

REVIEW

IMPROVEMENT OF THE RICE BREEDING IN INTENSIVE CROPPING SYSTEM IN THE MEKONG DELTA

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ABSTRACT

We summarize the impact of rice breeding in CLRRI for intensive cropping system of the Mekong Delta, a biggest area of rice cultivation in the country. The breeding program started in 1982-2007, since then 43 varieties were released as national varieties. Out of them, 12 were received from INGER, 71% varieties grown in the Mekong Delta area were bred from CLRRI. The breeding for durability of varieties against biotic constraints is more challenges in the future.

The changes of cropping practices

The Mekong Delta is a biggest area of 3.9 million ha for rice cultivation in the country. It produces more than 52 % of rice in the country and contributes 93 percent of the total rice export volume. During last five years, rice production of this Delta has increased more than 3 M tons from 15,997,500 tons in 2001 to 19,263,000 tons in 2005. Average rice yield has increased from 4.22 tons ha⁻¹ in 2001 to 5.03 tons ha⁻¹ in 2005. In 2006, nearly 1 M tons were lost due the to outbreak of BPH associated with viruses damaging rice crop; however, the average rice yield was estimated at 4.9 tons ha⁻¹ and total rice output of the Mekong Delta was remained 18.5 M tons. The Mekong Delta is one of most intensive rice crop practices, its development began in the late 1980s. The use of short and high yielding varieties, direct seeding with high density planting and high nitrogen application was rapidly adopted. In the irrigated area, rice is cropped 2 to 3 times per year, rice is also grown 7 crops per two years in some areas. The change of crop practices with asynchronous planting followed by new pest emergence and disease outbreaks made difficult to rice farmers to manage crop. An overuse of pesticides leads to environmental problems for a long run. Biotic factors are considered as one of major constraints to rice production in the delta. What are consequences? Indeed, it needs to be understood and to suggest for management strategy. Paper discusses on host-pathogen interaction and how to manage co-evolution in such a situation.

Breeding for durable resistance of modern varieties

Cuu Long Delta Rice Research Institute (CLRRI) has been working mainly on rice. Besides that there are the other institutions and universities are partially studying on rice as Institute of Agricultural Science of South Vietnam (IAS), Can Tho University (CTU), Ha Noi Agricultural University (HAU) and Vietnam Academy of Agricultural Sciences which consists of Institute of Agricultural Genetics (IAG), Food Crop Research Institute (FCRI), Agricultural Science Institute of Northern Central Vietnam (ASINCV) and National Institute of Plant Protection (NIPP). In the Mekong Delta, rice improvement over last twenty eight years has been achieved a great work. Recently, 71% varieties grown in the Mekong Delta were bred from CLRRI.

In breeding for most extensive cultivation areas, it has been concentrated on high yielding with good grain quality, blast, bacterial leaf blight and brown plant hopper resistance. Breeding for adverse soils such as drought, salinity, acid sulfate soil tolerance with high yield and good grain quality has also been paid more attention. Breeding for high vitamin A and Fe has also been done.

In 1986-2006, the released varieties as national varieties were high yield, good grain quality and resistant to brown plant hopper (BPH) and Blast. However, these varieties recently become susceptible to major insects and diseases such as brown plant hopper, blast, bacterial leaf blight, grassy and ragged stunt viruses. Interestingly, still some varieties have shown field blast resistance and drought/salinity/acid sulfate tolerance such as OM 576, IR 50404-57-2-2-3, AS 996, VND 95-20, OM 4498 and OM 5930 since released. Most of promising and leading varieties have the common ancestors as IR 64 and IR 48; therefore the new genetic resources are being looked for in breeding programs to prevent the narrow genetic base and then created genetic vulnerability because of the similarity in their genotype.

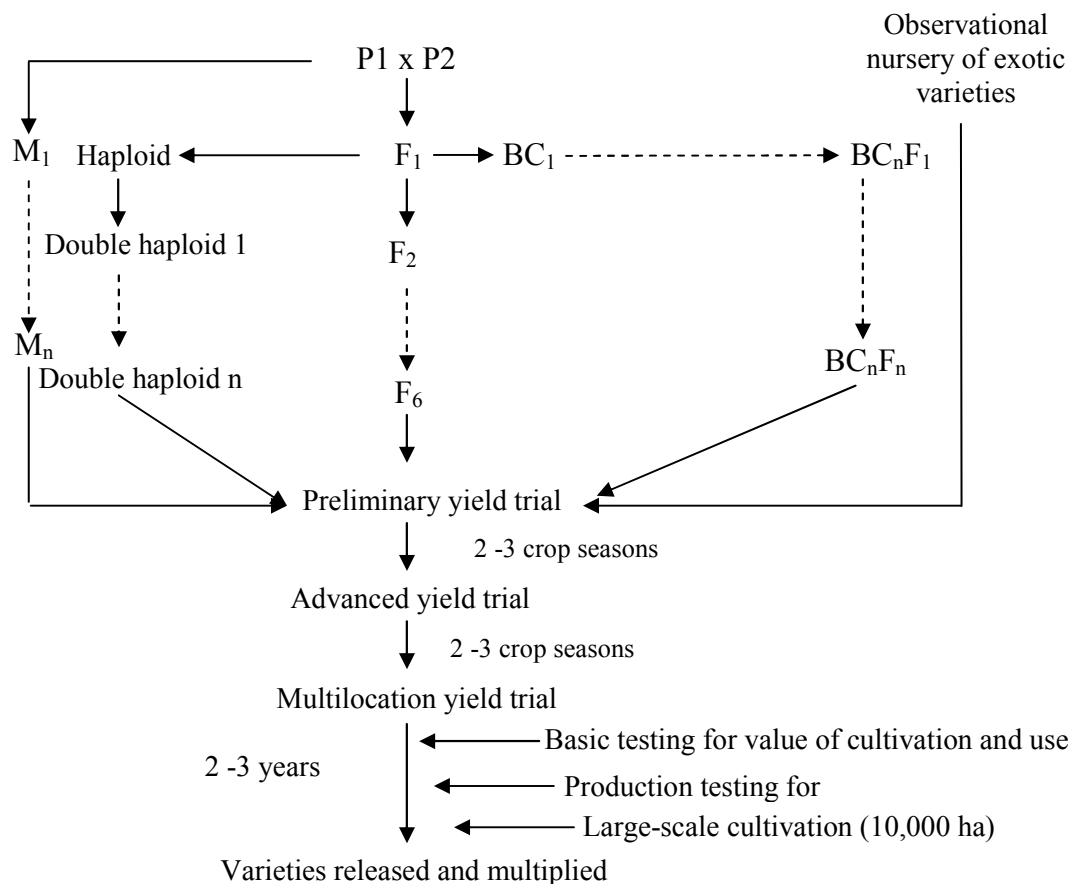
The varieties with high yielding and short growth duration <95 days come high on the list of priority. Because of export and consumers demand, varieties with no chalkiness of endosperm, high head rice, intermediate amylose content, soft gel consistency and aroma are also preferred. Besides that genetic resources resistant to Blast, BLB, BPH, RGSV, RRSV, Tungro and tolerant to drought and salinity are also needed.

Breeding methods being utilized

The most common breeding methods are pedigree and backcross with marker-assisted selection (MAS). Mutation, anther and tissue culture, transformation are also utilized in breeding programs.

MAS is applied in selection of some important characteristics such as amylose content, aroma, blast and bacterial leaf blight resistance, brown plant hopper resistance, salinity tolerance.

Flow chart of varietal release procedures



Released varieties in the country

In 2005, there were 66 varieties grown in the Mekong Delta Area. Of them, 43 were bred varieties, 9 were exotic varieties and 14 were local rice varieties. The leading varieties were OM 1490, OM 2517, OMCS 2000, Jasmine 85, OM 2718, IR 50404, VND 95-20, OM 2717, OM 576 and OM 3536 occupied 76% Mekong area.

CLRRI used some entries received from INGER in the hybridization work, the followings resulted in released varieties as IR 5, IR 8, IR 36, IR 42, IR 48, IR 50, IR 64, IR 66, IR 68, IR 5853-229, IR 19735-5-2-3-2, IR 32843, IR 2307-247-2-2-3, A69-1, IR 44592, IR 50401, IR 32893, MRC 19399, IR 59606, IR 19746-11-33, IR 529-640-3-2, IR 8423-132-622, IET 2938, IR 2588, Pelita 1 and IR 2513-26-5-3-2.

In CLRRI, breeding programs has been started since 1982. There were 43 varieties released from 1986-2006 as national varieties. Out of them, 12 were received from INGER as IR 42, IR 48, IR 64, IR 66, IR 19660, IR 62032, MRC 19399, IR 44595-70-2-2-3, IR 35546-17, IR 29723, IR 49517-23, and IR 59606 (Table 1). Only IR 42 and IR 64 are still cultivated but the area has reduced over time because they are susceptible to some important diseases and insects. The others are MTL 233 (IR 65610-24-3-6-3-2-3) and MTL 250 (IR 68077-64-2-2-2-2) introduced from Can Tho University and IR 50404-57-2-2-3 from Institute of Agricultural Science of South Vietnam.

Table 1: List of national varieties released in Southern Vietnam

No.	National varieties	Pedigree/Origin	National varieties	Pedigree/Origin
1	NN 4B	IR 42	27	OM 1723
2	NN 5B	IR 48	28	OM 1633
3	OM 89	IR 64	29	OM 2031
4	OM 80	IR 36 / IR 5853-229	30	CM 16-27**
5	OM 86-9	IR 21015-80-3-3-2	31	OMCS 2000
6	IR 66	IR 66	32	AS 996
7	OM 576-18	Hungary / IR 48	33	OM 1348-9
8	OM 597	IR 48 / IR 19735-5-2-3-2	34	OM 2395
9	IR 19660	IR 19660	35	OM 3536
10	OM 90-2	IR 44595-70-2-2-3	36	OM 1352
11	OM 90-9	IR 35546-17	37	DS 20
12	IR 29723	IR 29723	38	OM 2717
13	OM 269-65	IR 32843 / NN 6A	39	OM 2718
14	IR 49517-23	IR 49517-23	40	OM 2514
15	OM 997-6	Colombia / IR 64	41	OM 2517
16	OM 723-7	IR 2307-247-2-2-3 / A69-1	42	OM 4495
17	KDM 105	Thailand	43	OM 4498
18	OMCS 94	IR 59606	44	IR 50404***
19	OM 1589	IR 36 / IR 50	45	KSB 54
20	OMCS 95-5	OMCS 6 / IR 68	46	KSB 218-11-1
21	IR 62032	IR 62032	47	KSB 55
22	OM Fi1	MRC 19399	48	VND 95-19
23	TN 108	Tai Nguyen*	49	VND 95-20
24	OM 1706	OM 90 / OM 33	50	MTL 233
25	Tai Nguyen	Tai Nguyen*	51	MTL 250
26	OM 1490	OM 606 / IR 44592		

* mutation

** anther culture

***Varieties (bold letter) from IAS and CTU

Resistance of released varieties to blast (*Pyricularia grisea*)

Rice blast caused by *Pyricularia grisea* (Rossman *et al.* 1990), is one of major rice diseases in the Mekong Delta of Vietnam. Infected area increased from 1999 to 2003. During dry season 02-03, 189,000 ha were infected in a total of 1.6 M ha of direct seeded rice crop. Most of new releasing varieties were found to be susceptible to the disease.

Results from blast nurseries conducted since 1980-2004 indicated that most of previously released varieties were susceptible to blast, some of them are still considered as durable resistance and cultivated in large scale for more than 15 years. Nowadays, resistant varieties are overcome by blast pathogen with average of 1-2 years after released (Du and Loan 2004) (Table 2).

Table 2: Reaction of promising lines and varieties to blast (*Pyricularia grisea* Sacc.) scored at O Mon, Can Tho from 1980-2004

No.	Varieties	Year released/ scale	Years *													
			90	91	92	93	94	95	96	97	98	99	00	02	04	
1	IR 42	1980	5	+	+	+	+	+	+	+	+	+	+	+	+	+
2	IR 48	1980	1	-	-	-	-	-	-	-	-	+	+	+	+	+
3	IR 64	1984	1	-	-	-	-	-	-	-	-	-	-	+	+	+
4	OM 576	1986	4	-	+	+	+	+	+	+	+	+	+	+	+	+
5	IR 50404	1988	2	-	-	-	-	-	-	-	+	+	+	+	+	+
7	OM 1490	1992	1			(1)	-	-	-	-	-	+	+	+	+	+
8	OM 2037	1995	1					(1)	-	-	-	-	+	+	+	+
10	OM 2031	1997	1							(1)	-	-	-	+	+	+
15	VÑ 20	1997	7								+	+	+	+	+	+
15	KHAO 39	1998	9									+	+	+	+	+
11	OM 3536	2000	5											(5)	+	+
17	OMCS 2000	2000	7												+	+
18	OM 4495	2000	7												+	+
20	OM 2717	2000	9												+	+
19	OM 3242	2001	9												+	+
12	OM 2517	2002	3													(3)
13	OM 2490	2002	3													(3)
14	OM 2519	2002	3													(3)
21	OM 2718	2002	7													(7)
22	OM 2492	2002	9													(9)

* (-) resistant ; (+) susceptible.

The number in parenthesis indicates the reaction of variety to blast in the years after released

Identification of blast races using 129 blast isolates collected in many places of Vietnam (Noda *et al.* 1999) indicated 12 pathogenic groups based on their virulence to 12 Japanese differential rice varieties. It was also shown that none of isolates were virulent to differentials which carry genes *Pik-s*, *Pish*, *Pik*, *Piz*, *Pita-2*, *Piz-t* and *Pik-p*. Study intended recently to determine which resistance genes is more durable against blast over time and space using the same Kiyosawa's varieties and 31 monogenic lines under natural condition of blast nursery (Ou 1965). Results indicated that in one location tested, reaction can be changed over time (8 seasons) from resistant to susceptible and vice versa. Some resistance genes could express resistance to blast for almost of times such as *Pik-m* (Kanto-51), *Piz+ Pish* (Fukunishiki), *Pita-2+ Pish* (PiNo.4), *Piz-t* (Toride 1), *Pik-p* (K60). When observation was conducted in 10 locations then reaction was also different, effective resistance genes found in almost 10 locations tested such as *Piz*, *Pish* (Fukunishiki), *Piz-t* (Toride 1), *Pik-p* (K60) and *Pik-m* (Tsuyuke, 10 % susceptible)

Some interchanges of resistance and susceptibility such as *Pik-s+Pish* (Shin 2, 40 % susceptible), *Pia+Pi19(t)* (Aichi Asahi, 70 % of susceptible), *Pii+Pik-s* (Ishikari Shiroke, 30 % of susceptible),

Pik (Kusabue, 20 % susceptible), *Pi-ta* (Yashimorochi, 40 % susceptible), *Pita-2+Pish* (PiNo.4, 20 % susceptible), *Pib+Pi-sh* (BL1, 20 % susceptible), *Pit* (K59, 50 % susceptible). In this study some blast resistance genes have been identified to be more durability to blast pathogens such as *Pik-m* (Tsuyuake), *Piz+Pish* (Fukunishiki), *Piz-t* (Toride 1) and *Pik-p* (K60). However, some varieties of Kiyosawa's differential carry two resistance genes. Recently, reaction of 31 monogenic lines by natural infection of blast (multilocation test) and inoculation test with 540 isolates have been conducted (data not shown here). Differential system will be developed in Vietnam (Pham Van Du *et al.* 2007). In near future gene pyramiding is going to be set up for blast resistance breeding program at CLRRI.

Evaluation on resistance genes against rice bacterial leaf blight

In the Mekong Delta the bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae* was not serious from 1980 - 1995. But recently, severity has increased gradually over the years. Most of leading varieties become susceptible, especially Jasmine 85, OMCS 2000, OM2490, OM2492, OM2517, OM4498 and OM4656 that are grown in large scale area. Efficacy of chemical on this disease is not significant. Therefore, planting resistant varieties provides an effective control and up to the present most breeders concentrate on the development of highly resistant varieties.

In Vietnam, previous results on BLB showed that there were 14 bacterial leaf blight races in Northern Vietnam. Most of races were incompatible to resistance genes *Xa-7* and *xa-5*, the next was *Xa-21* and *Xa-4* (Phan Huu Ton và Bui Trong Thuy 2003). Noda *et al.* (1999) were classified 52 isolates -collected in Southern, Central, and Northern- into 6 races (A, B, C, D, E, F), race A was prevalent in the Mekong Delta and was incompatible to resistance genes *Xa3*, *xa5*, *Xa7*, *Xa17* and *Xa21*. *Xa4* gene was not durable as a major gene for high level of resistance but possibly durable as a minor gene for partial resistance (Koch and Parlevliet 1991). *Xa21* gene was identified in the wide species, *Oryza longistaminata* (Khush *et al.* 1990). It is resistant to all Philippine and Indian races of *Xanthomonas oryzae*. There were large residual effect in *Xa21* and *Xa4* genes, *xa5* had smaller and *xa13* had no residual effect (Li *et al.* 2001).

Evaluation under field condition was conducted to preliminarily assess resistance genes that are still effective and can be used in bacterial leaf blight resistance breeding program. Results indicated that these NILs of IRBB 1, IRBB 3, IRBB 4, IRBB 10, IRBB 11 and IRBB 21, carrying resistance genes *Xa1*, *Xa3*, *Xa4*, *Xa10*, *Xa11*, *Xa21*, respectively, were moderately resistant to *Xoo*. None of NILs were highly resistant or resistant to *Xoo* in Can Tho province. Evaluation of pyramiding lines showed that when in pair, the diseased leaf area and lesion length were increased in the case where one of resistance gene was compatible to *Xoo* and were decreased when both dominant resistance genes were incompatible to *Xoo*. For instance, *xa13 + Xa21* (IRBB 55) and *Xa4 + Xa21* (IRBB 52), respectively. High level of resistance was observed in combination of 3 dominant resistance genes *Xa4+Xa7+Xa21* (IRBB 62), the next was *Xa4+xa5+xa13+Xa21* (IRBB 60). Especially, IRBB 63 having three genes *xa5+Xa7+xa13* was resistant in combination but one-gene NILs were moderately susceptible to *Xoo* (Le Cam Loan *et al.* 2006). Residual effect and quantitative complementation should be mentioned in this case. According to Li *et al.* (2001), high level of resistance against virulent pathogen races resulted from the defeated gene pairs such as *xa13/xa5*, *xa13/Xa4*, *xa13/Xa21*, *xa5/Xa4* and *xa5/Xa21*. This has been referred to as quantitative complementation (Ogawa and Khush 1988; Yoshimura *et al.* 1996; Huang *et al.* 1997). Generally, in comparison between two-gene pyramiding lines, three-gene pyramiding lines, four-gene pyramiding lines and five-gene pyramiding lines, there was no clear difference regarding diseased leaf area and lesion length except IRBB60, IRBB62 and IRBB63. Field testing of rice with bacterial blight was influenced strongly by environment on development of this pathogen. Additional experiment should be done in artificial inoculation to confirm the above observation and using the different races prevalent in Mekong Delta area is necessary in determining which resistance genes against bacterial leaf blight are still effective in the Mekong Delta. The result of additional study will be useful in breeding program for bacterial leaf blight resistance.

Isolates of *Xoo* in all rice growing areas of the Mekong Delta are being collected and used in virulence analysis and determination of effective resistance genes for breeding purposes.

Reaction of leading varieties to rice viruses

The outbreak of rice viruses occurred in March 2006, the disease spread very rapidly to 51,507 hectares within 6 months (Huan 2006). One hundred twenty thousand hectares of summer-autumn rice crop had been devastated by the disease and BPH. Most of leading varieties grown in the delta were susceptible to viruses (Table 3). It is difficult for rice farmers to continue next crop with the same varieties. This urges the local authorities to take all preventive measures possible against BPH and virus infection. Results from surveys strongly suggest that RGSV and RRSV are associated with the yellowing syndrome of rice. The result also indicates that BPH population could be monitored for the presence of the two viruses by a serological method. Observations in the fields showed that 20 day-older seedlings of some varieties such as OM 576, OMCS 2000, OM 732-7, IR 50404 can tolerate to RGSV and RRSV infection. Most of varieties showed moderate susceptibility to virus infection under lower pressure of BPH population. Thus preventive measure could be suggested immediately to prevent further losses when we did not have effectively available resistance genes against viruses. The followings are suggested to farmers to manage the virus infection at time: Eradication of diseased plants in fields; Using light trap in monitoring BPH migration in order to decide the sowing date that is helpful for the crop escaping heavy pressure of BPH population landing on seedling stage; Synchronous planting in the affected areas are recommended; Planting of tolerant varieties to viruses, such as OM 4498, OM 5930, OMCS 2000, OM 576, IR50404, CL8; Avoiding the use of susceptible varieties, specially such as OM 1490, Jasmine 85, OM 2517, OM 2518. CLRRRI is lacking of genetic resources for resistance of rice viruses, however, some new lines introduced recently also susceptible to grassy stunt virus but tolerance to ragged stunt (Table 4). Crosses between *O. nivara* and others (if any) resistant to RGSV and the above varieties susceptible to RGSV but resistant to RRSV can be made in breeding programs for both RGSV and RRSV resistance.

Table 3: List of leading and promising varieties against rice viruses observed under field condition, Wet season 2006

No.	Varieties	Incidence *		
		YS	RRSV	RGSV
1	OM 5796	50.00	33.33	8.33
2	OM 5240	33.33	16.67	25.00
3	OM 3419	41.67	33.33	16.67
4	PR 26703-3B-P-J7	33.33	33.33	16.67
5	IR 59656-5K-2	33.33	25.00	16.67
6	OM 4102	33.33	41.67	16.67
7	MTL 474	33.33	16.67	16.67
8	OM 4944	25.00	25.00	16.67
9	BẠC LIÊU 16	50.00	8.33	33.33
10	MTL 385	41.67	8.33	16.67
11	OM 1490	25.00	41.67	16.67
12	MTL 388	16.67	8.33	25.00
13	OM 4668	33.33	50.00	16.67
14	BẠC LIÊU 29	33.33	25.00	0.00
15	BẠC LIÊU 13	50.00	25.00	8.33
16	OM 6073	33.33	25.00	0.00
17	OM 4218	33.33	33.33	16.67
18	MTL 465	41.67	41.67	8.33
19	BẠC LIÊU 17	66.67	16.67	8.33
20	C 5442-B-1	16.67	50.00	0.00

No.	Varieties	Incidence *		
		YS	RRSV	RGSV
21	OM 5637	75.00	16.67	8.33
22	OM 5932	33.33	16.67	16.67
23	OM 5644	33.33	25.00	8.33
24	OM 5643	33.33	8.33	16.67
25	OM 2409	41.67	16.67	0.00
26	OM 5635	41.67	58.33	25.00
27	MTL 416	66.67	25.00	8.33
28	OM 5933	16.67	58.33	0.00
29	VND 95-20	50.00	25.00	16.67
30	MTL 392	58.33	0.00	16.67
31	OM 5930	25.00	8.33	0.00
32	MTL 425	33.33	0.00	0.00
33	OM 5900	41.67	25.00	33.33
34	OM 4926	58.33	8.33	0.00

* YS=yellowing syndrome, RRSV=rice ragged stunt virus; RGSV=rice grassy stunt virus

Table 4: Reaction of new lines against rice viruses, Dry season 06-07

Code	Lines *	Incidence (%)	
		Grassy stunt	Ragged stunt
V1	-	100.00	0.00
V2	-	91.49	0.00
V3	IR69726-116-1-3	100.00	0.00
V4	IR69734-5-1-2	100.00	0.00
V5	IR69734-128-2-3	100.00	0.00
V6	IR73885-1-4-3-2-1-6	100.00	0.00
V7	IR31917-45-3-2	100.00	0.00
V8	IR54751-1-2-44-15-2-3	100.00	0.00
V9	IR54751-2-4-1-10-5-1	100.00	0.00
V10	IR71033-62-15-B	98.00	0.00
V11	IR71033-121-15-B	100.00	0.00
V12	IR65482-7-216-1-2-B	100.00	0.00
V13	IR65482-4-136-2-2-B	100.00	0.00
V14	IR65482-17-511-5-7-B	100.00	0.00
V15	IR65482-18-539-2-2-B	100.00	0.00
V16	IR71033-4-1-127-B	100.00	17.02
V17	IR64	100.00	0.00
V18	IR73885-1-4-3-2-1-6	100.00	0.00
V19	IR73382-85-9-1-2-1-1	97.87	6.38
V20	IR73382-85-9-1-2-1-4B	100.00	5.26
V21	IR73680-11-4-1-2-2-4-1	100.00	0.00
V22	IR73680-11-10-2-1-3-B-1	100.00	0.00
V24	IR73681-1-1-8-6-2	98.04	0.00
V25	IR77390-6-1-18-4-B	100.00	0.00
V26	IR77390-6-1-18-5-B	100.00	6.67
V27	IR77390-6-4-2-3B	100.00	0.00
V28	IR27142	97.96	0.00
V29	IR27269	100.00	0.00

Code	Lines *	Incidence (%)	
		Grassy stunt	Ragged stunt
V30	IR34612	100.00	0.00
V32	IR35449	100.00	0.00
V33	IR48630	100.00	0.00
V34	IR48639	100.00	0.00
V35	IR48712	100.00	0.00
V36	IR48787	100.00	0.00
V37	IR48882	100.00	3.33
V38	IR48898	97.62	0.00
V39	IR48937	96.55	0.00
V40	IR54217	100.00	0.00
V41	IR54234	100.00	0.00
V42	IR54236	97.44	0.00
V43	IR66854	100.00	0.00
V44	IR73653	100.00	0.00
V45	IR73768	100.00	0.00
V46	IR73880	100.00	4.17
V47	IR74655	100.00	0.00
V48	IR76971	100.00	0.00

* These new lines received from Division of PBGB, International Rice Research Institute, 2006.

Rice virus outbreak in the Mekong Delta from March 2006 suggested that the same history repeated in Asian rice countries. The Mekong Delta area is now in the list of priority of genetic resource against BPH associated with viruses for breeding purposes

Future expectations for genetic resources

In our breeding programs, the yield potential has reached plateau due to lacking novel genetic variation, besides that most of released and promising varieties become susceptible to major pests and diseases, so the realized yields of commercial varieties have rarely reached their potentials due to biotic and abiotic stresses. In the Mekong Delta, rice growers preferred the early growth duration rice <95 days, so genetic resources with growth duration <95 days are very precious for intensive rice production system. Outbreak of BPH associated viruses occurs in Mekong delta in 2006, all varieties are found to be susceptible to viruses, we need the source of resistance to rice viruses (RGSV, RRSV and Tungro) for our breeding program. Resources resistant to Blast, BLB, BPH and tolerant to drought, salinity are also needed. Aspects of host-pathogen interaction such as race distribution, virulence analysis, effective resistance genes should be studied. Marker-assisted selection will be applied to obtain good achievements in rice breeding for sustainability of production. Experience of past time suggested that horizontal resistance of varieties may contributes 50 % for successful of crop. The use of crop diversity, improvement of cultural practices, escape strategy in IPM package may help for the rest.

REFERENCES

- Huan, NH. 2006. Special report to MARD conference on BPH and yellowing syndrome in Mekong Delta and eastern parts of South of Vietnam.
- Huang N, ER Angeles, J Domingo, G Magpantay, S Singh, G Zhang, N Kumaravadiel, J Bennett, and GS Khush. 1997. Pyramiding of bacterial blight resistance genes in rice: marker-assisted selection using RFLP and PCR. *Theor. Appl. Genet.* 95: 313-320.
- Khush GS, E Bacalangco and T Ogawa. 1990. A new gene for resistance to bacterial blight from *O. longistaminata*. *Rice Genet. Newslett.* 7: 121-122.

- Koch M and JE Parlevliet. 1991. Residual effects of the *Xa-4* resistance gene in three rice cultivars when exposed to a virulent isolate of *Xanthomonas campestris* pv. *oryzae*. *Euphytica* 55: 187-193.
- Le Cam Loan, Vo Thi Thu Ngan, and Pham Van Du. 2006. Response of rice with different gene resistance to bacterial leaf blight (*Xanthomonas oryzae*). The 2nd conference of Vietnam Molecular Plant Pathology Society and the 5th national conference on plant pathology and molecular biology, HAU, 20-22/10/2006. 87-88pp.
- Li Z, A Sanchez, E Angeles, S Singh, J Domingo, N Huang, and GS Khush. 2001. Are the dominant and recessive plant disease resistance genes similar? : A case study of rice R genes and *Xanthomonas oryzae* pv. *oryzae* races. *Genetics* 159: 757-765.
- Noda T, Nagao Hayashi, Pham Van Du, Hoang Dinh Dinh and Lai van E. 1999. Distribution of pathogenic races of rice blast fungus in Vietnam *Ann. Phytopathol. Soc.Jpn.* 65 : 526-530.
- Noda T., Pham Van Du, Lai van E, Hoang Dinh Dinh, and H Kaku. 1999. Pathogenicity of *Xanthomonas oryzae* pv. *oryzae* strains in Vietnam. *Annals of the Phytopathological Society of Japan*: 65(3): 293-296.
- Ogawa T, and GS Khush. 1988. Major genes for resistance to bacterial blight. *In: Bacterial blight of rice. Proceedings of the International Workshop on Bacterial Blight of Rice, 14-18 March 1988. International Rice Research Institute, Manila, Philippines.* pp. 177-192.
- Ou. S.H. 1965. A proposal for an international program of research on the rice blast disease. *In: The Rice Blast Disease. The Johns Hopkins Press, Baltimore, Maryland,* pp. 441-446.
- Du, P. V. and L. C. Loan. 2004. Study on durability of resistance genes to blast disease (*Pyricularia grisea*) in the Mekong Delta. *In: Genetic and functional diversity of agricultural microorganisms, the 12th NIAS International workshop on genetic resources. National Institute of Agrobiological Sciences.*
- Pham Van Du, Le Cam Loan and Nguyen Duc Sang. 2007. Blast research in the Mekong River Delta of Vietnam. *In: A differential system for blast resistance for stable rice production environment. Yoshimichi Fukuta, Casiana M. vera Cruz and Nobuya Kobayashi (eds). Japan International Research Center for Agricultural Sciences (JIRCAS), Tsukuba, Japan.*
- Phan Huu Ton and Bui Trong Thuy. 2003. Pathogenicity of the bacterial leaf blight strains from Northern Vietnam. The 2nd National Conference on Plant Pathology and Molecular Biology. HAU, 23-25 October 2003. 78-86 pp.
- Rossman, AY, RY Howard and B Valent. 1990. *Pyricularia grisea*, the correct name for the rice blast disease fungus, *Mycology* 82: 509-512.
- Yoshimura, A., J. X. Lei, T. Matsumoto, H. Tsunematsu, S. Yoshimura. 1996. Analysis and pyramiding of bacterial blight resistance genes in rice by using DNA markers. *In: Rice Genetics III. Proceedings of the Third International Rice Genetics Symposium, G. S. Khush (ed.), International Rice Research Institute., P. O. Box 933, 1099 Manila, Philippines.* pp. 577-581.

Những cải thiện đối với chương trình lai tạo giống cho hệ thống trồng lúa thâm canh ở đồng bằng sông Cửu Long

Tóm tắt về hiệu quả của chương trình lai tạo giống của Viện nghiên cứu lúa đối với vùng sản xuất lúa thâm canh cao và trù phú nhất của cả nước, vùng ĐBSCL. Chương trình lai tạo giống mới bắt đầu từ 1982-2007, đã có 43 giống lúa được phóng thích và công nhận giống quốc gia. Trong số đó 12 được công nhận có nguồn gốc nhập nội, thuộc mạng lưới đánh giá vật liệu di truyền quốc tế của IRRI. Hiện nay 71% giống lúa trồng ở ĐBSCL có nguồn gốc lai tạo từ Viện lúa. Tuy nhiên, lai tạo giống kháng đối với các sâu và bệnh hại chính một cách bền vững đang là một trong những thử thách cho những nghiên cứu của Viện lúa trong tương lai.