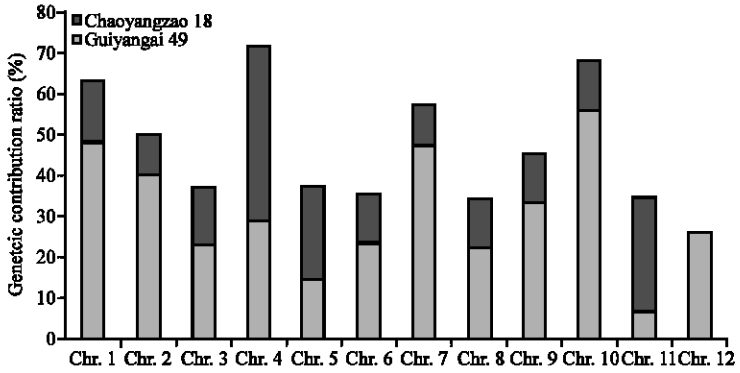

Fig. 4: Genomic Contributions of Chaoyangzao 18 and Guiyangai 49 to Guichao 2

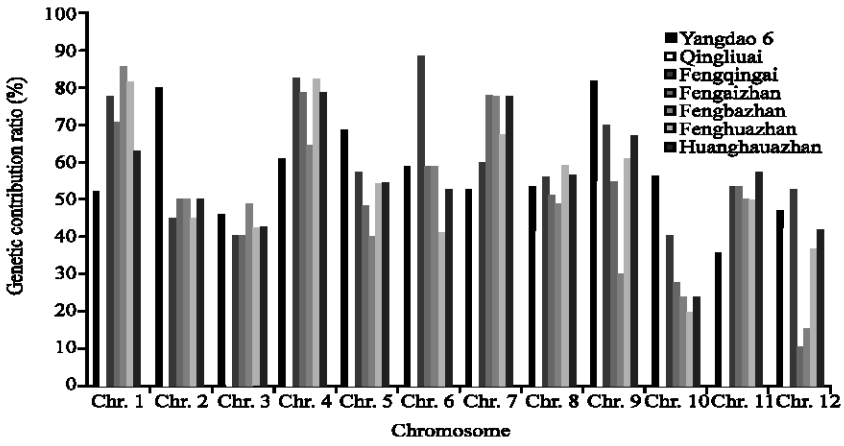

Fig. 5: Genetic contribution ratio of Guichao 2 to its derivatives

88.2%, to Fengqingai which came from chromosome 6. As a core parent, the amount of genetic components Guichao 2 contributed to its derivatives varied within a small range, from 49.7% (Qingliuai) to 59.5% (Fengqingai) and averaged 54.7%. In stark contrast with the whole genome level, the contribution of single chromosome varied over a large scale, from 33.1% (Chr.10) to 73.5% (Chr. 4) and averaged 54.0%.

Deliveries of genomic regions: As for genomic regions, there are 78 regions of Guichao 2 that were inherited by these derivatives; its contribution ratio ranged from 14.29 to 85.71% and averaged 47.25% (Table 3). Ten of these regions, RM3412-RM140, RM1339-RM1068, RM6997-RM6172, RM3524-RM3042, RM1388-RM1136, RM1353-RM1243, RM5508-RM3753, RM3395-RM3662, RM3662-RM44 and RM6643-RM2915 were found to be significantly important in the derivative cultivars, owing to all of them had the contribution ratio of 85.1%. Meanwhile, from the data shown in Table 3, we found that the 3 genomic regions with the highest contribution ratio all came from chromosome 4 and none of the 10 genomic regions listed above came from chromosomes 2, 3, 5, 6, 10, 11 or 12.

Table 3: Contribution ratio of genomic regions derived from Guichao 2

Chromosome	Genome region	Contribution ratio (%)	Chromosome	Genome region	Contribution ratio (%)	Chromosome	Genome region	Contribution ratio (%)
Chr.1	RM495-RM3148	42.86	Chr.5	RM7363-RM1237	14.29	Chr.9	RM5688-RM5799	42.86
Chr.1	RM1287-RM3412	57.14	Chr.5	RM3575-RM3800	14.29	Chr.9	RM6920-RM5515	71.43
Chr.1	RM3412-RM140	85.71	Chr.5	RM5401-RM3295	71.43	Chr.9	RM5515-RM5526	71.43
Chr.1	RM6681-RM5964	42.86	Chr.6	RM170-RM7639	71.43	Chr.9	RM296-RM3769	42.86
Chr.1	RM5964-RM5422	71.43	Chr.6	RM7639-RM190	28.57	Chr.9	RM3769-RM1896	28.57
Chr.1	RM1339-RM1068	85.71	Chr.6	RM190-RM6263	28.57	Chr.9	RM6771-RM5122	42.86
Chr.1	RM3520-RM104	71.43	Chr.6	RM1163-RM6176	42.86	Chr.9	RM5122-RM3700	57.14
Chr.2	RM1081-RM1234	71.43	Chr.7	RM1353-RM1243	85.71	Chr.9	RM3025-RM3492	14.29
Chr.2	RM5578-RM3858	42.86	Chr.7	RM1243-RM1134	71.43	Chr.9	RM3919-RM3249	14.29
Chr.2	RM332-RM5427	14.29	Chr.7	RM3755-RM7338	28.57	Chr.9	RM3249-RM3787	28.57
Chr.3	RM3400-RM1334	28.57	Chr.7	RM418-RM6394	57.14	Chr.9	RM6643-RM2915	85.71
Chr.3	RM7431-RM2453	28.57	Chr.7	RM432-RM3691	57.14	Chr.10	RM3311-RM6833	28.57
Chr.4	RM200-RM8213	14.29	Chr.7	RM3404-RM3826	28.57	Chr.10	RM6833-RM4455	14.29
Chr.4	RM8213-RM3658	71.43	Chr.7	RM5508-RM3753	85.71	Chr.10	RM4455-RM3283	14.29
Chr.4	RM3658-RM3471	42.86	Chr.7	RM3753-RM5397	42.86	Chr.10	RM3283-RM6142	42.86
Chr.4	RM3471-RM6659	42.86	Chr.7	RM1362-RM1306	71.43	Chr.10	RM6142-RM5758	42.86
Chr.4	RM6997-RM6172	85.71	Chr.8	RM5911-RM6369	14.29	Chr.10	RM3510-RM304	14.29
Chr.4	RM3524-RM3042	85.71	Chr.8	RM4955-RM3819	28.57	Chr.10	RM1146-RM5841	14.29
Chr.4	RM1388-RM1136	85.71	Chr.8	RM1148-RM3572	28.57	Chr.11	RM7283-RM3185	42.86
Chr.4	RM5320-RM2441	57.14	Chr.8	RM3572-RM5432	71.43	Chr.11	RM3185-RM1206	42.86
Chr.4	RM131-RM127	28.57	Chr.8	RM6429-RM3214	71.43	Chr.11	RM1206-RM7391	42.86
Chr.5	RM153-RM5816	57.14	Chr.8	RM3395-RM3662	85.71	Chr.11	RM6680-RM5349	14.29
Chr.5	RM6300-RM3334	71.43	Chr.8	RM3662-RM44	85.71	Chr.11	RM2596-RM3605	14.29
Chr.5	RM3334-RM1200	57.14	Chr.8	RM44-RM1384	14.29	Chr.11	RM4844-RM5926	71.43
Chr.5	RM3853-RM3777	42.86	Chr.8	RM3754-RM3761	14.29	Chr.12	RM1880-RM2851	57.14
Chr.5	RM3437-RM7363	42.86	Chr.9	RM8219-RM5688	42.86	Chr.12	RM20-RM6371	42.86

Note: 78 genetic regions were inherited from Guichao 2 by its derivatives, this table showed the contribution ratios of these regions

DISCUSSION

Core parents are particularly significant for selecting cultivars to breed because they are defined through analysis of good cultivars' pedigrees (Jun *et al*., 2009). Due to the fact that a core parent not only has excellent agronomic characteristics but also has a strong capacity to deliver crucial genetic regions associated with important traits to its descendants, it is helpful to select good cultivars. Guichao 2 has several characteristics that are considered ideal, such as a heavy panicle, a high number of grains, a high seed-set rate, a high thousand-grain weight and wide adaptability. These qualities have enabled Guichao 2 to act as a superior commercial cultivar and to be wildly cultivated all over China in the 1980s; in 1982, the cultivation area of this cultivar reached 2710 thousand ha in China. In addition, Guichao 2 has given rise to over thirty derivative cultivars. Since 1983, the cultivated area of Guichao 2 and 20 of its derivatives has amounted to 14.66 million ha. Yangdao 6, also designated as 9311, is a famous derivate line of Guichao 2 and its whole genome sequence was completed due to its outstanding field performance. Thus, analyzing and recognizing Guichao 2 on a genomic level will definitely benefit the breeding practice, especially for core parents and for the promotion of hybrid combinations in the future (Ge *et al*., 2009).

In this study we use SSR markers to perform genome-wide screening to evalutate genetic diversity and genetic structure of Guichao 2, its parents and derivatives. Previous researches prove molecular markers provide a powerful tool for locating and distinguishing these key genetic regions on the whole genome (Puchooa and Venkatasany, 2005; Tertivanidis *et al*., 2008; Yasmin *et al*.,

2006; Nazari and Pakniyat, 2008). While, microsatellite markers are widely utilized in genetic diversity analysis because of their abundant numbers, good polymorphisms and high repeatability (Guasmi *et al*., 2008; Belaj *et al*., 2007; Cao *et al*., 2006). Olufowote evaluated Seventy-one rice cultivars within-cultivar variation by using a combination of phenotypic, RFLP and microsatellite or simple sequence length polymorphism and results suggest that the use of four well-chosen microsatellites would be an efficient method for evaluating the heterogeneity of rice accessions (Olufowote *et al*., 1997). Gao *et al*. (2002) investigated genetic structure of five natural populations of common wild rice from China with 21 microsatellite loci and compare to estimates of genetic diversity and genetic differentiation detected by 22 allozyme loci and they found microsatellite markers are powerful high-resolution tools for the accurate assessment of important parameters in population biology and conservation genetics of *O. rufipogon* and offer advantages over allozyme markers.

Li *et al*. (2008) investigated genetic diversity of a wheat cultivar and its derivatives with 22 SSR markers, total of 133 alleles were detected among 54 materials and the number of alleles each primer pair ranged from 3 to15 with an average of 6.05. The PIC value ranged from 0.2606 to 0.8579, averaged at 0.6529. Genetic similarity varied from 0.549 to 0.962 with an average of 0.7474. While, according Chen *et al*. (2008) research, a set of 24 pairs of SSR primers with stable amplified band patterns were screened and a total of 126 alleles were scored. 3 to 11 alleles could be detected by each SSR primer with the average number of 5. 25. The genetic similarity (GS) between two cultivars among the 33 wheat cultivars (lines) varied from 0.373 to 0.794 and the average was 0.597. In this study, a total of 348 polymorphic markers and 833 polymorphic alleles were detected. The Polymorphic Information Content (PIC) value ranged from 0.15 to 0.95 and averaged 0.39. GS among the ten varieties varied from 0.751 to 0.926 with an average of 0.842. Compare with previous researches, it indicates the genetic diversity among these ten varieties is not abundant and the reason may be their close blood relationships. Cluster analysis showed the ten varieties could be grouped in two clusters. Cluster I consist of Guichao 2, its parents and a first generation; cluster II consist of other six derivatives and the two varieties which have direct genetic relationship always be grouped into a same sub-cluster of cluster II. These facts proved cluster analysis via SSR markers were corresponded with the pedigree and it was credible and reliable.

According to the results of SSR analysis, Chaoyangzao 18 transmitted more genetic components to Cuichao 2; especially Chr.10 of it had the greatest contributions to the chromosomes of Guichao 2. Guichao 2 transmitted 78 genomic regions to its derivatives and some of them should be considered significant. For instance, qPE9-1 was mapped to RM3025-RM3492; this is a main QTL of panicle erectness and improves plant architecture during rice domestication (Zhou *et al*., 2009). Gene Rf-4 was located on RM3510-RM304 and is a pollen fertility restoration gene for wild abortive-cytoplasmic male sterility in rice (Bharaj *et al*., 1995). OsGH3.13 is indole-3-acetic acid-amido synthetase gene and was mapped to RM6680-RM5349 (Zhang *et al*., 2009). A research indicated that rice could alter their architecture and enhance drought tolerance via down-regulation of indole-s-acetic acid by OsGH3.13 activation (Zhang *et al*., 2009). In addition, EL5 was mapped to RM332-RM542 and is an ubiquitin ligase gene that is involved in root development through maintenance (Koiwai *et al*., 2007).

CONCLUSION

The present results suggest rice core parent Guichao 2 inherited more genetic components from Chaoyangzao 18 than Guiyangai 49 and delivered some genetic regions to its derivatives and these

regions might be related to some major agronomic characters QTLs. Otherwise, genetic diversity among these ten cultivars is not abundant due to their close blood relationships.

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