Hue University Journal of Science: Natural Science
Vol. 134, No. 1S-2, 89–104, 2025 (Special Issue: CBA 2025)

pISSN 1859-1388
eISSN 2615-9678

Genetic Evaluation of 269 Rice Landraces for Grain Quality and Blast Resistance Genes

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(*Received: 30 June 2025; Revised: 14 August 2025; Accepted: 15 August 2025*)

Abstract. The overuse of agrochemicals has intensified the focus on breeding rice varieties with enhanced grain quality and resistance to major diseases. This study aimed to evaluate genetic variation related to grain quality and blast resistance in landrace rice varieties using gene-specific molecular markers. Five target genes, including *Wx, BADH2, GS3, Pi54*, and *Pi-ta*, were analyzed for their association with key traits. Among the accessions, 52 carried the *Wx* allele associated with low amylose content, 14 possessed the aromatic *BADH2* allele, and 99 carried the mutant *GS3* allele associated with long grain. For blast resistance, 17 genotypes harbored *Pi54* and 97 carried *Pi-ta*, both major resistance genes. The research highlights valuable allelic diversity for use in marker-assisted selection and the development of elite rice cultivars with improved grain quality and disease resistance.

Keywords: BADH2, GS3, Pi54 and Pi-ta, Landraces rice, Wx

1 Introduction

Landrace rice varieties are vital genetic resources that combine essential agricultural traits for sustainable farming with cultural significance. In Vietnam's Mekong Delta, these photoperiod-sensitive genotypes flower during the shorter days of October to November and are harvested at the year's end. Their dependable growth and ability to withstand heat led to consistent yields in a variety of environments, even those that are less than ideal. Landraces are essential for both in situ conservation efforts and modern breeding programs focused on improving grain quality and resilience to stress. With a rich diversity of alleles, they are well adapted to their local habitats. Furthermore, landrace rice varieties are essential for maintaining agricultural biodiversity and developing rice types resilient to climate challenges, given their extensive genetic variation and local adaptability. However, the area dedicated to their cultivation has decreased by 1.7%, now totaling 1.58 million hectares [1].

Genetic diversity underpins crop improvement strategies. In rice breeding, exploring genomic variation in landraces enables the targeted introgression of beneficial alleles through advanced methods such as marker-assisted selection (MAS), genome-wide association studies (GWAS), and genomic prediction. High-throughput genotyping and molecular markers are increasingly applied to dissect complex traits in traditional germplasm, supporting breeding under changing environmental conditions [2]. For instance, amylose content, crucial for determining rice cooking and eating quality, is primarily regulated by the *Wx (Waxy)* gene, which encodes the granule-bound starch synthase I (GBSSI) enzyme responsible for amylose synthesis [3]. Grain morphology, particularly length, is influenced by

variation in the *GS3* gene; a C to A transition in the second exon (A allele) has been linked to the elongation of rice grains in Oryza sativa [4]. Moreover, aroma is an economically significant quality trait that is primarily controlled by a loss-of-function mutation in the *BADH2* gene, which is closely linked to the molecular marker RG28 on chromosome 8. This mutation leads to the accumulation of 2-acetyl-1-pyrroline (2AP), the key volatile compound responsible for the characteristic fragrance in aromatic rice varieties [5]. Furthermore, with respect tof biotic stress resistance, the *Pi-ta* gene located on chromosome 12 encodes a nucleotide-binding site-leucine-rich repeat (NBS-LRR protein that confers resistance to *Magnaporthe oryzae*, the causal agent of rice blast disease [6].

The identification and incorporation of landrace rice accessions with superior grain quality and disease resistance are therefore essential for broadening the genetic base of elite cultivars. Integrating these valuable genetic resources into breeding pipelines will improve varietal resilience and grain quality, ultimately supporting food security and sustainability in rice production across the Mekong Delta and beyond.

2 Materials and Methods

2.1 Plant materials

The experiment was conducted on 269 traditional rice landraces preserved at the Plant Genetic Conservation Laboratory, Department of Genetics and Plant Breeding, College of Agriculture, Can Tho University.

2.2 Methods

DNA extraction

Genomic DNA was extracted using two-week-old fresh leaves following a modified CTAB protocol adapted from [7], optimized for high- quality DNA isolation in plant molecular studies. The quality and quantity of DNA were estimated using agarose gel electrophoresis and NanoDrop spectrophotometer. After quantification, all DNA samples were normalized to a final concentration of 50 ng/μL for use in PCR amplification in this study.

Table 1. Functional primer sequence for *Wx, BADH2, GS3, Pi54* and *Pi-ta*

Gene	Primer name	Primer Sequence	Chromosome	Size band (bp)
Wx	GF	TACAAATAGCCACCACA	6	387
	TR	GATCAGCCTAACCAAACA		
	GR	GGGAAACAAAGAATTATAAACATATATGTACAC		207
	TF	CATCAGGAAGAACATCTGCAAGT		235
BADH2	ESP	TTGTTTGGAGCTTGCTGATG	8	580
	EAP	AGTGCTTTACAAAGTCCCGC		
	INSP	CTGGTAAAAAGATTATGGCTTCA		355
	IFAP	CATAGGAGCAGCTGAAATATATACC		257
GS3	EFP	AGGCTAAACACATGCCCATCTC	3	365
	ERP	CCCAACTTCAGAAATTAAATG TGCTG		
	IRSP	AACAGCAGGCTGGCTTACTCTCTG		262

pISSN 1859-1388
eISSN 2615-9678

Gene	Primer name	Primer Sequence	Chromosome	Size band (bp)
	IFLP	ACGCTGCCTCCAGATGCTGA		147
Pi54	Pi54F	CAATCTCCAAAGTTTTCAGG	11	216
	Pi54R	GCTTCAATCACTGCTAGACC		359
Pi-ta	Pita-IF	CTCTGCCGTGGCTTCTATCTTTACTTG	12	201
	Pita-IR	ATCAAGTCAGGTTGAAGATGCATGGA		230
	Pita-GF	ATGGTTGATATACAATGGGTGGATTGG		382
	Pita-OR	CCCGAGAAAATATAGGACCTCCCATTAA		

PCR Amplification

Polymerase Chain Reaction (PCR) amplification was carried out in a total volume of 10 μL, comprising 5 μL of 2X PCR Master Mix (GoTaq Green Master Mix), 0.5 μL of each forward and reverse primer (10 pmol), 1 μL of DNA, and 3 μL PCR - grade water. PCR was conducted under the following cycling conditions: initial denaturation at 95°C for 5 minutes, followed by 35 cycles of 95°C for 30 seconds, annealing for 30 seconds (temperature depending on the annealing temperature of each primer, as listed in Table 2), extension at 72°C for 30 seconds, and a final extension at 72°C for 5 minutes. The PCR products were stored at 10°C. Amplified PCR products were separated by electrophoresis and stained with ethidium bromide (10 mg/mL) and visualized under UV light.

3 Results and Discusion

3.1 Genes Regulating Amylose Content

Amylose biosynthesis in rice is regulated by the granule-bound starch synthase 1 (GBSSI) enzyme, encoded by the *Waxy* (*Wx)* gene [8]. Several allelic variants of the *Wx* gene have been characterized in rice germplasm, including *Wx-in* [8] and Wx^b [9]. A key functional polymorphism, a G to T substitution at the first intron splice donor site, affects mRNA processing efficiency, leading to differences in GBSSI expression and ultimately determining amylose content. Based on this single-nucleotide polymorphism (SNP), [3] developed a molecular marker system comprising four primers: GF, TR, GR and TF. These form three diagnostic primer combinations: GF-TR amplifies a 387 bp fragment flanking the target region; GF-GR amplifies a 207 bp fragment indicative of the G allele (associated with high amylose content); and TF-TR amplifies a 235 bp fragment corresponding to the T allele (associated with low amylose content).

Genotypic analysis of amylose content in 269 landrace rice varieties (Fig 1) revealed that 214 landraces amplified a 207 bp fragment and a 387 bp fragment, corresponding to the high-amylose allele. Additionally, 52 landraces amplified the 235 bp and 387 bp fragments, indicating the presence of the low-amylose allele. The remaining 3 landraces exhibited all three bands, suggesting a heterozygous genotype carrying both alleles (Table 2). These results demonstrate the predominance of the high-amylose allele among landraces. Nevertheless, the presence of low-amylose and heterozygous genotypes provides useful germplasm for breeding programs targeting soft-textured or intermediate-quality rice.

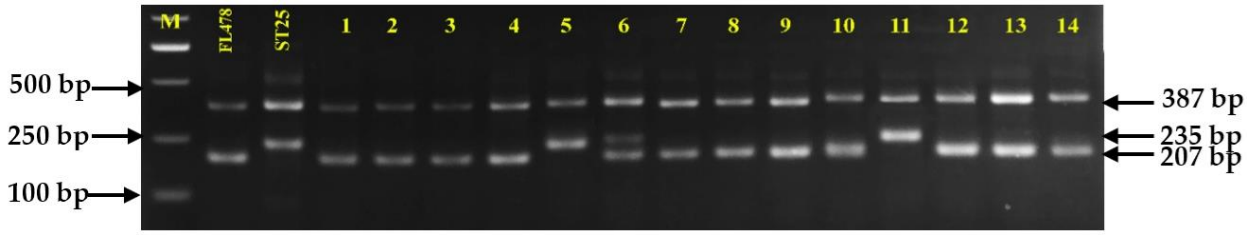

Fig. 1. PCR amplification profiles of the Wx gene in 14 out of 269 landrace rice varieties, visualized on a 2% agarose gel

(M: ladder DL2000plus; FL478: high-amylose control; ST 25: intermediate-amylose control; 1-13: experimental rice varieties listed in Table 2)

3.2 Gene Identification for Aromatic Trait

Aroma is an indispensable quality trait in rice, controlled by the *BADH2* gene. Mutations in this gene directly affect the biosynthesis of 2-acetyl-1-pyrroline (2AP), the compound responsible for the characteristic aroma of fragrant rice.

According to Bryan *et al.* [6], the *fgr* allele is located on chromosome 8. Specific mutations—including a 9-bp deletion, three single-nucleotide polymorphisms (SNPs) in exon 7, and a 8-bp deletion in exon 2—are strongly associated with the accumulation of 2AP and thus influence the aroma quality in rice. Genetic screening based on these mutations has become an effective and accurate tool in the development of aromatic rice lines within rice improvement programs.

Genotypic analysis of aroma-related traits in 269 rice cultivars (Fig 2) revealed that 231 cultivars exhibited the homozygous dominant genotype *Fgr/Fgr* (non-aromatic), with amplification bands at 355 bp and 580 bp. Fourteen cultivars carried the homozygous mutant genotype *fgr/fgr* (aromatic), showing bands at 257 bp and 580 bp. The remaining 24 cultivars displayed a heterozygous *Fgr/fgr* genotype, with bands corresponding to both the wild-type and mutant alleles. These results indicate that although non-aromatic rice types are more prevalent, aromatic genotypes still provide valuable genetic resources for the development of fragrant rice varieties (Table 2).

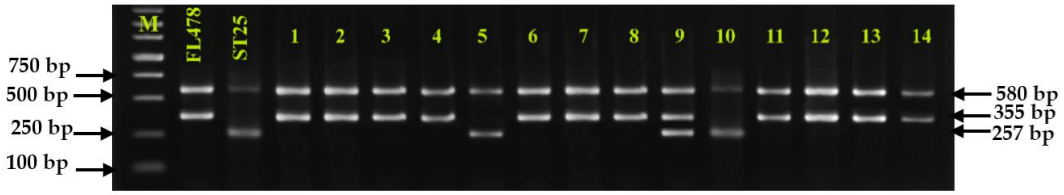

Fig. 2. PCR amplification profiles of the BADH2 gene in 14 out of 269 landrace rice varieties, visualized on a 2% agarose gel

(M: ladder DL2000plus; FL478: Non-aromatic control; ST25: Aromatic control; 1-14: experimental rice varieties listed in Table 2)

3.3 Genes Controlling Grain Length in Rice

Grain length in rice is a quantitative trait controlled by multiple genes. Among them, *GS3*, located on chromosome 3, is considered a key gene, accounting for approximately 80-90% of the phenotypic variation in grain length. This study applied the DRR-GL primer system to identify the genetic control of this trait [10]. Specifically, the EFP-ERP primer pair amplifies a 365 bp fragment used to detect general allelic variation associated with long-grain length; the EFP-IRSP primer pair

pISSN 1859-1388
eISSN 2615-9678

amplifies a 147 bp fragment to identify short-grain varieties (grain length <6.5 mm); and the ERP-IFLP primer pair amplifies a 262 bp fragment to characterize long-grain varieties (grain length >6.5 mm)

PCR amplification using the DRR-GL primer set, followed by electrophoresis on a 2% agarose gel in 269 upland rice varieties (Fig 3), showed that the EFP–ERP primer pair successfully amplified a 365 bp fragment in all samples, indicating the presence of both dominant and recessive alleles. The EFP–IRSP primer pair produced a 147 bp band in 152 varieties, corresponding to the short-grain trait. Meanwhile, the ERP–IFLP primer pair amplified a 262 bp band in 99 varieties, indicating the long-grain trait. The remaining 18 varieties displayed both bands, suggesting a heterozygous genotype (Table 2). Although short-grain types predominate, the substantial occurrence of long-grain genotypes highlights their potential utility in breeding programs aimed at enhancing grain morphology.

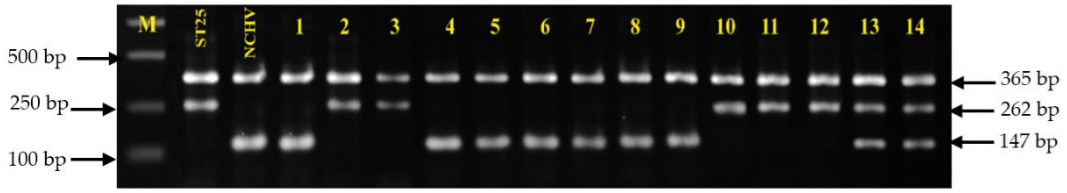

Fig. 3. PCR amplification profiles of the GS3 gene in 14 out of 269 landrace rice varieties, visualized on a 2% agarose gel

(M: ladder DL2000plus; ST25: long-grain control; NCHV: short-grain control; 1-14: experimental rice varieties listed in Table 2)

3.4 Blast Resistance Associated with the *Pi54* Gene

Rice blast disease is a persistent issue affecting rice cultivation across all major rice-growing regions worldwide. Incorporation of blast resistance genes into rice breeding programs is considered one of the most effective strategies for managing this disease [11]. Numerous studies have identified over 100 leucine-rich blast resistance genes and approximately 500 quantitative trait loci (QTLs) distributed throughout the rice genome. The *Pi54* gene, located on chromosome 11, contains a distinctive zinc finger domain outside the leucine-rich repeat (LRR) region, suggesting its role in pathogen recognition and transcriptional regulation to initiate defense responses. The *Pi54* MAS primer pair was designed to differentiate between resistant and susceptible alleles of the *Pi54* gene via PCR. Results showed that the varieties Te Tep and others that produced a 216 bp amplicon carry the resistant allele of *Pi54*, indicating potential resistance to blast disease. Furthermore, varieties yielding a 359 bp amplicon do not carry the *Pi54* resistance allele (Fig 4).

The PCR electrophoresis results of 269 landrace varieties using the *Pi54* molecular marker revealed that the susceptible control variety CO_{39} and 243 other varieties amplified a 359 bp band, indicating the absence of the *Pi54* blast resistance gene (Table 2). Conversely, the resistant control variety Te Tep and 17 landrace varieties amplified a 216 bp band, suggesting the presence of the *Pi54* resistance allele. These findings are consistent with the results reported by [10]. Additionally, 9 varieties showed amplification of both the 216 bp and 359 bp bands, indicating a heterozygous genotype at the *Pi54* locus. Despite a few landraces carrying the *Pi54* resistance allele, these genotypes represent valuable resources for introgressing blast resistance into breeding lines.

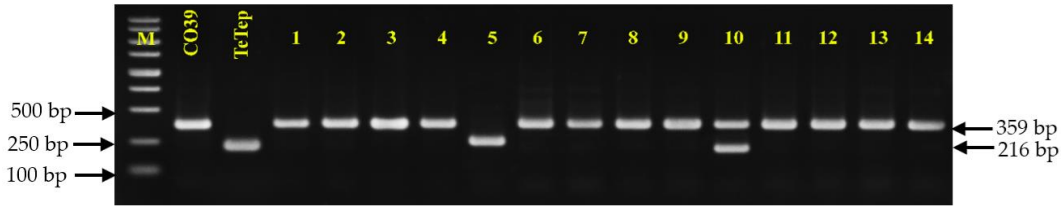

Fig. 4. PCR amplification profiles of the Pi54 gene in 14 out of 269 landrace rice varieties, visualized on a 2% agarose gel

(M: ladder DL2000plus; TeTep: Resistant check; CO39: Susceptible check; 1-14: experimental rice varieties listed in Table 2)

3.5 Blast Resistance Associated with the *Pi-ta* Gene

According to Bryan *et al.* [6], *Pi-ta* is among the most effective genes conferring resistance to rice blast disease. It is located near the centromere of rice chromosome 12, a region typically suppressed in recombination within the rice genome. [12] demonstrated that a nucleotide polymorphism within the *Pi-ta* gene can be effectively targeted using the molecular marker TPAP-Pita to distinguish between resistant and susceptible alleles. In this system, PCR amplification producing bands at 382 bp and 201 bp indicates a susceptible genotype, whereas bands at 382 bp and 230 bp correspond to a genotype carrying the resistant *Pi-ta* allele.

Based on PCR product analysis in 269 landrace rice varieties (Fig 5), 159 varieties amplified bands of 201 bp and 382 bp, indicating they did not carry the *Pi-ta* blast resistance gene, 97 varieties amplified bands of 230 bp and 382 bp, consistent with the presence of the *Pi-ta* resistance allele. The remaining 13 varieties showed amplification of all three bands (201 bp, 230 bp, and 382 bp), suggesting a heterozygous genotype at the *Pi-ta* locus (Table 2).

Although these indica rice varieties are considered pure lines due to being maintained through multiple generations of traditional cultivation, the genotyping results for *Pi-ta* reveal the presence of heterozygosity in modern systematic breeding processes; thus, morphological uniformity does not necessarily correspond to genetic homozygosity. Furthermore, the existence of heterozygosity at the *Pi-ta* locus reflects the genetic diversity within the indica rice population, which contributes to their adaptability to environmental conditions.

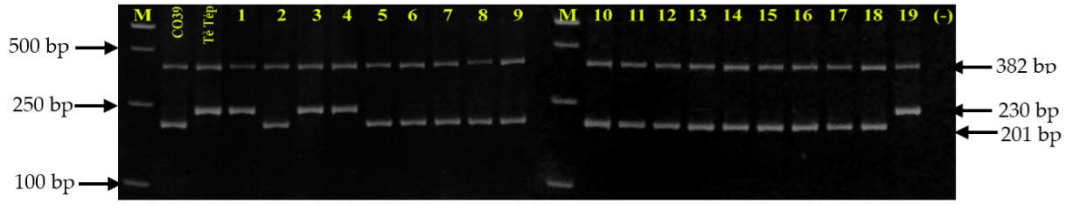

Fig. 5. PCR amplification profiles of the *Pi-ta* gene in 19 out of 269 landrace rice varieties, visualized on a 8% polyacrylamide gel

(M: ladder DL2000plus; TeTep: Resistant check; CO39: Susceptible check; 1-14: experimental rice varieties listed in Table 2)

3.6 Overall Comparison of Five Genes

A summary of the genetic analysis results for five target genes *(Wx, BADH2, GS3, Pi54, and Pi-ta)* in 269 landrace rice varieties is provided in Table 2.

pISSN 1859-1388
eISSN 2615-9678

Table 2. List of 269 Landrace Varieties, Source, and Genotypes in the Experiment

STT	Variety name	Source	Gene				
			Wx	*BADH2*	*GS3*	*Pi54*	*Pita*
1	Ba Bong Man 1	Ca Mau	G	N	S	S	R
2	Ba Co	Ca Mau	G	N	L	S	S
3	Ba Lon	Ca Mau	G	N	L	S	R
4	Ba Lu	Ben Tre	G	N	S	S	R
5	Nep Mong Chim 2	An Giang	T	A	S	R	S
6	Nang Lai 5	Tra Vinh	H	N	S	S	S
7	Ba Sa	Tien Giang	G	N	S	S	S
8	Brich Mao	Tra Vinh	G	N	S	S	S
9	Lua Soi 3	Tra Vinh	G	H	S	S	S
10	Tam Ruot Lua	Long An	G	A	L	H	S
11	To Nop Smal	An Giang	T	N	L	S	S
12	Chet Som 2	Vinh Long	G	N	L	S	S
13	Nep Mo 11	Ca Mau	G	N	H	S	S
14	Lun Can	Ca Mau	G	N	H	S	R
15	Ca Dung Bap	Tien Giang	G	N	S	S	S
16	Chang Lua	Vinh Long	G	N	S	S	S
17	Chim Dia	Ben Tre	G	N	S	S	S
18	Chum Ruot Lua 1	Bac Lieu	G	N	S	S	S
19	Chum Ruot Ran	Bac Lieu	G	N	L	S	S
20	Cu Ba	Bac Lieu	G	N	S	S	S
21	Doc Do 2	Tien Giang	G	N	S	S	S
22	Doc Do 3	Tien Giang	G	N	S	S	S
23	Dung Dinh Trang	Soc Trang	G	N	S	S	S
24	Duoi Trau 2	An Giang	T	N	L	S	S
25	Gie Vang	Tien Giang	G	H	S	S	R
26	Hong Xoi 2	Tien Giang	G	N	S	S	R
27	Huy Ky	Tien Giang	G	N	S	S	R
28	Huyet Rong 1	Hau Giang	G	N	S	S	S
29	La Tim	An Giang	G	N	S	R	R
30	Lem Bui 2	Ben Tre	G	N	S	S	S
31	Lon 2	An Giang	G	N	L	S	S
32	Long Tong 1	Tra Vinh	G	N	L	S	S

STT	Variety name	Source	Gene				
			Wx	*BADH2*	*GS3*	*Pi54*	*Pita*
33	Lua Hoi	Tra Vinh	G	A	S	S	R
34	Lua Lua	Ca Mau	G	N	L	S	R
35	Lua Thom 3	An Giang	G	N	L	S	S
36	Lun Bui 2	Binh Thuan	G	N	L	R	R
37	Lun Kien Giang	Ca Mau	G	N	S	S	R
38	Mat Chuoi To	Vinh Long	G	N	S	S	R
39	Long An 5	Vinh Long	G	N	S	S	R
40	Mong Chim Lun 2	Soc Trang	G	N	L	S	R
41	Mong Chim Lun 3	Soc Trang	T	N	L	S	S
42	Mot Bui Co Don	Ca Mau	G	N	L	S	R
43	Mot Bui Lun 1	Ca Mau	G	N	L	S	R
44	Nang Cho 2	Vinh Long	G	N	S	S	R
45	Nang Chiem	An Giang	G	N	S	S	R
46	Nang Co Do 2	Hau Giang	T	N	S	S	R
47	Nang Gao Gia 2	Hau Giang	T	N	L	S	S
48	Nang Keo 1	An Giang	G	N	S	S	R
49	Nang Minh 2	Long An	T	N	S	S	R
50	Nang Nieu 2	Ben Tre	T	N	S	S	R
51	Nang Nieu 3	Ben Tre	G	N	S	R	R
52	Nang Nu 2	Long An	T	N	L	S	R
53	Nang Pha	An Giang	T	N	L	S	R
54	Nang Phet 1	Tien Giang	T	N	S	S	S
55	Nang Quoc	Ben Tre	T	N	L	S	R
56	Nang Quot Dai	Ca Mau	T	N	L	S	S
57	Nang Ray	Long An	T	N	L	S	S
58	Nang Ray Trang	Tien Giang	T	N	S	S	S
59	Nang Sal	An Giang	G	N	L	S	S
60	Nang Sau 2	Long An	G	N	L	S	S
61	Nang Som	Hau Giang	T	N	S	S	S
62	Nang Tay Nau	An Giang	G	N	L	S	R
63	Nang Thom 2	Hau Giang	T	N	L	S	S
64	Nang Thom Muon	Long An	T	A	L	S	S
65	Nang Thuoc	Ben Tre	G	N	L	S	S

pISSN 1859-1388
eISSN 2615-9678

STT	Variety name	Source	Gene				
			Wx	*BADH2*	*GS3*	*Pi54*	*Pita*
66	Nang Tro 1	Tra Vinh	G	N	L	S	S
67	Nang Xoi	An Giang	T	N	L	S	S
68	Nanh Chon	Vinh Long	T	N	L	S	S
69	Nep Ba Kieu	Tra Vinh	T	N	L	S	R
70	Nep Bau 1	Tra Vinh	G	N	S	S	S
71	Nep Bun 1	An Giang	T	N	L	S	S
72	Nep Bun 6	Kien Giang	T	N	L	S	S
73	Nep Ca Ro 1	Can Tho	T	N	S	S	S
74	Nep Do 5	Ben Tre	T	N	S	S	S
75	Nep Gach Tom	Long An	T	N	L	S	S
76	Nep Han The	Ca Mau	T	A	S	S	S
77	Nep Hat Lon	Kien Giang	T	N	S	S	S
78	Nep Keo 3	Ben Tre	T	N	S	S	S
79	Nep Mau Luon 5	Can Tho	T	N	S	S	S
80	Nep Mo 9	Ca Mau	T	N	L	S	S
81	Nep Mo 17	Ben Tre	G	N	S	S	S
82	Nep Mot	Ca Mau	G	N	S	S	S
83	Nep Mua	Ben Tre	T	N	S	S	S
84	Nep Muong Do 2	Vinh Long	T	N	S	S	H
85	Nep Nam Ly	Tra Vinh	G	N	L	S	S
86	Nep Pain	Tra Vinh	G	N	L	S	S
87	Nep Ruoi Mua	Ben Tre	T	N	S	S	S
88	Nep Sap 3	Vinh Long	T	N	S	S	S
89	Nep Sap 4	Hau Giang	G	N	S	S	S
90	Nep Tam Sanh A	Tra Vinh	T	A	S	S	S
91	Nep Thu Thua	Long An	G	N	L	S	S
92	Nep Troi	Tra Vinh	T	N	L	S	R
93	Nep Trong Vo	Ca Mau	G	N	L	S	S
94	Nep Vo Dua	Ben Tre	G	H	L	S	S
95	Phi Nau	Tra Vinh	G	N	S	S	S
96	Quang Phat 2	Long An	G	N	H	S	H
97	Ruom Trang	Hau Giang	G	N	L	S	H
98	Sa Mo	Long An	G	N	S	S	S

STT	Variety name	Source	Gene				
			Wx	*BADH2*	*GS3*	*Pi54*	*Pita*
99	Sa Suc Vang	Hau Giang	G	N	S	S	S
100	Sen 2	Long An	G	N	L	S	S
101	So Thum	An Giang	G	N	S	S	S
102	Soc Do	Long An	G	N	L	S	S
103	Soc Nau 1	Tien Giang	G	N	S	S	S
104	Soc Nau 2	Long An	G	N	S	S	R
105	Soc Ran	Can Tho	G	N	S	S	H
106	Soc Sau 1	Long An	G	N	S	S	H
107	Soc Sau 2	Long An	G	N	S	S	S
108	Soc Vuon 1	Tien Giang	G	N	S	S	S
109	Soc Vuon 2	Tien Giang	G	N	S	S	H
110	Soi 1	Hau Giang	G	N	L	S	R
111	Soi 2	Hau Giang	G	N	L	S	H
112	Soi Da	Ben Tre	G	N	S	S	S
113	Soi Mieng	Long An	G	H	L	S	R
114	Song Doi	Hau Giang	G	H	S	S	R
115	Su An 1	Hau Giang	G	H	S	S	H
116	Tam Gia	Ca Mau	G	N	L	S	S
117	Tam Ruot 1	Tra Vinh	G	N	S	S	R
118	Tan Hung 2	Hau Giang	G	N	S	S	S
119	Tat No 2	Long An	G	N	S	S	H
120	Tau Bac	Ben Tre	G	N	S	S	R
121	Tau Bat	Tien Giang	G	N	S	S	R
122	Tau Bau	Kien Giang	G	H	H	S	S
123	Tau Bun Som	Ben Tre	G	N	L	S	R
124	Tau Chen	Kien Giang	G	N	L	S	S
125	Tau Huong 2	Ben Tre	G	N	S	S	S
126	Tau Huong 5	Ben Tre	G	A	L	S	S
127	Tau Rang	Ben Tre	G	N	S	S	R
128	Tay Lieu 5	Tra Vinh	G	N	L	S	R
129	Tay Nha Nuoc	An Giang	T	N	L	S	S
130	Tep	Long An	G	N	S	S	R
131	Tet Hanh 1	Ca Mau	G	H	L	S	R

pISSN 1859-1388
eISSN 2615-9678

STT	Variety name	Source	Gene				
			Wx	*BADH2*	*GS3*	*Pi54*	*Pita*
132	Tet Thom	Long An	G	N	L	R	S
133	Nang Minh 1 (130)	Long An	G	N	S	S	R
134	Thai Lan Muon	Ca Mau	G	N	L	R	S
135	Than Nong Bong Huong	Ca Mau	G	N	S	S	S
136	Than Nong Cao	Ben Tre	G	N	S	S	S
137	Than Nong Mua 1	Ca Mau	G	N	L	S	R
138	Than Nong Mua 2	Ca Mau	G	N	S	S	S
139	Thang Chim	An Giang	T	N	L	S	S
140	Them Dia	Ben Tre	G	N	S	S	R
141	Thom Nut Dit	Tra Vinh	G	N	S	S	R
142	Thom Nut Dit	Tra Vinh	G	N	L	S	S
143	Thom Ran	Hau Giang	G	N	L	S	S
144	Trai May	Kien Giang	T	N	L	S	S
145	Thuoc 1	Hau Giang	G	N	S	S	S
146	Tieu Doi 1	Long An	G	N	L	S	R
147	Tieu Doi 2	Long An	G	N	S	H	S
148	Tieu Xoi	Tien Giang	G	N	S	S	R
149	Tra Long 2	Ca Mau	G	N	S	S	S
150	Tra Vinh	Tien Giang	G	N	S	S	S
151	Tram Bong 2	Ca Mau	G	N	L	S	R
152	Trang Ba Lon 3	Kien Giang	G	N	L	S	S
153	Trang Trum 1	Kien Giang	G	N	L	S	R
154	Trang Trum2	Vinh Long	G	N	H	S	S
155	Trang Trum 7	Tra Vinh	G	N	S	S	S
156	Trang Trum 11	Vinh Long	G	N	S	S	S
157	Trang Don	Tra Vinh	G	N	S	S	S
158	Trang Hoa Binh	Ben Tre	G	N	L	S	R
159	Trang Hoc	Vinh Long	G	N	S	S	R
160	Trang Mot Bui	Ca Mau	G	N	L	S	R
161	Trang Tron	Ca Mau	G	N	S	S	R
162	Trieu Man	An Giang	G	N	S	S	S
163	Truong Hung Trang	Long An	G	N	S	S	S
164	Vang Bac	Vinh Long	G	N	S	S	S

STT	Variety name	Source	Gene				
			Wx	*BADH2*	*GS3*	*Pi54*	*Pita*
165	Xa Quay 2	Ca Mau	G	N	S	S	S
166	Nep Ong Doc	Tra Vinh	T	N	L	H	S
167	Ba So	Kien Giang	G	N	S	S	S
168	Me Huong	Khong	G	N	L	S	S
169	Tau Huong	-	G	A	S	H	S
170	Lun Can Dai	-	G	N	S	R	R
171	Nep Tet Hanh	-	G	N	L	S	S
172	Nang Huong Thanh Tra	-	G	N	S	S	H
173	Trang Tep	-	G	N	S	S	R
174	Nang Tet	Tra Vinh	G	N	S	S	S
175	Nep Thai Binh	Mien Bac	T	N	S	S	S
176	Cang Long	Tra Vinh	G	N	H	H	S
177	Trang Tep 1	Tra Vinh	G	N	L	S	S
178	Phi 4	Tra Vinh	T	N	S	S	S
179	Trang Lun 3	Tra Vinh	G	N	S	S	R
180	Trang Lun 4	Tra Vinh	G	N	S	S	S
181	Nang Tet 1	Tra Vinh	G	N	S	S	S
182	Rach Gia 1	Tra Vinh	H	N	H	S	R
183	Rach Gia 5	Tra Vinh	G	H	L	S	R
184	Lua Soi 1	Tra Vinh	G	N	S	S	S
185	Lua Soi 2	Tra Vinh	G	N	S	S	S
186	Lua Soi 4	Tra Vinh	G	N	S	S	S
187	Lua Soi 5	Tra Vinh	G	H	S	S	S
188	Nep Do 4	Tra Vinh	H	N	S	H	R
189	Nang Lai 1	Tra Vinh	G	N	S	H	R
190	Nang Lai 4	Tra Vinh	G	N	S	S	R
191	Ba Rong	Tra Vinh	G	N	S	S	S
192	Nang Tet 1	Tra Vinh	G	N	S	H	S
193	Tai Nguyen	Tra Vinh	G	N	S	S	R
194	Bong Sen	Tra Vinh	G	N	S	S	S
195	Trang Tra Vinh	Tra Vinh	G	N	S	S	R
196	Nep Do	Tra Vinh	G	N	L	S	R
197	Lua Den	Tra Vinh	G	N	S	S	H

pISSN 1859-1388
eISSN 2615-9678

STT	Variety name	Source	Gene				
			Wx	*BADH2*	*GS3*	*Pi54*	*Pita*
198	Nep Go Cong	Tra Vinh	G	N	L	S	R
199	Mot Bui	Tra Vinh	G	N	S	S	S
200	Hai Hoanh	Tra Vinh	G	N	S	S	R
201	Trang Lun	Tra Vinh	G	N	S	S	S
202	Nep Mo	Tra Vinh	G	N	S	S	R
203	Nep Than	Tra Vinh	G	N	L	S	S
204	Tai Nguyen Lun	Tra Vinh	G	N	S	S	R
205	Trang Lua	Tra Vinh	G	N	S	S	S
206	Tai Nguyen 204	Tra Vinh	G	N	S	S	S
207	Soi	Tra Vinh	G	N	S	S	S
208	Trang Tep (206)	Tra Vinh	G	N	S	S	S
209	Nang Nhen Thom	An Giang	G	H	L	S	S
210	Do Nom	PleiKu	G	N	S	S	R
211	Kung Nel	An Giang	G	N	S	S	R
212	Lua Thom Mua	An Giang	G	N	L	S	S
213	Srau Khoop	An Giang	G	N	S	R	R
214	Trang Tep	An Giang	G	N	S	R	R
215	Ir 65610	An Giang	G	A	L	S	R
216	Xo Thom	An Giang	G	N	S	S	S
217	Ba Thiet	An Giang	G	N	S	R	R
218	Lem Bui	Ben Tre	G	N	S	S	S
219	Ba Trang	Ca Mau	G	H	L	S	R
220	Ngoc Nu	Ca Mau	G	N	L	S	R
221	Nep Trung Cut	Ca Mau	G	N	S	S	S
222	Tet Hanh Lun	Ca Mau	G	N	H	S	R
223	Tet Ran	Ca Mau	G	N	S	S	S
224	Nep Dai	Ca Mau	T	N	H	S	S
225	Tet Hanh Dot Bien	Ca Mau	G	N	H	S	R
226	Nam Tai	Ca Mau	T	N	S	S	R
227	Vang 3 Danh	Ca Mau	G	N	H	S	S
228	Trang Tron (226)	Ca Mau	G	N	L	S	S
229	Trang Tron	Ca Mau	G	N	S	S	R
230	Nang Tung Chum	Ca Mau	G	N	L	S	S

STT	Variety name	Source	Gene				
			Wx	*BADH2*	*GS3*	*Pi54*	*Pita*
231	Tai Nguyen	Ca Mau	G	N	S	S	R
232	Trang Hoang Anh	Ca Mau	G	N	S	S	R
233	Trang Ba Lon	Ca Mau	G	N	H	S	H
234	Lun Can	Ca Mau	G	N	H	S	R
235	Vang That Hong	Ca Mau	G	N	H	S	S
236	Tai Nguyen	Ca Mau	G	N	L	S	S
237	Trang Sua	Ca Mau	G	N	L	S	R
238	115	Ca Mau	G	N	L	S	R
239	To Nop Ao Vang	Kien Giang	G	N	L	S	S
240	Trang Thai Lan	Kien Giang	G	N	H	S	R
241	Lun Can Trang	Kien Giang	G	N	S	S	R
242	Nep Chlan	An Giang	T	N	L	R	R
243	Nep Chol Hol	An Giang	G	N	S	R	S
244	Sma Sa Kom	An Giang	G	N	H	H	H
245	Ta Nop Smal	An Giang	G	N	S	S	R
246	Musaline	An Giang	G	N	S	S	S
247	Nang Nhen Thom	An Giang	G	H	S	R	R
248	Lua Thom Mua 247	An Giang	G	H	S	R	R
249	Too Nop So	An Giang	G	H	S	R	S
250	Bong Mdy	An Giang	T	H	L	R	S
251	To Nop Oop	An Giang	G	H	S	S	R
252	Lua Chanh	An Giang	T	A	L	R	S
253	Lua Chao	An Giang	G	H	S	S	R
254	Me Huong	-	G	A	L	S	S
255	Lua Thom	-	G	A	L	S	S
256	Thom Lua	-	G	A	S	S	S
257	Nang Thom Som	-	G	H	L	S	S
258	Nanh Chon	-	G	A	S	S	S
259	Chau Hang Vo	-	G	H	H	S	S
260	Nep Do 7	Tien Giang	T	H	L	S	S
261	Nep Doc	Tien Giang	G	N	L	S	R
262	Nep Mo 6	Tra Vinh	T	N	L	S	S
263	Nep Mu U 4	Soc Trang	T	N	S	S	S

pISSN 1859-1388
eISSN 2615-9678

STT	Variety name	Source	Gene				
			Wx	*BADH2*	*GS3*	*Pi54*	*Pita*
264	Nep Sap 1	Long An	T	H	L	S	R
265	Tai Nguyen Gao Trang	Ca Mau	G	H	S	S	R
266	Than Nong Duoi	Ca Mau	G	H	H	S	S
267	Trang Chum 10	Vinh Long	G	N	S	S	S
268	Lun Minh Hai	Kien Giang	G	N	L	S	S
269	Srdu Ca Don	Kien Giang	G	N	L	S	S

Wx: T: Low-amylose content, G: High amylose content; BADH2: A: Aroma, N: None aroma; GS3: L: Long-grain, S: short grain; Pi-ta & Pi54: R: Resistant; S: Susceptible, H: Heterozygous

4 Conclusion

In conclusion, the study showed that 214 out of 269 rice varieties carried genotypes associated with high amylose content, while 52 landrace rice varieties carried the genotypes indicative of low amylose content, and 3 varieties were heterozygous. Regarding aroma, 231 out of 269 rice varieties lacked the fragrance-related genotype, 14 possessed the aromatic genotype, and 24 were heterozygous. For the gene regulating grain length, 153 varieties carried the short-grain genotype, 99 carried the long-grain genotype, and 18 varieties were heterozygous. In terms of blast resistance, 17 landrace rice varieties carried the *Pi54* resistance gene, and 97 varieties carried the *Pi-ta* gene. Meanwhile, 243 and 159 varieties did not carry the *Pi54* and *Pi-ta* resistance genes, respectively, and 9 (*Pi54*) and 13 (*Pi-ta*) varieties were heterozygous. Moreover, the accessions Nep Mong Chim 2, Bong Mdy, Lua Chanh, Nep Chlan, and Nep Sap 1 were identified as possessing genotypes associated with low amylose content and blast resistance.

5 Recommendation

The landrace accessions identified in this study constitute genetic resources for breeding rice cultivars with enhanced grain quality and blast resistance.

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