

Genetic diversity and structure of *indica* rice varieties from two heterotic pools of southern China and IRRI

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Abstract

Investigation of genetic diversity and the relationships among varieties and breeding lines is of great importance to facilitate parental selection in the development of inbred and hybrid rice varieties and in the construction of heterotic groups. The technology of single nucleotide polymorphism (SNP) is being advanced for the assessment of population diversity and genetic structures. We characterized 215 widely cultivated *indica* rice varieties developed in southern China and at the International Rice Research Institute (IRRI) using IRRI-developed SNP oligonucleotide pooled assay (OPA) to provide grouping information of rice mega-varieties for further heterotic pool study. The results revealed that the Chinese varieties were more divergent than the IRRI varieties. Two major subpopulations were clustered for the varieties using a model-based grouping method. The IRRI varieties were closely grouped and separated clearly from the majority of the Chinese varieties. The Chinese varieties were subclustered into three subgroups, but there was no clear evidence to separate the Chinese varieties into subgroups geographically, indicating a great degree of genetic integration of alleles and shared ancestries among those high-yielding modern varieties.

Keywords: Chinese variety; genetic diversity; hybrid rice; IRRI variety; single nucleotide polymorphism markers

Introduction

High-yielding varieties (HYVs) and elite germplasm derived from semi-dwarf rice breeding since the 1960s have been applied either on a large scale in rice

production or as parents in developing new inbred and hybrid rice varieties. Germplasm exchange among breeding programmes promotes new variety development, but it may also increase genetic similarity as all breeding programmes pursue limited common variety traits.

Crop heterosis is significantly increased by combining genetically distinct parental materials, i.e., parents belonging to distinct heterotic pools. Heterotic pools can be identified through the study of agro-morphological differentiation and the characterization of genetic diversity

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at the DNA level via molecular markers. Detection of DNA polymorphisms has been extensively employed as a mean to assess genetic diversity and its relationship to heterosis in maize (Lee *et al.*, 1989; Dudley *et al.*, 1991; Boppenmaier *et al.*, 1993; Reif *et al.*, 2003) and rice (Xie, 1993; Zhang *et al.*, 1994, 1995). Early studies have shown that heterotic rice hybrids in China were derived from distant parents of different geographical origins or ecotypes or subspecies (Yuan, 1977). Two heterotic pools, i.e., early-season *indica* varieties in the regions of the Yangtze River Valley and mid- or late-season *indica* varieties from South and Southeast Asia (mainly the varieties developed at the International Rice Research Institute (IRRI) in the Philippines) were identified for the three-line Chinese hybrid rice (Yuan, 1977; Lu and Xu, 2010) with many commercial hybrids developed. Parental selection based on distant relations geographically and biotype differences have been the most important factors for heterotic hybrid development, but the recent development of super high-yielding hybrids in China has involved many crosses between subspecies or parents derived from subspecies. The development of heterotic rice hybrids still relies mostly on the breeders' trial-and-error approach. It is both urgent and justified to explore the genetic relationships and diversity of parental populations more widely and in more detail for further hybrid rice breeding. The study of genetic variation among southern Chinese and IRRI rice varieties attracts the interest of rice breeders since *indica* is the major cultivated rice in southern China and in other tropical Asian countries, and it provides a rich source of germplasm as hybrid rice parents.

Detection and analysis of genetic diversity in rice germplasm have been immensely facilitated with the use of molecular markers (Collard *et al.*, 2008; Moose and Mumm, 2008). Single nucleotide polymorphisms (SNPs) are widely becoming the marker of choice due to their high-throughput capacity, cost-effectiveness, efficiency, and abundant type of polymorphisms to potentially increase the speed and efficiency of research and breeding activities (McNally *et al.*, 2009; McCouch *et al.*, 2010; Chen *et al.*, 2011; Thomson *et al.*, 2012). SNP marker profiling of rice germplasm has shown great genetic variability and significant differentiation among rice subspecies or landraces (Zhao *et al.*, 2011), yet none of the documented studies has so far dealt with genetic diversity in HYVs and their potential application for heterotic pools.

In this study, using SNP markers, we evaluated the population structure of southern Chinese and IRRI rice varieties that have been popularly cultivated on a large scale of production and/or are also used extensively in rice breeding programmes as donor parents, but, most importantly, those varieties represent the two known rice heterotic pools. This study aims to characterize and analyse the population structure and diversity based on

SNP molecular markers, and to provide baseline data and references for parental selection to further the studies on rice heterotic pools.

Materials and methods

Plant materials

Plant materials for the study comprised 215 diverse *Oryza sativa* L. *indica* varieties selected from 11 provinces in southern China (161) and IRRI (54). The Chinese samples were from the rice germplasm bank at the China National Rice Research Institute (CNRRI) and originated from Anhui (6 varieties), Fujian (17), Guangdong (33), Guangxi (6), Henan (5), Hubei (6), Hunan (18), Jiangsu (3), Jiangxi (23), Sichuan (17) and Zhejiang (27). The IRRI samples were the lowland irrigated inbreds historically released as commercial varieties, including from IR8 (released in 1966) to IRRI154 (released in 2009) (see Table S1, available online only at <http://journals.cambridge.org>). All of the CNRRI and IRRI varieties were both commercial rice cultivars grown on a large scale and parents that were widely used in various rice breeding programmes in China and in South and Southeast Asian countries. Information on all the IRRI varieties is available from the IRRI database (<http://www.iris.irri.org/germplasm/>) while the information on all the Chinese varieties can be requested from the website <http://chinariceinfo.com> or <http://icgr.caas.net.cn>.

DNA extraction and SNP genotyping

All of the samples were cleaned and purified using single-seed-descent in the previous generations. Genomic DNA from the samples was isolated from three to five leaves of 21-d-old plants per line using the modified cetyltrimethylammonium bromide method (Murray and Thompson, 1980). The isolated DNA was RNase-treated and the final concentration was normalized to 50 ng/ μ l. The GoldenGate Genotyping Protocol of the Veracode Technology was applied in SNP genotyping, which was carried out at the Molecular Marker Applications Laboratory at IRRI. RiceOPA2.1, a 384-plex oligonucleotide pool assay (OPA) designed for *indica/indica* genotypes (Thomson *et al.*, 2012), was used as markers.

SNP data generation and analysis

Scan results were generated from Illumina's BeadXpress Reader, from which the allele calls generated from the GenomeStudio software were then corrected using

ALCHEMY software (Wright *et al.*, 2010). Genetic diversity and distances measured 14. Cavalli-Sforza chord (CSChord) (Cavalli-Sforza and Edwards, 1967) were estimated using PowerMarker v3.25 (Liu and Muse, 2005). Principal coordinate analysis (PCA) of the Chinese and IRRI samples was performed based on the CSChord (Cavalli-Sforza and Edwards, 1967) distance matrix using GENALEX 6 (Peakall and Smouse, 2006). The model-based program STRUCTURE (Pritchard *et al.*, 2000) was used to infer population structure and to assign individual varieties into subpopulations. Models with a putative number of subpopulations (K) from 1 to 10 with admixture and correlated allele frequencies were considered (Falush *et al.*, 2003). Ten independent runs with 20,000 burn-in cycles and 10,000 iterations for each K were implemented based on trial runs of the program. To determine the uppermost level of the K value, Evanno's ΔK was used (Evanno *et al.*, 2005). With the same settings of program parameters, STRUCTURE was rerun for assignments of individual Chinese varieties into subgroups based on the maximum of inferred ancestry of individuals. For a graphic view of the parental classification of the Chinese samples, cluster analysis with the 384 SNP markers was carried out using PowerMarker with neighbour-joining tree and viewed in MEGA 5 (Tamura *et al.*, 2011).

Results

Genetic diversity of the Chinese and IRRI varieties

Each of the SNP markers, except three showing monomorphism (id3002191, id6010434 and wd5001329), gave two alleles per locus across all of the Chinese and IRRI varieties and resulted in an average of 1.9922 alleles per locus (Table 1). An additional 4 and 37 markers were found monomorphically among the Chinese and IRRI varieties, respectively, when they were analysed separately.

It was observed that the diversity measurements - gene diversity, polymorphism information content (PIC) and genetic distance across all of the samples, were 0.3136,

0.2529 and 0.2869, respectively, which were higher than those indices measured from each individual sample source (CNRRI and IRRI). However, the major allele frequency for all the varieties was 0.7690, which was lower than that estimated from the individual sample sources. Compared with the IRRI varieties, the Chinese samples showed higher values in all of the diversity indices measured except for the major allele frequency. Specifically, the average genetic distance of the Chinese varieties was 0.2720, which was significantly ($P < 0.001$) higher than the average genetic distance (0.2412) of the IRRI varieties. Both sets of the samples have a minimum of zero distance between pairs, but the maximum distances were 0.5311 and 0.3658, respectively, among the pairs in the Chinese and IRRI variety populations. As for the genetic distance distributions, both populations were skewed to the left, with skewness coefficients of -0.1300 and -0.0944 and medians of 0.2817 and 0.2436 for the Chinese and IRRI varieties, respectively (Fig. 1). More pairs (87.3%) of the genetic distances among the IRRI varieties ranged from 0.20 to 0.35 compared with 71.6% of the pairs of the Chinese varieties within that range.

Three pairs among the Chinese varieties (Aijiaonante vs. Xianfeng1hao, Xingheng1hao vs. Jiefang1hao, and Nantehao vs. Zhechang3hao) and two pairs of the IRRI varieties (IR52 vs. IR58 and IRRI146 vs. IRRI150) showed the same SNP genotypes based on RiceOPA2.1 markers.

PCA and population structure

PCA was used to characterize the population structure of the varieties from the two sample sources. The first and second axes of the PCA accounted for 44.5 and 16.0% of the allele variation among populations (Fig. 2). The analysis revealed two clusters among the varieties. All IRRI varieties but one (IR60) were clustered closely together and were clearly separated from the majority of the Chinese varieties. IR60 was an outlier of the IRRI variety group and was closely associated with the

Table 1. Diversity statistics (mean) of the Chinese and IRRI varieties

Measures	All lines	Chinese variety				IRRI variety
		Overall	Subgroup 1	Subgroup 2	Subgroup 3	
Major allele frequency	0.7690	0.7898	0.8575	0.7493	0.8136	0.8115
No. of alleles per locus	1.9922	1.9896	1.9089	1.9740	1.8828	1.9036
Gene diversity	0.3136	0.2936	0.2070	0.3324	0.2573	0.2626
PIC value	0.2529	0.2388	0.1724	0.2655	0.2092	0.2137
Genetic distance*	0.2869	0.2720	0.1889	0.3137	0.2172	0.2412

PIC, polymorphism information content.

*Significant differences ($P < 0.001$) for group means of genetic distances between the Chinese and IRRI varieties, and among the subgroups within the Chinese varieties.

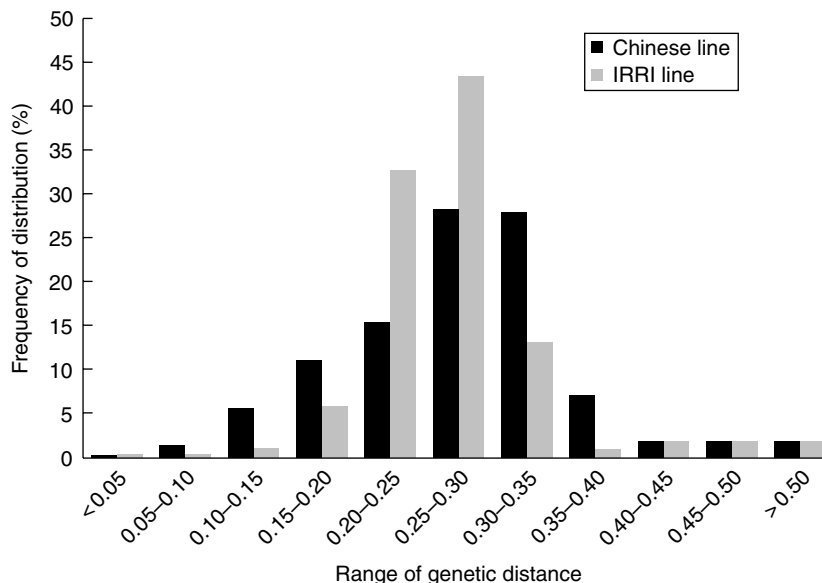


Fig. 1. Distribution of genetic distances of the Chinese and IRRI varieties.

majority of the Chinese varieties, specifically close to the varieties from Guangdong province. On the other hand, the Chinese varieties were scattered over a wide range, but most of the varieties from Guangdong were clustered together and showed a relatively close relationship with the IRRI varieties compared with other Chinese varieties from different provinces. However, there was no clear evidence to separate the Chinese varieties by province in the PCA.

Genetic relationships and differentiation

The two distinct groups (subpopulations) clustered by PCA based on the CSChord genetic distance were verified by the STRUCTURE analysis, which predicted $K = 2$ as the optimum number of subpopulations (Fig. 3). Individual varieties were assigned into subpopulations based on the maximum population inferred clusters (see Table S1, available online only at <http://journals.cambridge.org>).

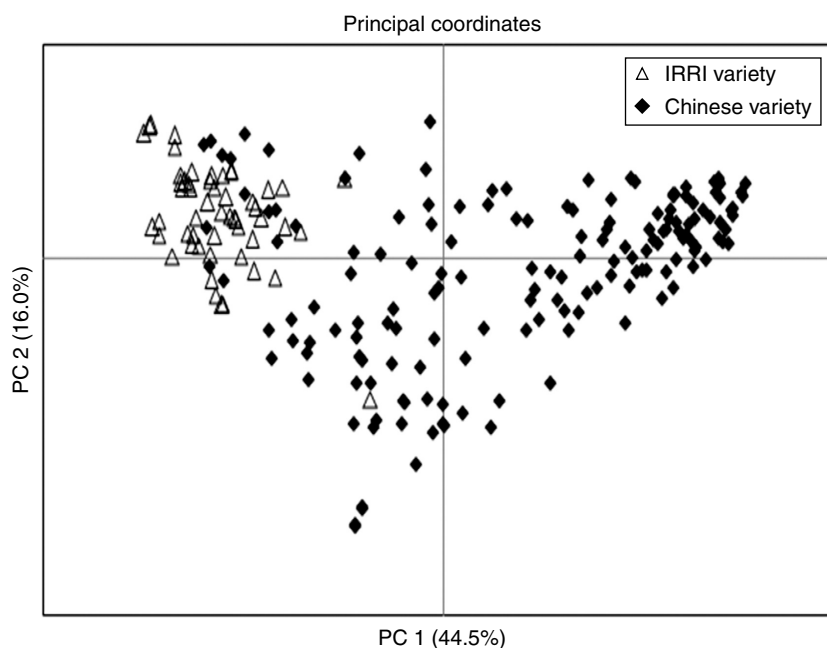


Fig. 2. PCA of 215 Chinese and IRRI rice varieties using IRRI SNP RiceOPA2.1 based on CSChord 1967 distance estimates. PC 1 and PC 2 are the first and the second principal coordinates, respectively. Numbers in parentheses refer to the proportion of variance explained by the principal coordinate.

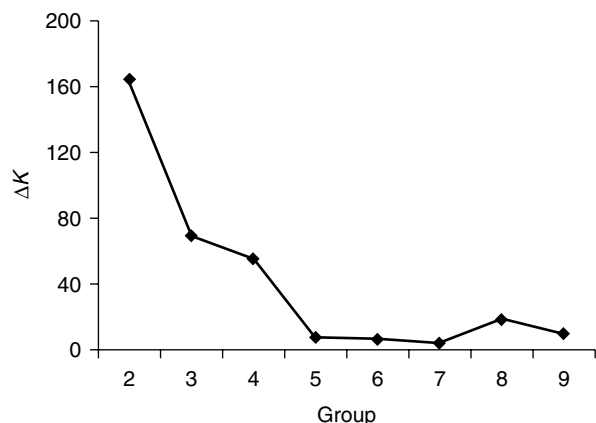


Fig. 3. Likelihood distribution of subpopulations of the Chinese and IRRI varieties based on the average of ΔK over ten runs for each K value.

The STRUCTURE analysis showed that 94 samples were in subpopulation 1, all composed of the Chinese varieties, and 121 samples in subpopulation 2, which included 67 Chinese varieties and all of the 54 IRRI irrigated inbreds. It was observed again that there was no clear separation to distinguish the individual varieties based on provincial origins among the Chinese varieties. Twenty-one of the 33 varieties from Guangdong were clustered in subpopulation 2, indicating a relatively close association with the IRRI varieties in comparison with varieties from other provinces.

The Chinese varieties were subclustered into three subgroups with 21, 86 and 54 varieties in subgroup 1, subgroup 2 and subgroup 3, respectively, at the second step of STRUCTURE analysis. It was observed again that the varieties from the different provinces were distributed across the subgroups without clear evidence of separation into subgroups by provinces (see Fig. S1, available online only at <http://journals.cambridge.org>). The varieties in subgroup 2 were obviously more diverse than the varieties in subgroup 1 or subgroup 3, as indicated in the diversity measurements (Table 1). The average genetic distance of the subgroup 2 varieties was 0.3137, which was significantly ($P < 0.001$) higher than those measured in subgroup 1 (0.1889) and subgroup 3 (0.2172), showing a divergent population structure in subgroup 2, followed by the varieties in subgroup 3 and subgroup 1 within the Chinese samples.

Discussion

SNP markers

Five rice OPAs were developed at IRRI for the rice SNP platform (Thomson *et al.*, 2012). Our samples

were screened using OPA2.1, which was designed for the *indica/indica* populations. As Thomson *et al.* (2012) pointed out, the OPA provides reasonably high polymorphism rates for the targeted germplasm pools, and it could have “an intrinsic bias” affecting the interpretation of diversity results due to the SNP markers being selected with a particular objective in mind, rather than at random. However, the OPA2.1-selected SNP markers are spaced across the genome, informative within and between different germplasm groups, and they have been validated for diversity analysis and fingerprinting of more than 500 rice varieties and breeding lines at IRRI (Thomson *et al.*, 2012). Therefore, we believe that the data generated from this study provide a fair estimation for the genetic diversity for our samples, even though these markers can be further improved for the SNP marker selection of maximum marker efficiency. In this study, 3, 4 and 37 markers showed monomorphism across all of the samples, among the Chinese varieties, and among the IRRI varieties, respectively. The monomorphism of SNP markers in this study is understandable because we used an existing SNP marker package for the diversity analysis. Some markers are not specifically designed and selected for diversity estimation of the population we used. However, those monomorphic markers could be replaced with other markers to provide maximum marker information, especially for those IRRI varieties sharing many ancestral parents in the crosses and that are closely related genetically.

Diversity

It is reasonable to conclude that, among the Chinese and IRRI varieties selected in this study, the Chinese varieties are more divergent than the IRRI varieties based on the marker profiling. These Chinese varieties are from many regions geographically with diverse rice-growing environments, but all of them are *indica* varieties adapted to the lowland irrigated rice ecosystem. On the other hand, IRRI has been expanding its germplasm sources with more parents involved in variety development. Parents used in irrigated inbred breeding have increased dramatically in the last 20 years (Fig. 4). For example, the pedigree records showed that the number of parents involved in breeding crosses of IR8, IR36, IR64 and IRRI116 (all mega-varieties released in 1966, 1976, 1985 and 1997, respectively), and IRRI154 (released in 2009) were 3, 16, 22, 32 and 43, respectively, showing that the parents in the variety pedigrees increased significantly over the years. However, the IRRI varieties, even though they have been cultivated on more rice area under more diverse environments than the Chinese varieties, are still less diverse than the Chinese varieties, as

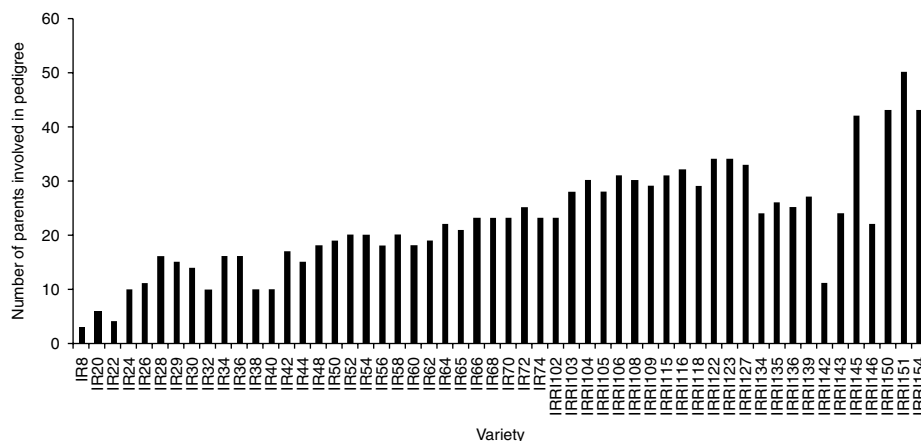


Fig. 4. Parents involved in variety development of the IRRI irrigated inbred varieties.

indicated in this study. We urgently need to diversify IRRI germplasm to be able to adapt to various rice-growing environments and to meet the challenges of climate and rice ecosystem changes. For the hybrid rice breeding programme at the IRRI, specifically, it is more urgent to develop divergent germplasm since the parents and germplasm used in hybrid rice breeding are mostly derived from the IRRI inbred breeding programmes. These sources of limited hybrid rice germplasm are further restrained to only a tiny portion of germplasm available due to the maintaining and restoring requirements. This could be one reason that a lower hybrid heterosis than that of hybrid rice in China is observed in the tropics where IRRI hybrid rice germplasm has been popularly used. With the help of molecular marker tools, hybrid rice germplasm should be regularly monitored and evaluated for genetic composition and population structure to better understand the parental genetic basis and to enhance heterosis.

All of the Chinese varieties used in this study are improved semi-dwarf HYVs that are widely grown for rice production. They showed a diverse admixture among the groups without a clear separation by province, showing a great degree of genetic integration of alleles. The admixed parents are likely to be the result of shared ancestry in developing varieties due to the widespread use of HYVs. Some of the Chinese varieties, such as those in subgroup 2, are closely allied with the IRRI varieties. This could be due to the sharing of ancestry among those *indica* varieties with the same semi-dwarf background and a large quantity of IRRI germplasm imported into China, specifically to Guangdong province which has a similar rice ecosystem to the tropical environment, in the last four decades. Germplasm exchange domestically and internationally in China has been playing a very important role in raising the yield potential for local varieties with an accelerated integration of new alleles from different regions and

sources, and this greatly enhanced the expansion of the germplasm breeding pools. However, an increased concern is that common HYVs and elite lines/traits are pursued by all of the breeders over the regions, which results in a great similarity of genotypes and phenotypes among the new varieties observed in national and regional rice yield trials. This may result in some unique genes or traits adapted to local environments being lost during line selection under well-controlled selection environments with an increased risk of making the rice ecosystem vulnerable.

Rice heterotic groups

Heterotic hybrids are usually derived between heterotic pools that are defined as those germplasm groups differentiated genetically from each other and can produce superior hybrids when they are crossed. Heterotic pools in rice have not been fully and clearly defined. The concept of rice subspecies or groups clustered based on genetic molecular markers, such as those classified as *aus*, *indica*, aromatic, temperate *japonica* and tropical *japonica* (Zhao *et al.*, 2010), is different from the definition of heterotic pools. Heterosis magnitude may be correlated with groups based on molecular markers, but most of the time, the hybrids derived from different subspecies are not applied in commercial production because of various problems with hybrids. However, in general, parental diversity is one of the major contributors to the magnitude of heterosis of hybrid rice, even within a subspecies. The Chinese experience teaches that heterotic rice hybrids are always derived 28 from genetically distance parents. Shanyou 63, a specific hybrid that dominated hybrid rice production in southern and Central China with more than 50% of hybrid rice area coverage in the 1990s, was bred from the parents of ZS 97 and MH H63. These

two lines are also the most widely used parents in China either directly as parents for other hybrids or as crossing donors in parental breeding. ZS 97 is a typical early-season *indica* variety from southern China and MH 63 is an excellent restorer line derived from a cross involving an IRRI variety (IR30). These two varieties are the representative parents from the two heterotic pools (early-season *indica* varieties in southern China as female parents and low-latitude *indica* varieties from IRRI or from other Southeast Asian countries as male parents) identified for three-line hybrid rice in China. However, both of them were clustered into the same subgroup in our study (see Fig. S1 and Table S1, available online only at <http://journals.cambridge.org>) with a small genetic distance compared with pairs in other different subgroups. It is noteworthy that many commercial hybrids have been produced from ZS 97, but no heterotic hybrids have been found or commercialized in varieties associated closely with ZS 97, i.e. some hybrid rice parents derived from ZS 97 crosses have not produced heterotic hybrids as good as ZS 97 itself. Some alleles of *japonica* rice were found in ZS 97 (McNally *et al.*, 2009). It is not clear what role those *japonica* alleles played for the combining ability of heterotic hybrids and what genetic factors contributed molecularly to the heterosis of ZS 97 hybrids. Molecular profiling of those varieties associated closely with ZS 97 and MH 63 and further hybridization studies may provide some hints of understanding the basis of hybrid heterosis in hybrid rice and to further enhance heterosis in the three-line hybrids as well as to serve as a guideline reference for developing two-line hybrid rice. Hybrid heterosis has not been fully explored among the parents from our parental groups based on molecular markers. Heterotic pools in hybrid rice could be different from the parental groups clustered by molecular markers. However, information from molecular markers with field studies of heterotic pools will offer great help in developing heterotic hybrids by selecting parents from different heterotic pools or specific molecular combinations. Parental classification with assignment of populations and individual varieties into groups would help to develop heterotic rice hybrid and provide a basis for parental selection based on heterotic pools.

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References

- Boppenmaier J, Melchinger AE, Seitz G, Geiger HH and Herrmann RG (1993) Genetic diversity for RFLPs in European maize inbreds III. Performance of crosses within versus between heterotic groups for grain traits. *Plant Breeding* 111: 217–226.
- Cavalli-Sforza LL and Edwards AWF (1967) Phylogenetic analysis: models and estimation procedures. *American Journal of Human Genetics* 19: 233–257.
- Chen HD, He H, Zou YJ, Chen W, Yu RB, Liu X, Yang Y, Gao YM, Xu JL, Fan LM, Li Y, Li ZK and Deng XW (2011) Development and application of a set of breeder-friendly SNP markers for genetic analyses and molecular breeding of rice (*Oryza sativa* L.). *Theoretical and Applied Genetics* 123: 869–879.
- Collard BCY, Vera Cruz CM, McNally KL, Virk PS and Mackill DJ (2008) Rice molecular breeding laboratories in the genomics era: current status and future considerations. *International Journal of Plant Genomics*, Article ID 524847: 25.
- Dudley JW, Saghai Maroof MA and Rufener GK (1991) Molecular markers and grouping of parents in maize breeding programs. *Crop Science* 31: 718–723.
- Evanno G, Regnaut S and Goudet J (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology* 14: 2611–2620.
- Falush D, Stephens M and Pritchard JK (2003) Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genetics* 164: 1567–1587.
- Lee M, Godshalk EB, Lamkey KR and Woodman WW (1989) Association of restriction fragment length polymorphisms among maize inbreds with agronomic performance of their crosses. *Crop Science* 94: 1023–1030.
- Liu K and Muse SV (2005) PowerMarker: an integrated analysis environment for genetic marker analysis. *Bioinformatics* 21: 2128–2129.
- Lu ZM and Xu BQ (2010) On significance of heterotic group theory in hybrid rice breeding. *Rice Science* 17: 94–98.
- McCouch SR, Zhao K, Wright M, Tung CW, Ebana K, Thomson M, Reynolds A, Wang D, DeClerck G, Ali ML, McClung A, Eizenga G and Bustamante C (2010) Development of genome-wide SNP assays for rice. *Breeding Science* 60: 524–535.
- McNally KL, Childs KL, Bohnert R, Davidson RM, Zhao K, Ulat VJ, Zeller G, Clark RM, Hoen DR, Bureau TE, Stokowski R, Ballinger DG, Frazer KA, Cox DR, Padhukasahasram B, Bustamante CD, Weigel D, Mackill DJ, Bruskiewich RM, Ratsch G, Buell CB, Leung H and Leach JE (2009) Genome-wide SNP variation reveals relationships among landraces and modern varieties of rice. *Proceedings of the National Academy of Sciences of the United States of America* 106: 12273–12278.
- Moose SP and Mumm RH (2008) Molecular plant breeding as the foundation of the 21st century crop improvement. *Plant Physiology* 147: 969–977.
- Murray MG and Thompson WF (1980) Rapid isolation of high molecular weight plant DNA. *Nucleic Acids Research* 8: 4321–4326.
- Peakall R and Smouse PE (2006) GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. *Molecular Ecology Notes* 6: 288–295.

- Pritchard JK, Stephens M and Donnelly P (2000) Inference of population structure using multilocus genotype data. *Genetics* 155: 945–959.
- Reif JC, Melchinger AE, Xia XC, Warburton ML, Hoisington DA, Vasal SK, Srinivasan G, Bohn M and Frisch M (2003) Genetic distance based on simple sequence repeats and heterosis in tropical maize populations. *Crop Science* 43: 1275–1282.
- Tamura K, Peterson D, Peterson N, Stecher G, Nei M and Kumar S (2011) MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular Biology and Evolution* 28: 2731–2739.
- Thomson MJ, Zhao K, Wright M, McNally KL, Rey J, Tung CW, Reynolds A, Scheffler B, Eizenga G, McClung A, Kim H, Ismail AM, Ocampo M, Mojica C, Reveche MY, Dilla-Ermita CJ, Mauleon R, Leung H, Bustamante C and McCouch SR (2012) High-throughput single nucleotide polymorphism genotyping for breeding applications in rice using the BeadXpress platform. *Molecular Breeding* 29: 875–886.
- Wright MH, Tung CW, Zhao K, Reynolds A, McCouch SR and Bustamante CD (2010) ALCHEMY: a reliable method for automated SNP genotype calling for small batch sizes and highly homozygous populations. *Bioinformatics* 26: 2952–2960.
- Xie FM (1993) Hybrid performance and genetic diversity as revealed by RFLPs in Rice (*Oryza sativa* L.). PhD Thesis, Texas A&M University.
- Yuan LP (1977) Practice and theory of breeding hybrid rice. *Scientia Agricultura Sinica* 10: 27–31.
- Zhang Q, Gao YJ, Yang S, Ragab R, Saghai Maroof MA and Li ZB (1994) A diallel analysis of heterosis in elite hybrid rice based on RFLPs and microsatellites. *Theoretical and Applied Genetics* 89: 185–192.
- Zhang Q, Gao YJ, Saghai Maroof MA, Yang SH and Li JX (1995) Molecular divergence and hybrid performance in rice. *Molecular Breeding* 1: 133–142.
- Zhao K, Wright MH, Kimball J, Eizenga G, McClung AM, Kovach M, Tyagi W, Ali ML, Tung CW, Reynolds A, Bustamante CD and McCouch SR (2010) Genomic diversity and introgression in *O. sativa* reveal the impact of domestication and breeding on the rice genome. *PLoS ONE* 5: 1–11.
- Zhao K, Tung CW, Eizenga GC, Wright MH, Ali ML, Price AH, Norton GJ, Islam MR, Reynolds A, Mezey J, McClung AM, Bustamante CD and McCouch SR (2011) Genome-wide association mapping reveals a rich genetic architecture of complex traits in *Oryza sativa*. *Nature Communication* 2: 467.