



Molecular markers for starch quality in rice

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Abstract

We investigated population structure of 416 rice accessions mostly collected in China. Substantial phenotypic and genotypic diversity in this germplasm set was found. Association analysis based on population structure using molecular markers for starch biosynthesis genes indicated that the *Wx* and *SSIIa* genes are strongly associated with apparent amylose content (AAC) and pasting temperature (PT) ($P < 0.001$). In addition, genome-wide association mapping identified five and seven SSRs that were associated with AAC and PT, respectively.

Introduction

- Rice starch, comprising ~90% of total grain dry weight of milled rice, strongly influences cooking and eating quality. DNA markers are widely accepted as potentially valuable tools for crop improvement in rice.
- Identifying genetic variants underlying rice quality is a challenging task facing plant breeders. Linkage mapping, and more recently, association or linkage disequilibrium (LD) mapping have been applied to elucidate the genetic basis of natural variation in important quantitative traits.
- In conventional linkage mapping studies, the LD required for mapping quantitative trait loci is generated as a result of the mating design, whereas association studies exploit the LD already present in the population of interest.
- We evaluated the population structure and genetic diversity of a set of 416 rice materials mainly collected in China, developed functional markers for starch biosynthesis genes, and conducted association mapping for starch quality based on the estimated population structure.

Materials & Methods

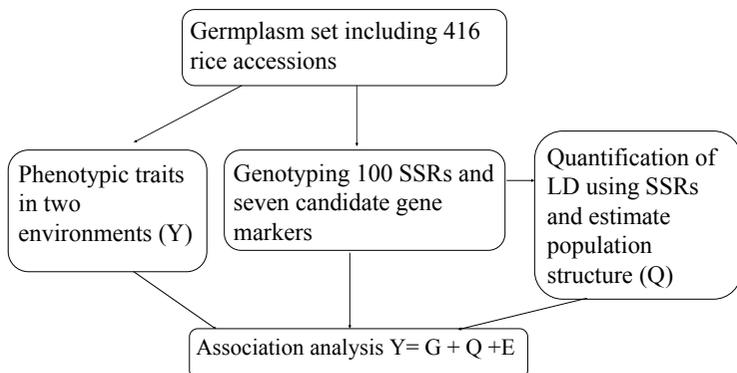


Figure 1. The scheme and procedures of association mapping, including germplasm choice, estimation of population structure, trait evaluation, identification of candidate polymorphisms, and statistical analysis

Results

A total of 100 SSR markers, randomly distributed across the genome, were used to evaluate the genetic diversity of the rice population. All of the 100 SSR markers were polymorphic across the 416 rice accessions and a total of 390 alleles were detected. The average number of alleles per locus was 3.9, ranging from 2 to 9. The average gene diversity was 0.4736, ranging from 0.0473 to 0.7618. The average PIC value was 0.4214, ranging from 0.0466 to 0.7216.

The model-based simulation of population structure using SSRs showed that the likelihood was maximized when the number of populations was set at seven, suggesting that these rice accessions can be grouped into seven subpopulations, as inferred from the model, here denoted as POP1, POP2, POP3, POP4, POP5, POP6 and POP7, respectively (Fig. 2). All *japonica* rice clustered into POP5.

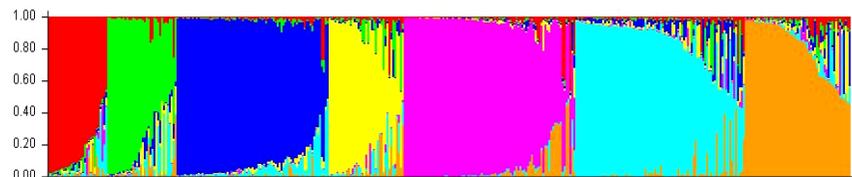


Figure 2. Population structure of 416 rice accessions based on 100 SSRs ($K=7$) Each accession is represented by a thin vertical line, which can be partitioned into seven colored segments that represent the probabilities of individual membership (Q) to the seven clusters, and then all accessions were sorted by Q.

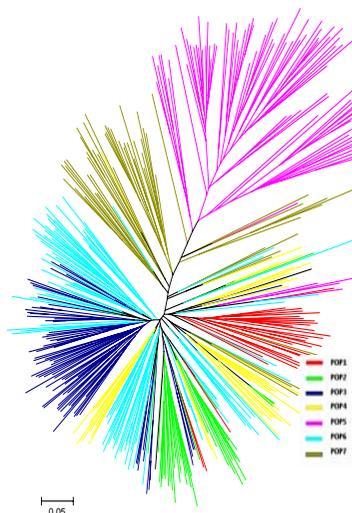


Figure 3. Unrooted neighbor-joining tree of 416 rice accessions based on Nei's genetic distance

The neighbor-joining tree revealed genetic relationships reasonably consistent with the STRUCTURE model-based membership assignment. However, a few rice accessions were displaying as admixtures in different clusters. These "misplaced" rice accessions were breeding lines derived from *indica/japonica* crosses. With few exceptions, the neighbor-joining tree showed that the rice accessions could be well differentiated according to their subspecies affiliation, i.e. *indica* or *japonica*.

Substantial variation existed in nearly all the agronomic and quality traits measured in this diverse germplasm set of 416 rice accessions grown in 2006 and 2007 (Table 1).

Seven starch biosynthesis gene markers have been genotyped (Fig. 4) (Bao et al. 2006a,b). We performed structure-based association mapping for starch quality using both candidate gene mapping and genome-wide association mapping. In candidate gene mapping, the *Wx* and *SSIIa* genes could be identified as strongly associated with AAC and PT respectively ($P < 0.001$). Genome-wide association mapping identified five and seven SSRs that were associated with AAC and PT, respectively. Among them, RM253, RM276 and RM484 have been detected by QTL mapping before. Two markers, RM253 and RM276, closely linked to the *SSIIa* gene, explained 5-10% of the variation of PT. Their associations with PT could be a result of LD with *SSIIa*.

Table 1 Descriptive statistics and percentage of phenotypic variation explained by population structure for 25 agronomic traits

Trait	Year	Mean \pm SD	Range	H^2	R
Agronomic traits					
Heating date (days)	2006	73.2 \pm 12.5	50.0-126.0	0.976	34.4
	2007	73.4 \pm 12.4	51.0-119.0		32.7
Plant height (cm)	2006	105.3 \pm 27.0	54.3-182.4	0.908	46.6
	2007	110.8 \pm 30.2	53.0-188.1		42.9
Flag leaf length (cm)	2006	36.2 \pm 9.5	15.4-77.3	0.782	23.1
	2007	36.8 \pm 9.0	15.9-66.7		23.8
Flag leaf width (cm)	2006	1.73 \pm 0.27	0.90-2.68	0.802	9.3
	2007	1.70 \pm 0.26	1.00-2.63		7.9
Grain length (mm)	2006	8.44 \pm 0.90	6.76-11.18	0.686	31.9
	2007	8.52 \pm 0.91	6.77-11.21		30.7
Grain width (mm)	2006	2.99 \pm 0.35	2.19-4.07	0.711	39.1
	2007	3.03 \pm 0.36	2.26-4.86		42.1
Grain length/width ratio	2006	2.87 \pm 0.56	1.87-4.64	0.991	40.1
	2007	2.86 \pm 0.55	1.83-4.47		40.9
Panicle length (cm)	2006	24.2 \pm 4.0	13.1-38.4	0.918	18.6
	2007	23.3 \pm 3.6	13.1-23.3		15.5
1000-grain weight (g)	2006	23.2 \pm 3.3	12.9-33.4	0.906	6.2
	2007	22.8 \pm 4.6	12.6-34.8		6.0
Starch quality traits^b					
Apparent amylose content, AAC (%)		23.1 \pm 5.7	1.6-32.6	na	41.5
Peak viscosity (RVU)		242 \pm 33.5	81.7-305.4	na	11.5
Hot paste viscosity (RVU)		173 \pm 30.9	43.0-248.1	na	14.9
Cool paste viscosity (RVU)		308 \pm 51.8	56.5-409.1	na	21.3
Breakdown (RVU)		69 \pm 19.7	19.6-141.3	na	18.2
Setback viscosity (RVU)		69 \pm 37.1	-82.6-193.2	na	27.0
Pasting temperature, PT ($^{\circ}$ C)		74.9 \pm 2.8	67.5-81.5	na	18.3
Hardness (g)		29.2 \pm 11.1	0.8-61.1	na	43.6
Grain color traits					
<i>L</i> *	2006	51.8 \pm 9.5	14.1-67.4	na	8.5
<i>a</i> *	2006	3.46 \pm 2.90	-12.9-13.8	na	21.1
<i>b</i> *	2006	14.3 \pm 2.1	-1.8-18.7	na	6.7
<i>C</i>	2006	15.1 \pm 1.4	9.48-19.7	na	9.5
<i>H</i> $^{\circ}$	2006	72.5 \pm 31.0	-193.3-101.4	na	7.0
Nutritional quality traits					
Phenolics (mg GAE/l)	2006	208.1 \pm 155.6	108.1-1244.9	na	8.0
Flavonoids (mg RE/l)	2006	134.6 \pm 20.6	88.51-286.29	na	5.0
Antioxidant capacity (mMTAEC) 2006		0.474 \pm 0.752	0.0120-5.533	na	8.4

^aPercentage of phenotypic variation explained by population structure. ^bData from Bao et al. (2006a, b). na, not available

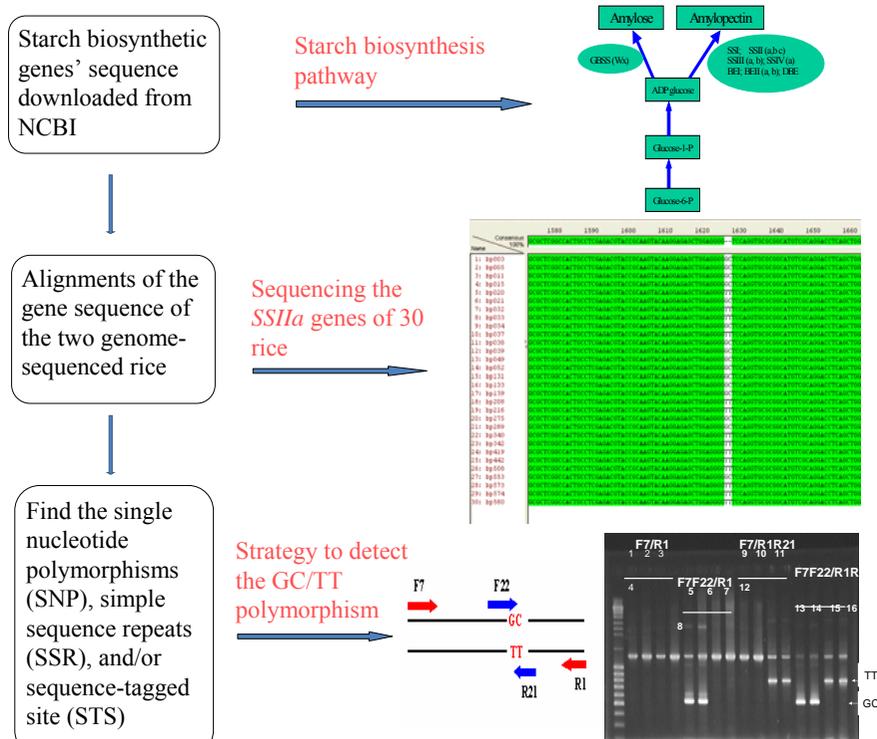


Figure 4. Strategies to discover functional molecular markers for starch biosynthetic genes

Table 2 Association of starch synthesizing gene markers (left) and SSRs (right) with apparent amylose content (AAC) and pasting temperature (PT) based on population structure

Gene markers	AAC		PT		Markers	Chromosome	Position	P	R^2
	P	R^2	P	R^2					
AAC									
<i>Wx</i> SNP	1.02E-105	0.3979	1.04E-04	0.0313	RM122	5	0	5.01E-04	0.0217
					RM161	5	96.9	4.00E-04	0.0225
					RM346	7	47	2.70E-06	0.0444
<i>Wx</i> SSR	2.64E-95	0.3968	0.008	0.0464	RM336	7	61	0.001	0.0328
					RM126	8	57	4.13E-04	0.0187
PT									
<i>SSIIa</i> SSR	6.51E-11	0.0689	0.1584	0.0109	RM253	6	37	3.88E-05	0.0520
					RM276	6	40.3	1.13E-10	0.1042
<i>Sbe1</i> SNP	3.73E-04	0.0188	4.43E-65	0.4312	RM346	7	47	2.48E-04	0.0449
					RM278	9	77.5	1.38E-05	0.0523
<i>Sbe1</i> STS	0.0217	0.0141	0.0162	0.0217	RM222	10	11.3	7.50E-04	0.0395
	0.0016	0.0145	0.0034	0.0179	RM484	10	97.3	9.76E-04	0.0295
<i>Sbe3</i> SNP	0.8005	9.39E-05	0.9824	1.04E-06	RM206	11	102.9	5.52E-04	0.0460

References

- Bao JS, Corke H, Sun M (2006a) Nucleotide diversity in starch synthase IIa and validation of single nucleotide polymorphisms in relation to starch gelatinization temperature and other physicochemical properties in rice (*Oryza sativa* L.). Theor Appl Genet 113: 1171-1183
- Bao JS, Corke H, Sun M (2006b) Microsatellites, single nucleotide polymorphisms and a sequence tagged site in starch-synthesizing genes in relation to starch physicochemical properties in nonwaxy rice (*Oryza sativa* L.). Theor Appl Genet 113: 1185-1196