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Date received: 28/10/2016
Date reviewed: 15/11/2016
Reviewer: Dr. Dang Minh Tam
Date approved for publication: 20/12/2016

EVALUATION AND TESTING OF TROPICAL RICE VARIETIES UNDER TEMPERATE CLIMATE IN RUSSIA

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Abstract

Breeding of rice varieties for Northern temperate regions always faces difficulty and therefore needs to have diverse sources of materials collected from tropical regions. A study of the collection of tropical rice materials with economically important quantitative traits has been carried out and a considerable variation was found. A positive correlation was recorded between the panicle length and plant height; weight of panicles and weight of 1000 grains; the number of grains per panicle and the ratio of fertile grains. The study results will provide pre-breeding materials for improving productivity and resistant ability of popular rice varieties in Russia.

Keywords: rice, collection, donors, sustainability, productivity

INTRODUCTION

Rice (*Oryza sativa* L.) is a staple food of more than half of the world's population. The global diversity of varieties is a genetic basis for breeding efforts aimed at maintaining the productivity of rice. In most Asian countries, it is known to be rich in rice germplasm. International Rice Research Institute (IRRI) has the most genetically diverse and comprehensive collection of rice in the world (Jackson MT, 2002).

Rice is grown in Northern zones of the Russian Federation. Rice is annually cultivated in Kuban, Don, Volga and in the Far East with approximately 200 thousand hectares. In Rostov region alone, rice is sown yearly with 14-15 thousand hectares (Kostylev PI. *et al*., 2004). In this regard, the main focus of rice breeding in this area is the generation of middle-stress resistant varieties with high productivity, well adapted to local conditions (Usatov AV. *et al*., 2004). The problem of their generation must be addressed through the study of various sources of materials and separated from the sources of agronomic characters for inclusion in the selection process, which will be allowed to more effectively develop new high-yielding varieties of rice.

The aim of this study was to conduct a comprehensive study on the collection of rice samples from IRRI (Philippines) and AGI (Institute of Agricultural Genetics, Vietnam) and to select pre-breeding materials for breeding of new tolerant lines under stress factors.

MATERIALS AND METHODS

50 donor samples of rice subspecies *indica* from the collection of AGI, carrying genes *Saltol* (salt tolerance), *Sub 1* (resistance to flooding), *Xa* (resistance to bacteriosis) *AG* (anaerobic germination), and others were used and control varieties were Boyarin and Uzhanin.

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Methods used in the study were followed by VIR (Lyakhovkin AG, 1982) and ARRIGC (Kostylev PI, 2011). Sample seeds were sown on May 4 with coded plots of 0.6 m^2/plot and three replications. Data processing was followed by BA Dospehov (1985).

RESULTS AND DISCUSSIONS

Rice samples from IRRI (Philippines) and AGI were sown in greenhouse under controlled conditions for seedling growth and development and then planted on experimental plots at ARRIGC.

Table 1. Characteristics of the donor rice varieties in Proletarsk, 2015

Number of plots 2015	Name of the variety	Origin	Characteristics	Period before flowering (days)	Plant height (cm)	Panicle length (cm)
st	Boyarin	ARRIGC	Standard	76.0	86.0	15.3
st	Uzhanin	ARRIGC	Standard	86.0	103.0	18.3
8261	QR1	AGI	Amylose	114	64.1	12.6
8262	QR2	AGI	Amylose	109	79.2	21.4
8254	SHPT-1	AGI	High yield	117	90.8	17.0
8255	DT 57	AGI	High yield	117	64.5	21.8
8256	FL 478	AGI	*Saltol*	114	67.4	21.5
8257	IR 45427-2B-2-2N-1-1	AGI	*Saltol*	114	71.8	23.4
8259	IR 74099-3R-3-3	AGI	*Saltol*	110	78.4	25.6
8260	NSiC Rc 106	AGI	*Saltol*	110	73.3	26.0
1006	BR 47	IRRI	*Saltol*	105	96.5	23.3
1032	D18 (Khang Dan)	AGI	*Sub1*	131	91.7	19.7
1033	D27 KD	AGI	*Sub1*	131	93.3	18.3
1034	D149 KD	AGI	*Sub1*	126	95.0	21.5
1015	IR86385-48-2-1-B	IRRI	*Sub1 + Saltol*	131	83.3	19.0
1022	IR86385-87-1-1-B	IRRI	*Sub1 + Saltol*	117	81.7	16.3
1024	IR86385-99-2-1-B	IRRI	*Sub1 + Saltol*	126	76.7	21.0
1026	IR86385-117-3-1-B	IRRI	*Sub1 + Saltol*	126	86.7	16.5
1027	IR86385-122-1-1-B	IRRI	*Sub1 + Saltol*	131	70.0	18.0
1029	IR86385-194-2-1-B	IRRI	*Sub1 + Saltol*	117	83.3	18.0
1030	IR86385-248-2-1-B	IRRI	*Sub1 + Saltol*	126	80.0	18.7
1008	Khao Hlan On	IRRI	*AG*	126	153.3	18.3
1009	Kharsu 80A	IRRI	*AG*	113	140.0	22.7
1010	Mazhan Red	IRRI	*AG*	115	123.4	22.7
1044	IRBB 62	IRRI	*Xa4, Xa7, Xa21*	129	60.0	15.7
1041	IRBB 5	IRRI	Xa5	124	56.7	12.0
1042	IRBB 7	IRRI	*Xa7*	131	81.7	14.5
	Minimum			*76.0*	*56.7*	*12.0*
	Maximum			*131.0*	*153.3*	*26.0*
	Average			*116.5*	*87.6*	*19.2*
	Standard deviation			*11.9*	*26.5*	*3.9*

A study of the collection of materials on a range of signs have had a large difference in the growth duration, plant height, panicle length, number of spikelets and grains per panicle, length and width of grains, 1000 grain weight and grain weight with panicle. Half of the samples was recorded to be late maturing, photosensitive, and in our conditions did not flower. The growth duration of some varieties was a major limitation factor. Some varieties with growth duration of more than 130 days could not ripen. In 2015, growing season was in warm conditions, especially, the temperature regime in the summer and in September was 2.3 - 5.2S above long-term average. The amount of active temperatures in the period of April - September accounted for 2900°C, even in some locations with 3505°C which contributed to the maturation of the grain, even very late maturing varieties.

The collection of samples of different growing season showed range of days to flowering: from 105 to 131 days to flowering (later not analyzed). It was 29 - 55 days longer than the standard variety Boyarin (Table 1).

With the use of greenhouse, the environmental factors (temperature, humidity, light) could be controlled for enhancing growth and development of tropical varieties to full maturity. The growth duration of BR47 was 105 days, QR2 was 109 days and NSiC Rc 106 was 110 days, respectively. Almost varieties carrying genes *Sub 1* and *Xa* had growth duration longer than 131 days. If adding one month to maturity (in the greenhouse) the overall growing duration will be more than 160 days.

Besides, the plant height of studied varieties was diversified and varied from 56 to 153 cm (Table 1). The predominant form of 70 - 90 cm with semi-dwarf genes could contribute to the increase of harvest index. This was the optimal size for the production of rice varieties. Varieties with high plant height were the donors of genes anaerobic germination (AG) such as Khao Hlan On (153 cm), Kharsu 80A (140 cm) and Mazhan Red (123 cm). The plants of these varieties could be greatly elongated and grown in the deep water layer. However, they all were perished when ripening. The rest of the samples had a modern semi dwarf characteristics with erect leaves and long drooping panicles. Bushy plants with sufficient space food showed very high and reached 25 fertile tillers (Fig. 1).

The length of the flag leaf ranged from 21.2 to 30.5 cm (26.7 in average), the width - from 1.0 to 1.7 cm (average 1.4 cm).

The sample collections have been characterized by a large variety of panicle sizes and shapes, which depended on the length of the central axis, the number of nodes on it, the length of the side branches, the number and distribution of spikelets on lateral branches. All samples were indicated drooping tropical type panicles. Panicle length of the studied samples ranged from 12 to 26 cm (Table 2), whereas the standard Boyar was 15.3 cm. In contrast, to the rest of the samples it was dense, compact, and upright. Panicle length was positively correlated with plant height ($r = 0.22 \pm 0.10$), grain panicle weight ($r = 0.23 \pm 0.10$) and 1000 grain weight ($r = 0.6 \pm 0.10$).

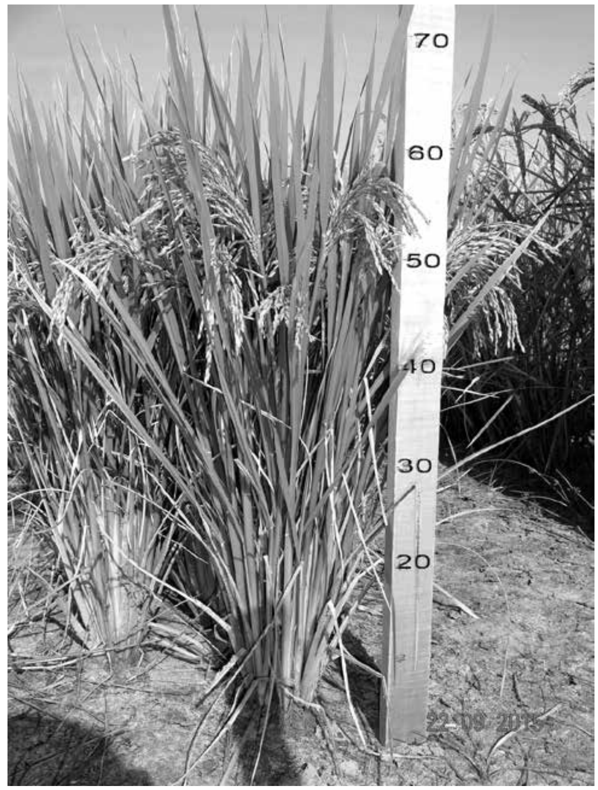

Figure 1. Plants varieties QR 1 in Proletarsk September 22, 2015

The number of spikelets on the panicle - one of the main signs of the productivity of rice. The number of spikelets per panicles varied over a wide range from 91.5 to 268 units (Table 2). Most of the spikelets formed in panicles varieties D18 (Khang Dan), KD Sub1 D149 and SHPT-one were fertile while the spikelets of earlier sample BR 47 were low fertile.

Simultaneously, there was a high sterility of spikelets associated with increased dryness of the air, the fertility of tropical varieties ranged from 55.6 to 89.9% (in standard 92.7 - 94.0%). Therefore, the number of grains was formed substantially as follows: from 65.3 to 196.7 units (Table 2). Analysis of the relationship signs showed that the number of grains per panicle correlated with fertility ($r = 0.48 \pm 0.18$) and weight of grain panicle ($r = 0.86 \pm 0.11$).

By weight of grain panicle ranged from 1.46 to 4.90 g (Table 2). They were divided into two groups: The panicle weight of 1.46 - 2.5 g, accounting for 41%, and

2.6 - 4.9 g for 59%, respectively. The highest panicle weight was recorded at varieties QR2, SHPT-1, IR 74099-3R-3-3 and standard Southerner with more than 4 g.

Under the conditions of the Rostov area with good lighting and the optimum temperature conditions showed to be favorable for the formation of rice with high weight of 1000 grains. In our studies, 1000 grain weight varied from 16.9 to 29.1 g, and from 29.5-31.8 g of the control varieties. Especially, grains of QR2 had aroma and high amylose content (18-20%). Correlation analysis showed that the weight of grains was positively related to the length of the panicle (r = 0.36 ± 0.18) and weight of grain panicle (r = 0.44 ± 0.18), but negative with the number of empty spikelets on the panicle (r = -0.45 ± 0.18) and growing period (r = -0.71 ± 0.15).

Table 2. Characteristics of the donor rice varieties in Proletarsk, 2015 (continued)

Number of plots 2015	The number of spikelets per panicle (pcs)			Fertility spikelets (%)	Weight grain panicle (g)	The weight of 1000 grains (g)	Spikelets length (mm)	Spikelets width (mm)
	Viable grains	Floate grains	Total					
Boyarin	110.0	7.0	117.0	94.0	3.50	31.8	8.5	3.5
Uzhanin	140.0	11.0	161.0	92.7	4.13	29.5	8.8	3.4
8261	124.3	35.4	159.7	77.8	3.20	25.7	7.8	2.4
8262	156.5	17.5	174.0	89.9	4.24	27.1	8.6	2.3
8254	168.3	77.2	245.5	68.6	4.90	29.1	8.2	2.7
8255	137.7	53.4	191.1	72.1	3.07	22.3	9.0	2.7
8256	123.9	49.4	173.3	71.5	3.16	25.5	8.9	2.6
8257	108.2	41.6	149.8	72.2	3.00	27.7	8.2	2.9
8259	156.8	38.1	194.9	80.5	4.25	27.1	8.6	2.6
8260	130.2	14.8	145.0	89.8	3.67	28.2	9.9	2.2
1006	68.0	23.5	91.5	74.3	1.50	22.0	8.3	2.4
1032	196.7	71.3	268.0	73.4	3.79	19.3	7.9	2.6
1033	169.3	76.7	246.0	68.8	3.50	20.7	8.0	2.7
1034	160.3	104.0	264.3	60.7	3.81	21.7	8.3	2.8
1015	74.3	59.3	133.6	55.6	1.78	24.0	9.3	2.7
1022	88.5	57.6	146.1	60.6	1.95	22.0	8.2	2.7
1024	76.4	59.4	135.8	56.3	1.99	26.0	9.8	2.2
1026	76.3	37.7	114.0	67.0	1.99	25.9	8.8	2.4
1027	65.3	49.0	114.3	57.1	1.46	22.3	9.1	2.5
1029	135.8	47.7	128.7	74.0	3.26	24.0	9.1	2.5
1030	67.7	40.3	108.0	62.7	1.68	23.4	8.5	2.5
1008	148.0	48.6	196.6	75.3	2.66	18.0	8.5	2.6
1009	67.7	49.2	116.9	57.9	1.90	28.0	8.1	3.4
1010	99.5	70.3	169.8	58.6	2.69	27.0	7.7	2.6
1044	95.3	54.0	149.3	63.8	1.80	18.9	8.7	2.5
1041	103.3	52.0	165.3	66.5	1.69	16.9	8.8	2.6
1042	129.0	52.7	181.7	71.0	2.27	17.6	8.7	2.6
Minimum	*65.3*	*7.0*	*91.5*	*55.6*	*1.46*	*16.9*	*7.7*	*2.2*
Maximum	*196.7*	*104.0*	*268.0*	*94.0*	*4.90*	*31.8*	*9.9*	*3.5*
Average	*118.6*	*48.6*	*165.5*	*71.1*	*2.87*	*24.3*	*8.6*	*2.7*
Standard deviation	*41.6*	*22.3*	*54.0*	*9.9*	*1.1*	*4.2*	*0.6*	*0.3*

The examined samples had a narrow grain mainly, from 2.2 to 2.8 mm (3.4 - 3.5 mm in standard) (Table 2, Fig. 2). The length of spikelets varied from 7.7 to 9.9 mm. The longest grain varieties were NSiC Rc 106 and IR86385-99-2-1-B (Table 2).

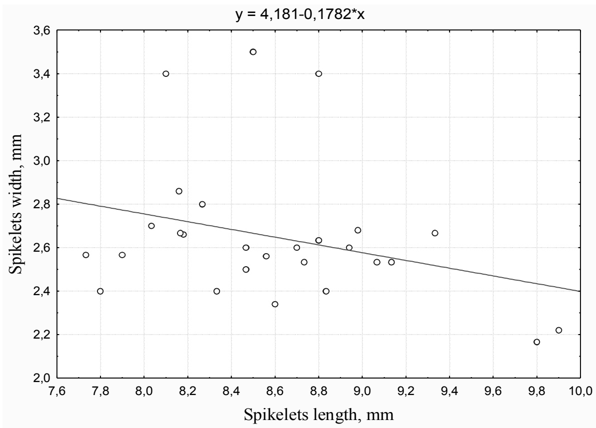

Figure 2. Distribution of rice samples in length and width of spikelets

Of great importance revealed resistance to bacteriosis caused by *Xanthomonas*. The disease appears on leaves and greatly reduces grain yield in early infection of susceptible varieties. This problem is very severe in Russia and in some parts of the world, but it may occur in connection with what is necessary to use in the selection process forms the donor immune gene *Xa*. Samples with high resistance to the disease IRBB 62, IRBB 5, IRBB 7 were crossed in 2015, with early ripening varieties Contact and Boyarin. Presence of genes in breeding will be carried out by PCR analysis. A line by crossing vigorously sprouting varieties Khao Hlan On, Kharsu 80A and Mazhan Red with a grade Contact and hybrid lines [9305 (Pi1 + 2 + 33 + ta + -b) × INBARA 3 (Sub-1)],

Magnat × TDK 1 (Sub 1), INBARA 3 (Sub-1) × Boyarin, IR 64 (Sub-1) × Comandor to combine in a single genotype of different genes.

In the study, salinity resistant genes of rice (Saltol) from donors IR 52713-2B-8-2B-1-2, IR 74099-3R-3-3, NSIC Rc 106) and flooding of a deep layer of water (Sub 1) (BR-11, CR-1009, INBARA-3, TDK-1) from Asian donors were also transferred to domestic variety. In 2013, hybrids were obtained with early ripening varieties. In the last year, F3 was selected as valuable recombinants to be adapted to Russian conditions. The conducted study of the collection of rice created a possibility to use interest genes for developing varieties for specific soil and climatic conditions of Rostov regions. Again, output of the study must refer to the early and medium growth duration of 110-120 days and enjoy the yields of 8-10 t/ha. Plants have to be resistant to lodging, shattering, diseases and abiotic stress factors. This model is the basis for the variety of our selection work.

CONCLUSIONS AND RECOMMENDATIONS

(1) Study collection of tropical donors rice subspecies *indica* contains varieties can ripen in the northern rice under Russian and interbreed with local varieties maturing subspecies *Japonica*.

(2) A positive correlation between the length of the panicles with plant height, mass of grain panicle and 1000 grain weight; the number of grains per panicle - fertility and weighing of grain panicle.

(3) For the breeding selected resistant to such stress factors such as salinity, flooding, disease, rice forms the complex agronomic characters. Spend their hybridization with domestic ripeing varieties.

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Date received: 25/10/2016
Date reviewed: 16/11/2016
Reviewer: Dr. Tran Danh Suu
Date approved for publication: 20/12/2016

GENETIC VARIATION OF WILD RICE IN VIETNAM

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Abstract

The study aimed at identifying rice gene pools carrying blast resistant genes via phenotyping and genotyping for wild rice in Vietnam. The experiments were carried out at CLRRI (Cuu Long Delta Rice Research Institute) laboratories, greenhouses and experimental fields, Thoi Lai, Can Tho, from 2011 October to 2015 October. Major research activities consisted of evaluating the genetic diversity of wild rice accessions. A total of 101 accessions of some wild rice species in the genebank of Cuu Long Rice Research Institute, Vietnam were used to clarify the diversity using SSR markers. Molecular diversity analysis using 38 polymorphic SSR markers revealed among the 101 accessions. The 101 Vietnam accessions generated 2 clusters at 0.76 similarity coefficient. Some with the same variety names were grouped into different clusters. Genotyping blast resistance among wild rice via molecular markers as SSRs (simple sequence repeats) showed the results of a total of 101 wild rice accessions were classified into two cluster groups A , and B based on the polymorphism data for 120 alleles of 38 SSR markers. Te Tep varieties including *O. punctala-1 , O. latifolia-1, O. nivara-1* were categorized into group B. The other two groups A (98 accessions) as an LTH -type control was also categorized into group A. Phenotyping blast resistance among wild rice for blast isolates collected from the Mekong Delta. Against 13 standard differential blast isolates which were selected based on the reactions to monogenic lines for targeting 101 resistance genes as the differential accessions, these resistant of rice accessions were investigated. Based on the cluster analysis, these accessions were classified into three groups, A, B and C.

Keywords: Blast, genetic diversity, SSR markers, wild rice

INTRODUCTION

Recent advances in molecular biology, principally the development of the polymerase chain reaction (PCR) for amplifying DNA, DNA sequencing and data analysis have resulted in powerful techniques which can be used for the screening, characterization and evaluation of genetic diversity. With molecular marker techniques, powerful tools have been developed so that genetic resources can be accurately assessed and characterized. Several types of molecular markers are available for evaluating the extent of genetic variation in rice (Ni *et al.*, 2002). These include restriction fragment length polymorphism (RFLP) (Botstein *et al.*, 1980), random amplified polymorphic DNA (RAPD) amplified fragment length polymorphism (AFLP)), and microsatellites or simple sequence repeats (SSR) (Mc. Couch, 1988, Temnykh *et al.*, 2000 and Lang *et al.*, 2009). Development of host plant resistance is the most effective means of disease management. As many as genes conferring resistance some genes for resistance to blast have been identified to various races of the pathogen have been identified and utilized in rice breeding programs. To evaluate the genetic backgrounds and introgression of resistance genes from donor varieties, the graphical genotypes of the population were constructed using 38 simple sequence repeats. However, large-scale and long-term cultivation of varieties carrying a single gene for resistance resulted in a significant shift in pathogen race frequency with the consequent breakdown of resistance in these cultivars. This report the gene for blast resistance, genes identified wild rice.

Characterization and evaluation of diversity among traditional varieties will provide plant breeders information necessary in the identification of initial materials for hybridization to produce varieties with improved productivity and quality.

The objectives of the study are: To evaluate genetic diversity of the wild rice accessions in the genebank of Cuu Long Rice Research Institute, Vietnam using morphological characters and microsatellite markers.

Genetic diversity of Vietnam wild rice species using SSR markers.

MATERIALS AND METHODS

Plant materials

A total of 102 accessions of several wild rice species included and 2 checked varieties such as Te Tep and LHT rice (data are not shown).

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