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# Evaluation on Genetic Quality and Traits of Rice Landraces in the Taihu Lake Area

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**Abstract** In this paper, with 511 rice landraces in the Taihu Lake area as test materials, we select 19 starch synthesis-related intragenic molecular markers to detect the genetic quality of starch, and compare them with 86 bred varieties. The results show that the average polymorphic information content (PIC) of japonica landraces is 0.1726, slightly higher than the average PIC (0.1101) of the bred japonica rice varieties. Based on Nei's genetic distance between materials, UPGMA method is used for clustering, and all study materials are divided into 6 groups. Group I mainly includes indica rice, the bred japonica rice varieties are mainly concentrated in the first half of Group II and Group III, and the japonica landraces are mainly concentrated in the second half of Group III, and Group IV, V, VI. Both of them are in different regions, and there has been genetic differentiation. According to the national standard of high quality rice, it is found that many rice landraces in the Taihu Lake area have good quality and traits, and these varieties can be used for future high quality breeding.

**Key words** Taihu rice production area, Intragenic molecular marker, Starch synthesis-related gene, Diversity

## 1 Introduction

The genetic basis of China's rice breeding varieties is weak and narrow, the genetic diversity of the bred varieties decreases gradually, and the genetic differences between the bred parents are very close<sup>[1-5]</sup>. With increasing levels of breeding, the simplification trend of crop variety extension is increasingly evident, resulting in loss of considerable genes and reduction of genetic diversity<sup>[6-8]</sup>. Jin Weidong *et al.*<sup>[9]</sup> use 60 pairs of SSR markers to study the genetic differences between the varieties currently promoted in the Taihu Lake area, and find that the average similarity coefficient between varieties reaches 0.902. Taihu Lake Basin began rice production as early as 8000 years ago<sup>[10]</sup>, and japonica rice was mainly cultivated. Long-term natural evolution and artificial selection have brought rich rice genetic resources in the region<sup>[11-12]</sup>, but so far, the breeding has been only limited to a few landraces such as Huangke Zaonianri, Aininghuang and Laohudao, and the utilization potential of the vast majority of resources has not been tapped. With the development of molecular biology, some genes are found to be related with starch formation or rice quality formation, including granular starch synthase gene (*Wx*), branching enzyme gene (*Sbe1*, *Sbe3*), soluble starch synthase gene (*Sss1*), iso-amylase gene (*Isa*) and limit dextrinase or R enzyme gene (*Pull*). Wu Hongkai *et al.*<sup>[13]</sup> use *Wx* gene to study the RVA profile, and find that all eight eigenvalues of RVA play a major role, and have significant epistasis effect on amylopectin biosynthesis-related genes *Sbe1*, *Sss1*. With 53 indica and japonica varieties

and the high-yielding rice varieties bred in recent years as materials, Yan Changjie *et al.*<sup>[14]</sup> design molecular marker of *Wx*, *Sbe1* and *Sbe3* genes and analyze the genetic effect of three gene loci. Chen Feng *et al.*<sup>[15]</sup> use *Wx*, *Sbe1*, *Sbe3* markers to analyze the effect of three genes on rice physicochemical quality and RVA profile characteristics, and find that there are significant differences in starch physicochemical properties among different genotype varieties (AC, GC, RVA), and there are also significant differences in the combined effects of three genes between different genotype combinations. Jin Weidong *et al.*<sup>[9]</sup> use SSR (Simple Sequence Repeat) to conduct the polymorphic DNA analysis on the core germplasm of 129 japonica landraces resources in Taihu Lake Basin, and the results show that there are not only rich genetic variations, but also a lot of rare allelic variations for the germplasm of the japonica landraces in Taihu Lake Basin. Yu Ping *et al.*<sup>[16]</sup> use 45 pairs of SSR primers to analyze the genetic diversity of 224 japonica landraces in Taihu Lake Basin, and find that the SSR diversity of japonica landraces is low and there are many rare allelic genes. Luo Bing<sup>[17]</sup> uses SSR primer to analyze the genetic diversity of 42 japonica rice varieties in the Taihu Lake area, and the results show that the average genetic similarity coefficient between the varieties is 0.6100, the test materials are highly similar, and the average PIC of each polymorphic locus is 0.4966. Debjani *et al.*<sup>[18]</sup> use 36 pairs of SNP to mark 12 rice chromosomes and analyze the genetic diversity of 6984 rice varieties in Northeast India, and find that PIC is 0.004-0.375, and genetic diversity is 0.006-0.500. Mehrzad *et al.*<sup>[19]</sup> use 52 primers distributed on 12 pairs of chromosomes to detect the genetic diversity of 94 genotypes of rice, and find that the highest and lowest PIC content is 0.892 and 0.423, respectively. In this study, we use the internal marker of starch synthesis gene closely related to rice quality to detect the marker genotypes of rice landraces in Taihu

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Lake Basin, and carry out the genetic diversity analysis and evaluation. According to UPGMA method, clustering is performed on 511 rice materials and 86 bred rice varieties, to reveal the genetic

differences in quality gene between rice landraces resources in Taihu Lake Basin.

**Table 1 Starch synthesis-related intragenic molecular marker**

Target gene	Molecular markers	Primer sequence	Marker type	Distinguishable allele
<i>Wx</i>	ND	ND-F: CACAGCAACAGCTAGACAACCAC ND-R: CACGACGACGGAGGGGAAC	STS	<i>Wx</i> / <i>wx</i>
	PCR-AccI	pAg: ACCATTCTTCAGTTCTTTTG pBg: ATGATTTAACGAGAGTTGAA	CAPS	<i>Wx<sup>a</sup></i> / <i>Wx<sup>b</sup></i>
	(CT) <sub>n</sub>	F: CTTTGTCTATCTCAAGACAC R: TTGCAGATGTTCTTCTGATG	SSR	(CT)8/(CT)11/(CT)16/(CT)17/(CT)18/(CT)19/ (CT)20
	(AATT) <sub>n</sub>	F: TGCATCTTTTCATTGCTCGTT R: ACCCCTGGATGTTTCTCT	SSR	(AATT) <sub>5</sub> /(AATT) <sub>6</sub>
<i>GBSSII</i>	S004	S004-F: TTGCTGCGAATTATCTGCG S004-R: ACCTCCTCCCCTCTTTTGC	STS	<i>GBSSII<sup>a</sup></i> or hybrid/ <i>GBSSII<sup>b</sup></i>
<i>SBE1</i>	S005	S005-F: GAGTTGAGTTGCGTCAGATC S005-R: AATGAGGTTGCTTGCTGCTG	STS	<i>Sbe1<sup>j</sup></i> / <i>Sbe1<sup>i</sup></i>
<i>SBE3</i>	S006	S006-F: TCGGTCCTAATATTTTGGCGCTG S006-R: CCTTAACTTGACACCGAATCC	STS	<i>Sbe3<sup>j</sup></i> / <i>Sbe3<sup>i</sup></i>
	488/489	488: GATCCGTTTTTGTGTGCCC 489: CCTCCTCTCCGCCGATCCTG	STS	<i>SssI<sup>j</sup></i> / <i>SssI<sup>i</sup></i> / <i>SssI<sup>a</sup></i> / <i>SssI<sup>b</sup></i>
	S001	S001-F: GTAGGCAAGCTGCTACTTGT S001-R: CTTGAGGCGCTAATCAGGT	STS	Having band/having no band
	PCR-HaeII	SSSI-22: CCAAGCCTGTAATAATAAG SSSI-23: CACGCTAAACGAAGAAAT	CAPS	<i>SssI<sup>j</sup></i> / <i>SssI<sup>i</sup></i>
<i>SSSII-1</i>	S008	S008-F: CACCCACCGTTCTACTATGC S008-R: TCCATAGTTTCAATGAGATTGCTC	STS	<i>SSSII-1<sup>a</sup></i> / <i>SSSII-1<sup>b</sup></i> / <i>SSSII-1<sup>c</sup></i>
<i>SSSII-2</i>	S009	S009-F: AGATTGAACTCAGGACTTGGTG S009-R: TCTATGGGCTCTATCCTTACTAGG	STS	<i>SssII-2<sup>j</sup></i> / <i>SssII-2<sup>i</sup></i>
	PCR-TaqI	S003-F: GCACTCCTGCCTGTTTATCTGAAG S003-R: CTCGTACAGCTTGAAGTATCCAG	CAPS	<i>SSSII-3<sup>a</sup></i> or <i>SSSII-3<sup>b</sup></i> / <i>SSSII-3<sup>c</sup></i>
	PCR-BanII	S020-F: GGTTCCTCGGTGAAGATGGC S020-R: CTGGTCCCAGCTGAGTCC	CAPS	<i>SSSII-3<sup>a</sup></i> or <i>SSSII-3<sup>c</sup></i> / <i>SSSII-3<sup>b</sup></i>
<i>SSSIII-1</i>	S010	S010-F: AAGAAGGGAAGGGAGTCAGC S010-R: GCCATCTCCATTGCCAGC	STS	<i>SSSIII-1<sup>a</sup></i> / <i>SSSIII-1<sup>b</sup></i> / <i>SSSIII-1c</i> / hybrid
	S011	S011-F: GACCAACCGATTACCTTCTT S011-R: TTGCTCTTTTCTCAACCTGT	STS	<i>SSSIII-2<sup>a</sup></i> or <i>SSSIII-2<sup>c</sup></i> / <i>SSSIII-2<sup>b</sup></i>
	PCR-XbaI	S012-F: AAGTCCTTCGGCTTACTATTCC S012-R: GGAGAAGGAACATAACAGGGAC	CAPS	<i>SSSIII-2<sup>a</sup></i> / <i>SSSIII-2<sup>b</sup></i> or <i>SSSIII-2<sup>c</sup></i>
<i>SSSIV-1</i>	AY2	AY2-F: GCTTTCAGTTGTGTATGGATT AY2-R: TGAGAGTTTTACCTTATGGGAC	STS	<i>SSSIV-1<sup>a</sup></i> / <i>SSSIV-1<sup>b</sup></i>
<i>SSSIV-2</i>	AY1	AY1-F: TTCGTTCTCAGTACTCTGCTCCT AY1-R: TTGCTAATGAATGTGCTGTGGTA	STS	<i>SSSIV-2<sup>a</sup></i> / <i>SSSIV-2<sup>b</sup></i> / <i>SSSIV-2<sup>c</sup></i>
<i>ISA-1</i>	S015	S015-F: ATAGATGCTAATGTGATGTGGC S015-R: TGGTATAGGCACAACCGTAGA	STS	<i>ISA<sup>a</sup></i> / <i>ISA<sup>b</sup></i>
<i>PULL</i>	S016	S016-F: CTGTATGGACTGAGTAGTCGATGG S016-R: TGAGCCTCATCTGCCAGACT	STS	<i>PUL<sup>a</sup></i> / <i>PUL<sup>b</sup></i>
<i>AGPlar</i>	S017	S017-F: CGTTCAGGTTACGGCAATCA S017-R: GGAAGGTTGCTGATGTGGAG	STS	<i>AGPlar<sup>a</sup></i> / <i>AGPlar<sup>b</sup></i> / <i>AGPlar<sup>c</sup></i>
<i>AGP<sub>sma</sub></i>	S018	S018-F: TCTATTCTCAGCCCTCCAACC S018-R: GTGTGTTTAGAGGTGCTTTTGG	STS	<i>AGP<sub>sma</sub><sup>a</sup></i> / <i>AGP<sub>sma</sub><sup>b</sup></i>
<i>AGPiso</i>	PCR-EcoRI	S019-F: TGGAAATGGGAACTCTATTATTGG S019-R: TCCCAACCTCTACCTTCAAATG	CAPS	<i>AGPiso<sup>a</sup></i> / <i>AGPiso<sup>b</sup></i> / hybrid

2 Materials and methods

511 rice landraces in the Taihu Lake area are planted in Suzhou Academy of Agricultural Sciences, including 423 japonica landraces, 15 glutinous rice landraces, 39 japonica glutinous rice landraces, 29 indica landraces, 5 indica glutinous rice landraces, and 86 varieties bred from a wide range of sources. At the seedling stage, the sampling and DNA extraction are conducted, and intra-genic marker detection is conducted in the laboratory (Table 1). These marker loci are related to 19 starch synthesis genes. In autumn, these materials are harvested in batches, and some quality traits are measured, such as apparent amylose content, gel consistency and gelatinization temperature<sup>[20-21]</sup>.

**2.1 Marker genotype detection** SDS method is used to extract DNA, and the corresponding primers in each sample are used for PCR amplification, and if it is CAPS molecular marker, there is also a need to perform the corresponding enzyme digestion of PCR product. PCR product or enzyme digestion product separates DNA fragments of different sizes by 1% agarose or 6% polyacrylamide gel electrophoresis. Electrophoresis conditions are selected based on the size of the difference in polymorphic bands. If it is greater than 50 bp, the agarose gel is used, and it is stained with EB after electrophoresis; if it is smaller than 10 bp, the polyacrylamide gel is used. After electrophoresis, the silver staining method is used to display DNA bands, and the results are scanned by ScanMaker 3830 (Microtek, Shanghai, China).

**2.2 Statistical analysis** One locus is detected for one pair of

primers, and each polymorphic band is one allele. The allele of all test materials is recorded. The software PowerMarker 3.25<sup>[22]</sup> is used for general statistical analysis, to obtain number of alleles, allelic variation frequency, genetic diversity, polymorphic information content (PIC)<sup>[23]</sup>, and other parameters. The Nei's genetic distance matrix between individuals and subgroups is further calculated, unweighted pair-group method with arithmetic means (UPGMA) is used for genetic clustering analysis, and MEGA4.0 is used for observing clustering map.

3 Results and analysis

**3.1 Analysis of starch synthesis-related genetic diversity** The japonica landraces and the bred japonica rice varieties are compared (Table 2), and the results show that the average genetic diversity of japonica landraces is 0.1988, ranging from 0.0094 to 0.6520, and the average PIC is 0.1726, ranging from 0.0094 to 0.5887. The polymorphism of (CT)*n* genetic locus is highest, while the polymorphism of Pull genetic locus is lowest. The average diversity of the bred japonica rice gene is 0.1282, ranging from 0.0000 to 0.5116, and the average PIC is 0.1101, ranging from 0.0000 to 0.3929. The polymorphism of SSSIII-2 genetic locus is highest, while the polymorphism of Wx, AATT, SSSVI-2 genetic loci is lowest. By comparison, it is found that the japonica landraces have higher genetic diversity and PIC than the bred japonica rice varieties.

Table 2 Genetic diversity of the japonica landraces and the bred japonica rice varieties

Gene	Japonica landraces			The bred japonica rice		
	Number of alleles	Genetic diversity	PIC	Number of alleles	Genetic diversity	PIC
Wx	3.000 0	0.510 7	0.391 8	1.000 0	0.000 0	0.000 0
(CT) <i>n</i>	8.000 0	0.652 0	0.588 7	2.000 0	0.334 7	0.278 7
AATT	2.000 0	0.085 8	0.082 1	1.000 0	0.000 0	0.000 0
GBSSI	2.000 0	0.102 8	0.097 5	2.000 0	0.024 7	0.024 4
Sbe1	2.000 0	0.492 2	0.371 0	2.000 0	0.348 8	0.287 9
Sbe3	2.000 0	0.055 1	0.053 6	2.000 0	0.048 8	0.047 6
SSSI	4.000 0	0.113 5	0.111 5	2.000 0	0.024 7	0.024 4
SSSI-1	3.000 0	0.498 2	0.383 2	3.000 0	0.118 4	0.113 8
SSSI-2	2.000 0	0.115 4	0.108 7	2.000 0	0.024 7	0.024 4
SSSI-3	3.000 0	0.117 2	0.113 7	3.000 0	0.393 4	0.325 3
SSSIII-1	4.000 0	0.243 9	0.226 7	3.000 0	0.141 3	0.135 9
SSSIII-2	3.000 0	0.137 3	0.130 6	3.000 0	0.511 6	0.392 9
SSSVI-1	2.000 0	0.115 4	0.108 7	2.000 0	0.024 7	0.024 4
SSSVI-2	2.000 0	0.037 1	0.036 4	1.000 0	0.000 0	0.000 0
Isa-1	2.000 0	0.123 6	0.116 0	2.000 0	0.072 2	0.069 6
Pull	2.000 0	0.009 4	0.009 4	2.000 0	0.024 7	0.024 4
AGPlar	3.000 0	0.112 7	0.109 2	2.000 0	0.072 2	0.069 6
AGP <sub>sma</sub>	3.000 0	0.107 9	0.103 8	2.000 0	0.072 2	0.069 6
AGP <sub>iso</sub>	2.000 0	0.147 8	0.136 9	2.000 0	0.199 7	0.179 7
Mean	2.842 1	0.198 8	0.172 6	2.052 6	0.128 2	0.110 1

**3.2 Clustering analysis based on genetic distance** Based on the Nei's genetic distance between materials, the UPGMA method

is used for cluster analysis of 511 rice materials and 86 bred rice varieties. The entire group can be divided into six categories, as

shown in Fig. 1. From the cluster diagram, it is found that the bred japonica rice varieties are mainly in the right upper half of Group II and Group III, and japonica landraces are mainly concentrated in the second half of Group III, Group IV, V, VI. Both of them are in different areas, and there have been significant genetic differentiation. Group I mainly includes indica landraces. It is also found that a small number of cultivars are still mixed in the landraces, and show consistent performance in terms of allele combination. In the tree diagram, the bred varieties Yangdao 6 and Shuijing 3 are genetically close to landraces Shuijingbaidao and Xishihuang. By contrast, a few landraces are also included in the bred varieties. In the tree diagram, the landraces Lujingqing and Sujing 5 are genetically close to the bred varieties Huaidao 11 and Nanjing 44. The results show that for the rice germplasm resources in the Taihu Lake area, there is great similarity and small genetic difference between a few landraces and a few bred varieties, while there is a small similarity between most landraces and the bred varieties, and they are in different groups, with great genetic difference.

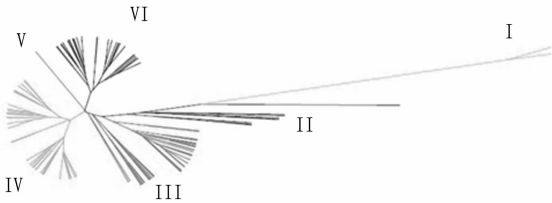


Fig. 1 Clustering of 511 landraces and 86 bred varieties

**3.3 Classification of quality traits** Based on national standards of quality rice<sup>[24]</sup>, the landraces are classified (Tables 3, 4 and 5). In terms of gel consistency trait, when indica rice  $\geq$

70mm, japonica rice  $\geq 80$ mm, indica glutinous rice  $\geq 100$ mm, japonica glutinous rice  $\geq 100$ mm, it is at the first level. It can be seen from Table 4 that the indica rice has 5 landraces with first level gel consistency, accounting for 0.978% of total landraces in the Taihu Lake area; the japonica rice has 109 landraces with first level gel consistency, accounting for 21.33% of total landraces; the japonica glutinous rice has 21 landraces with first level gel consistency, accounting for 4.11% of total landraces; the indica glutinous rice has only one landrace (Majinnuo) with first level gel consistency. Based on national standards of amylose content, when indica rice dry basis content is 17% – 22%, japonica rice dry basis content is 15% – 18%, indica glutinous rice dry basis content is  $\leq 2.0\%$ , japonica glutinous rice dry basis content is  $\leq 2.0\%$ , it is at the first level. Table 4 shows that the indica rice has 18 landraces with first level of amylose, accounting for 3.52% of total landraces in the Taihu Lake area; the japonica rice has 156 landraces with first level of amylose, accounting for 30.53% of total landraces; the japonica glutinous rice has 10 landraces with first level of amylose, accounting for 1.96% of total landraces. Based on national standards of gelatinization temperature<sup>[25]</sup>, when indica rice  $> 4$ , japonica rice  $> 6$ , glutinous rice  $> 6$ , it is at the first level. Table 3 shows that the indica rice has 6 landraces with first level gelatinization temperature, accounting for 1.17% of total landraces in the Taihu Lake area; the japonica rice has 137 landraces with first level gelatinization temperature, accounting for 26.81% of total landraces; the glutinous rice has 3 landraces with first level gelatinization temperature, accounting for 0.59% of total landraces. In summary, the gel consistency, gelatinization temperature or amylose content can reach first level for most of japonica landraces in the Taihu Lake area.

Table 3 The japonica landraces reaching the first level standard in the Taihu Lake area

Varieties	Type	AC 15% – 18%	GT > 6	GC $\geq 80$	Varieties	Type	AC 15 – 18%	GT > 6	GC $\geq 80$
345	Japonica rice	1	1		Lidongdao	Japonica rice	1	1	
Aibaidao	Japonica rice		1	1	Lidongqing	Japonica rice	1		1
Aidatou	Japonica rice	1	1		Ligengqing	Japonica rice	1	1	
Aijidaluzhong	Japonica rice	1		1	Longgouzhong	Japonica rice	1		1
Aijidaluzhong	Japonica rice	1		1	Luhuangzhong	Japonica rice		1	
Aijiguang	Japonica rice	1	1		Luhuangzhong	Japonica rice	1		1
Aijihuang	Japonica rice	1	1		Lujingqing	Japonica rice	1	1	
Aijiaotaihuqing	Japonica rice	1	1		Lujingqing	Japonica rice	1		1
Aizibaigetou	Japonica rice	1	1		Luoshuangqing	Japonica rice			
Baidiegu	Japonica rice	1		1	Luoshuangqing	Japonica rice			1
Baikelaolaiqing	Japonica rice	1	1		Luoshuangqing	Japonica rice			1
Baikelaolaiqing	Japonica rice	1	1		Luoshuangqing	Japonica rice		1	
Baimangduanzhong	Japonica rice	1		1	Manluzhong	Japonica rice	1		1
Baimangduanzhong	Japonica rice	1			Muduzhong	Japonica rice		1	1
Baishidao	Japonica rice	1	1		Putauluzhong	Japonica rice	1		1
Baijidao	Japonica rice			1	Sanzhaoqi	Japonica rice	1		1
Baoxintaihuqing	Japonica rice	1	1	1	Sanguangdao	Japonica rice		1	1
Buxigui	Japonica rice	1	1		Sanpingtou	Japonica rice		1	1
Changshuhuang	Japonica rice	1	1		Shanghaiqing	Japonica rice		1	
chiguwandao	Japonica rice	1		1	Shanghaiqing	Japonica rice			1

Varieties	Type	AC 15% – 18%	GT > 6	GC ≥ 80	Varieties	Type	AC 15 – 18%	GT > 6	GC ≥ 80
Dadaosuitou	Japonica rice	1	1		Shiluzhong	Japonica rice	1		1
Daheitouhong	Japonica rice		1	1	Shuangjiangqingnuodao	Japonica rice			1
Daliangdao	Japonica rice	1	1		Suzhouqing				
	Japonica rice			1					
Daluzhong	Japonica rice	1		1	Tieganyishixing	Japonica rice	1		1
Damandao	Japonica rice	1	1		Tiegandao	Japonica rice	1	1	
Daqingzhong	Japonica rice	1		1	Tuoguoshan	Japonica rice			1
Dasuitoujingdao	Japonica rice	1	1		Wanbague	Japonica rice	1	1	
Daichangqing	Japonica rice	1	1	1	Wanluohandao	Japonica rice	1	1	
Diezhong	Japonica rice	1		1	Wannuodao	Japonica rice			1
Dingzhuangdao	Japonica rice	1	1		Wangjiadao	Japonica rice	1	1	
Dongting 2	Japonica rice	1	1		Wumangwanbagetou	Japonica rice	1	1	
Duanmangmengzijingdao	Japonica rice			1	Wumangyedao	Japonica rice	1		1
Duiguzhong	Japonica rice	1		1	Wumangzaodao	Japonica rice			1
Fenghuangdao	Japonica rice	1	1		Wuxiyedao	Japonica rice	1		1
Gaidaoqing	Japonica rice	1	1		Wuqitou	Japonica rice	1	1	1
Guangtou 853	Japonica rice			1	Xidao 16	Japonica rice	1		1
Guangtoudadao	Japonica rice		1	1	Xihongke	Japonica rice	1		1
Heidao	Japonica rice			1	Xiangjingdaonuo	Japonica rice			1
Heikeluhuabai	Japonica rice		1	1	Xiangjingdaonuo	Japonica rice			
Hongkenuo	Japonica rice	1			Xiangjingdaonuodao	Japonica rice			1
Hongkenuo	Japonica rice			1	Xiangzhunuo	Japonica rice			1
Hongkenuo	Japonica rice	1			Xiangzhunuoquan	Japonica rice			1
Hongmangnuo	Japonica rice	1	1		Xiaohongzao	Japonica rice			1
Hongmangxiangjingdaonuo	Japonica rice			1	Xiaoluohan	Japonica rice	1	1	
Hongmuxiqiu	Japonica rice			1	Xiaoluohanhuang	Japonica rice		1	
Huangjingdao	Japonica rice	1	1		Xiaomai 2	Japonica rice	1	1	
Jijiaohong	Japonica rice			1	Xiaoqingzhong	Japonica rice	1	1	
Jijingdao	Japonica rice	1	1		Xiekehuan	Japonica rice		1	1
Jiangbeinuo	Japonica rice			1	Yanhongdao	Japonica rice	1		1
Jiangxinuo	Japonica rice			1	Yangfeilaifeng	Japonica rice			1
Jiangyinza	Japonica rice			1	Yangzaonianri	Japonica rice	1	1	
Jinghuang	Japonica rice	1	1		Yeli X	Japonica rice	1	1	
Jintannuo	Japonica rice			1	Yiliqi	Japonica rice	1		1
Jintannuo	Japonica rice			1	Yilizi	Japonica rice	1		1
Jingdaogunuo	Japonica rice			1	Zaoshiri	Japonica rice	1	1	
Jiuciqing	Japonica rice	1	1		Zao 7 – 312	Japonica rice	1		1
Laodiegu	Japonica rice	1		1	Zaoguangtou	Japonica rice			1
Laohuangdao	Japonica rice	1	1		Zhoujiadao	Japonica rice	1	1	
Laohuangdao	Japonica rice		1						
Laowandao	Japonica rice	1		1					

**Table 4 The glutinous rice and japonica glutinous rice landraces reaching the first level standard in the Taihu Lake area**

Varieties	Type	AC ≤ 2.0%	GT > 6	GC ≥ 100	Varieties	Type	AC ≤ 2.0%	GT > 6	GC ≥ 100
Aizinuo	Glutinous rice			1	Huangnuo	Japonica glutinous rice	1		1
Ebusinuodao	Glutinous rice	1		1	Jiangyinnuo	Japonica glutinous rice	1		
Huangjinnuo	Glutinous rice			1	Jinhuanuo	Japonica glutinous rice	1		1
Huangjingnuodao	Glutinous rice	1		1	Jintainuo	Japonica glutinous rice			1
Huangnuo	Glutinous rice	1		1	Jingdaogunuo	Japonica glutinous rice			1
Huangnuo	Glutinous rice	1		1	Maonuo	Japonica glutinous rice	1		1
Qiangdaonuo	Glutinous rice	1		1	Niaoxiunuo	Japonica glutinous rice			1
Shuijingnuo	Glutinous rice			1	Putanuo	Japonica glutinous rice			1
Xichainuo	Glutinous rice	1		1	Wushinuo	Japonica glutinous rice			
Xueliqingnuodao	Glutinous rice	1	1	1	Yangnuodao	Japonica glutinous rice			1

Varieties	Type	AC≤2.0%	GT>6	GC≥100	Varieties	Type	AC≤2.0%	GT>6	GC≥100
Guozinuo	Japonica glutinous rice			1	Yangxiandaonuo	Japonica glutinous rice	1		1
Hongkenuo	Japonica glutinous rice				Yishixing	Japonica glutinous rice	1		1
Hongmangnuo	Japonica glutinous rice			1	Zaonuodao	Japonica glutinous rice			1
Huajiaonuo	Japonica glutinous rice	1		1	Zhimanuo	Japonica glutinous rice	1		1
Huangsanshinuodao	Japonica glutinous rice	1		1					

Table 5 The indica landraces reaching the first level standard in the Taihu Lake area

Varieties	Type	AC17% - 22%	GT>4	GC≥70	Varieties	Type	AC17% - 22%	GT>4	GC≥70
Guiyuanhuang	Indica rice			1	Xiandao	Indica rice	1		
Dadaotou	Indica rice	1			Yangxiandao	Indica rice	1		
Hongmangyishixing	Indica rice	1			Wanduzixiandao	Indica rice	1	1	
Jiaobaixiandao	Indica rice			1	Datougui	Indica rice		1	1
Wanxiandao	Indica rice	1			Liushiri	Indica rice		1	
Wuxidao	Indica rice			1	Xiandao	Indica rice	1		
Jiangyinzao	Indica rice	1			Duzixiandao	Indica rice	1		
Zaohonglian	Indica rice	1		1	Wujianguangzao	Indica rice	1		
Jianlizi	Indica rice	1			Bashirizao	Indica rice	1	1	
Taihuliushizi	Indica rice	1			Wanjinxiaandao	Indica rice	1		
Bashizi	Indica rice	1			Taihuxiandao	Indica rice	1		
Wujiangxiandao	Indica rice	1	1						

4 Conclusions and discussions

In this study, with 511 rice landraces in the Taihu Lake area as test materials, we choose 19 starch synthesis-related intragenic molecular markers to detect the genetic quality of starch, and compare them with 86 bred varieties. The genetic diversity of rice landraces in Taihu Lake Basin is slightly lower than that of the bred rice varieties in 6 genetic loci (*AGP<sub>sma</sub>*, *AGP<sub>iso</sub>*, *Pull*, *SSS III-2*, *SSSII-3*, *Sbe3*), but the average genetic diversity or PIC value of landraces is slightly higher than that of the bred rice varieties. The bred varieties are selected from a wide range of sources, such as American rice, Japanese rice and some domestic varieties from the south to the north, while the landraces are all local varieties in Taihu Lake Basin. From the results of cluster analysis, all study materials are divided into 6 groups, and Group I mainly includes the commonly used indica rice; the bred japonica varieties and the japonica landraces are concentrated in different regions, and there has been genetic differentiation. Therefore, it is necessary to study and utilize the quality genetic diversity of landraces so as to broaden the genetic basis of future breeding of high-quality new rice varieties. The materials selected in this study are selected from nearly 1000 landraces in the Taihu Lake area according to the differences in quality traits. According to the national standards of high quality rice, in terms of amylose content, gelatinization temperature and gel consistency, 67 landraces reach the first level standard in one trait; 95 landraces reach the first level standard in two traits; 4 landraces reach the first level standard in three traits. Although these old landrace resources have high plant and low resistance to lodging, they still make good performance in starch quality traits, and these varieties can be used to broaden the genetic basis of starch synthesis gene and quality breeding in the future.

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