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RICE GENETIC RESOURCE CONSERVATION AND UTILIZATION IN THE MEKONG DELTA

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ABSTRACT

During 2000 to 2010, genetics and plant breeding division at CLRRI has collected complement samples for rice gene bank in Mekong delta. More than 90% of the varieties collected from Mekong are indica. Highly significant differences among the various traits in the 196 traditional varieties were obtained for grain length, grain width, percentage of unfilled grains, 1,000-grain weight. Differences were not statistically significant for panicles per plant. Mean of allele number per locus and each chromosome reveal much lower in the improved varieties than landrace varieties. The best selections released directly as commercial varieties included OM4498, OM5930, OM6073, OM4900, OM6161(lowland and good quality); OM 6162, OM 6840 (drought tolerance); and OM5629 (salt tolerance); OM5981 (acid sulfate soil), OM6071 and OM6877 (BPH resistance).

Keywords: conservartion . Resource germplasm ,morphological marker, SSR marker

INTRODUCTION

Food insecurity especially for the poor and marginal household neglected and slow agricultural economy. The world is changing rapidly, and so is germplasm resource in Vietnam must be conserved well. With a new structure based on its strategy CLRRI toward 2000 -2010 and beyond, work plan for 2011-2020, and with a drastically reduced work force, we are adjusting to a new situation. What we must retain, at all cost, is the highest quality standards needed to safeguard the germplasm already collected. We also will make all effort to minimize further losses in the genetic resource base, including field collecting in critical areas. CLRRI will continue to play an active role in the conservation and use of plant genetic resources, especially in establishing and enhancing contacts among the different provinces and international genetic resources centres across boundaries of disciplines, and climatic regions. The plant germplasm of our globe must remain common property. The free flow of genetic materials among researchers working on food production must be safeguarded.

Collecting land races of rice

During 2000 to 2010, genetics and plant breeding division at CLRRI has collected complement samples for rice gene bank in Mekong delta (Table 1). Comprehensive and systematic collecting of landraces in Kien Giang, An Giang, Long An, Tien Giang and Ben Tre was accomplished. In addition, more than 90% of the varieties collected from Mekong are indica. Each year, selected traditional varieties in the Gene Bank at CLRRI are entered in the screening nurseries for evaluation against different stresses. If germplasm bank entries are to be effectively utilized by rice scientists around the nation, we should be characterized and evaluated appropriately, taking into consideration the genetic variation that exists among insects and pathogens as well as the variations in physical and chemical stresses. A total of 1,000 rice accessions included 55 upland rice, 800 lowland and 250 swampy rice (Table 1). Number of varieties for each ecosystem and type of domestication has been recognized. Nearly 1,000 germplasm accessions have been entered in various: 158 were screened for good quality properties, 51 for adaptation to rainfed upland rice culture, and 144 for resistance to blast and 100 for resistance to bacterial blight. Other screening involving fewer than 30 accessions each, included

rainfed lowland, deepwater, salinity, blast, bacterial blight, sheath blight, ragged stunt virus, white back plant hopper, stem borer, gall midge, leaf folder, and thrips. Some accessions found promising for tolerance to different stresses across locations. Some of these have been utilized in various breeding programs, and the progenies of some crosses have been released as leading varieties for 10 recent years.

Agro-morphological characters

Analysis of variance: For each of the 11 quantitative traits, the mean, range (maximum and minimum), standard deviation, coefficient of variation (CV), mean standard error, and F value were calculated.Results show that most of the quantitative traits are highly variable. With respect to maturity, the earliest maturing genotype matured in 148 days while the maximum number of days to maturity was 159 days. Maximum values were obtained in grain yield (95.gr) in case of the variety Nang Loan Doc, Mao Chao (86.03 gr). Some varieties yielded two low (19.08 g)such as Bong Sen. Panicle length of some varieties were two high such as Nop Rum (28 cm/panicle), Nep Ruoi Xanh (26.41 cm/panicle) Tien Nu. Number of filled grains/panicle obtained 123.6 (77.8%) in case of Lua Ba Trang. Their high fertility indicated good materials to be potentially used by plant breeders for varietal improvement in the future (Lang et al. 2009)

Highly significant differences among the various traits in the 196 traditional varieties were obtained for grain length, grain width, percentage of unfilled grains, 1,000-grain weight. Differences were not statistically significant for panicles per plant.

Divergence analysis by markers.

The first cluster A contained one up land rice genotypes and two lowland ones. The second cluster, B, is the largest cluster contained 126 (90.2 %) rice varieties. Most of this cluster contained lowland rice landraces. The second cluster was divided into two sub clusters, B1, B2, The first sub cluster B1 contained 122 rice landraces including 26 upland rice genotypes. The second sub cluster B2 included for rice accessions.

Table 1. Classification of rice varieties in Vietnam based on the SSR marker polymorphism patterns

Cluster	Sub cluster	No. of rice varieties and percentage (%)						
		Indica type						Total
		Landrace			Improved			
		L	**U**	**S**	**L**	**U**	**S**	
A	1	1 (0.7)	1 (0.7)	0 (0.0)	1 (0.7)	0 (0.0)	0 (0.0)	3(2.1)
	2	1 (0.7)	0 (0.0)	0 (0.0)	1 (0.7)	0 (0.0)	0 (0.0)	2 (1.4)
Total		**2 (1.4)**	**1 (0.7)**	**0** (0.0)	**2 (1.4)**	**0** (0.0)	**0** (0.0)	**5 (3.5)**
B	1	48 (34.3)	26 (18.6)	11 (7.8)	37 (26.6)	0 (0.0)	0 (0.0)	122 (87.4)
	2	1 (0.7)	1 (0.7)	1 (0.7)	1 (0.7)	0 (0.0)	0 (0.0)	4 (2.8)
Total		**49 (35)**	**27 (19.3)**	**12 (8.6)**	**38 (27.3)**	**0 (0.0)**	**0 0(0.0)**	**126 (90.2)**
C	1	3 (2.1)	0 (0.0)	0 (0.0)	3 (2.1)	0 (0.0)	0 (0.0)	6 (4.2)
	2	1 (0.7)	0 (0.0)	0 (0.0)	1 (0.7)	0 (0.0)	0 (0.0)	2 (1.4)
Total		**4 (2.8)**	**0 (0.0)**	**0 (0.0)**	**4 (2.8)**	**0 (0.0)**	**0 (0.0)**	**8 (5.6)**
D		0 (0.0)	1 (0.7)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (0.7)
Total		**0 (0.0)**	**1 (0.7)**	**0 (0.0)**	**0 (0.0)**	**0 (0.0)**	**0 (0.0)**	**1 (0.7)**
Grand Total		**55 (39.2)**	**29 (20.7)**	**12 (8.6)**	**44 (31.5)**	**0 (0.0)**	**0 (0.0)**	**140 (100)**

*U= Upland; L=Lowland; S=Swampy

The third cluster C composed of 8 (5.6%) varieties. The cluster C is divided into two sub clusters, C1 and C2. Most varieties of the third cluster are lowland genotypes; three for landrace

and three for improved varieties. The second sub cluster C2 consisted of two low land landraces, and one lowland improved genotype. Final cluster D has only one upland landrace variety.

Table 2. Mean number of alleles based on microsatellites on different rice chromosomes.

Cluster	Sub cluster	Mean of allele no. per SSR marker												Mean
		Chromosome												
		1	2	3	4	5	6	7	8	9	10	11	12	
A	1	1.33	0.00	4.00	1.00	2.33	15.67	1.00	1.67	1.00	1.67	1.00	2.67	**2.78**
	2	0.00	1.00	2.00	0.00	5.00	10.00	1.00	2.00	1.00	1.00	0.00	2.00	**2.08**
	Mean	**0.67**	**0.50**	**3.00**	**0.50**	**3.67**	**12.83**	**1.00**	**1.83**	**1.00**	**1.33**	**0.50**	**2.33**	**2.43**
B	1	1.49	2.48	2.93	0.53	1.84	17.72	2.38	3.82	1.72	2.36	0.93	3.07	**3.44**
	2	1.50	3.00	4.00	0.75	4.50	25.00	3.00	5.00	2.75	3.00	1.50	4.00	**4.83**
	Mean	**1.50**	**2.74**	**3.47**	**0.64**	**3.17**	**21.36**	**2.69**	**4.41**	**2.24**	**2.68**	**1.22**	**3.53**	**4.14**
C	1	0.33	2.00	2.67	1.00	4.33	22.33	3.00	6.00	3.67	4.00	1.00	3.67	**4.50**
	2	0.00	0.00	5.00	0.00	4.00	24.00	0.00	2.00	3.00	0.00	1.00	4.00	**3.58**
	Mean	**0.17**	**1.00**	**3.83**	**0.50**	**4.17**	**23.17**	**1.50**	**4.00**	**3.33**	**2.00**	**1.00**	**3.83**	**4.04**
D		2.00	2.00	6.00	1.00	6.00	32.00	1.00	6.00	3.00	3.00	2.00	5.00	**5.75**
	Mean	**2.00**	**2.00**	**6.00**	**1.00**	**6.00**	**32.00**	**1.00**	**6.00**	**3.00**	**3.00**	**2.00**	**5.00**	**5.75**
Mean		**1.09**	**1.56**	**4.08**	**0.66**	**4.25**	**22.34**	**1.55**	**4.06**	**2.39**	**2.25**	**1.18**	**3.67**	**4.09**

Mean of allele number per locus and each chromosome reveal much lower in the improved varieties than landrace varieties (Table 2). The mean of allele number per locus of cluster A, B, C and D is 2.43, 4.14, 4.04 and 5.75, respectively.

Germplasm assessment for biotic and abiotic stresses

Brown planthopper:

Brown plant hopper (BPH) [*Nilaparvata lugens* (Stal.)] has been a major pest of rice in Mekong delta with the outbreak in 260,000 ha in 2006 (Huan et al. 2006). It destroyed all rice fields planted to susceptible cultivars. BPH became a particularly damaging pest in Southern Vietnam following the introduction of high-yielding, semidwarf rices, such as OM1490, grown under high levels of nitrogenous fertilizer application. Expansion of irrigation systems that allow year-round rice cultivation exacerbated the problem. BPH sucks rice plant sap and causes the crop to wilt and dry (hopper burn syndrome). It also transmits grassy stunt and ragged stunt viral diseases. Developing resistant varieties is the most practical solution to the BPH problem, and varietal resistance is the key component in integrated pest management programs. Breeding for BPH resistance again started in 2007 with new strategy. Since then, more than 140 rice accessions and even more breeding lines have been evaluated. BPH thrives on susceptible varieties but not on resistant ones. We also have identified germplasm with tolerance or moderate resistance that would minimize biotype selection without loss of yield. Minor genes for BPH resistance that block biotype selection are being identified. BPH resistant donors to BPH were pinpointed as Pkaanpa, Xương Ga Trang, Ro cu, Tolut, Cuong Trau and Nang Keo.

Identification and incorporation of new BPH resistance gene into modern rice cultivars are importance breeding strategies. In this study, the rice genetics of resistance to the important rice hopper has been instigated in details. The reaction to BPH of 114 varieties suggested new donors for resistance to BPH at CLRRI such as: IK01500,

Babawee, IKO1537, IR68077, IR69726, IR68059 and OM6602. These are possibly good breeding materials. The F_2 populations from the crosses of TN1/Babawee and OM 2864-5-2-1/Babawee have been exploited with one dominant gene combined one recessive. In case of IR64/IR70441-3-3-1-2-3-1-1-3 and AS996/Basmati 370-3-1-5-1-7 segregated in the ratio of 7:9. This indicated two recessive and complematary genes control the resistance. In term of Mong Chim/Koi Kum segregated in the ratio of 15:1 expected based on independent segregation of two dominant and duplicate genes. On the other hand, in the F_3 populations, five crosses segregated in the ratio of 15:1. Thus two crosses of Jasmine 85/OM2517, OM4498/OM2502); two cross of OM4900/OM5993, OM4498/OM5993; two crosses of OM4900/OM5992, OM2517/OM2718; one cross of OM5930/IR36; and OM2517/OM2514 segregated into 9:1; 23:1; 13:1; 25:1; and 7:1, respectively.

In case of 42 crosses in a diallele set, F_1's plants mostly expressed susceptibility in two crosses as NGD/ PTB33 and NGD/ KT. They exhibited resistance at score 3.

The BC_1 of OM4498/TL, OM4900/IKO1537, OM4498/ASD7, OM2514/TL exhibited resistance at the score 1.

In case of OM2514/TL, the F_2 progenies segregated into the ratio of 55:9. This indicated the independent segregation of three dominant genes with inhibitor action by one recessive allele.

In case of OM4498/ASD7, the progenies segregated into the ratio of 1:3. It means one recessive gene controlling the resistance. This is *bph-2* gene.

Looking to the future, we need clarify the allelic relationships among resistance genes in TL, PSBRC 8, IK 01537, ARC 10550 with more details.

Wide hybridization has provided new opportunities for incorporating pest resistances from wild species. Using embryo rescue techniques, we have transferred resistance from Oryza *officinalis* to *O. sativa* while maintaining yield and grain quality. Biotechnological advances on the horizon will provide broad opportunities to tap novel sources of resistance to BPH and other pests. Although the challenges are formidable, the genetic arsenal and understanding of host plant resistance to pests are being enriched every day. This will provide opportunities to stabilize production, a major goal of resistance breeding. Accessions of wild species were also screened for BPH resistance, to compare the distribution of resistance genes in wild species with those in cultivated varieties. We tested 334 accessions comprising 4 wild species populations and 22 natural hybrids brown plant hopper resistance, using primers. Although only a few cases of resistance to BPH such as *O. officinalis*, more than half tested accessions showed resistance to BPH.

Bacterial blight

More than 400 rice varieties from Mekong delta have been tested for resistance to bacterial blight (BB) since 2000. From their reaction to 13 races at Mekong provinces; resistant varieties were broadly classified into five varietal clusters. Varieties belonging

to the 7 main clusters were mostly found in Mekong Delta.

One hundred and sixty six local accessions, and 25 parent lines of hybrid rice genotypes were used as materials for screening leaf blight resistance using 13 bacterial races at Mekong delta. There were five landraces that exhibited their resistance to bacterial races like IRBB21, three cultivars significantly reacted to IRBB5 and 58 cultivars to the race No 4 and No 6 as IRBB13. These cultivars were subsequently genotyping using RG556, RG136 and PTA248 for detecting *xa-5*, *xa-13* and *Xa-21* genes, respectively. PCR products of materials using RG556 and PTA248 did not detect *xa-5* and *Xa-21*. Marker RG136 was assisted to select 5 local rice accessions and 3 parent lines of hybrid rice genotypes containing *xa-13* gene. A susceptive modern cultivar (IR24) and the resistant local rice (Nang Som) were used to develop their backcross populations to transfer recessive *xa-13* gene into the HYVs. Bacterial blight resistant gene, *xa-13*, was not detected from the first BC generation. Screening 130 plants with IR24 genotype in BC_1F_2 population, we found 20 plants showing resistance to at least 6 races including race 4 and race 6 (typical resistance

phenotype of *xa-13* gene). These plants were genotyped for 5 microsatellite markers (RM21, RM114, RM122, RM164, and RM190), of which 2 markers RM21 and RM190 showed polymorphic bands with the accuracy of 55% and 50%, respectively.

As compared to BB pathogen reaction, these plants had not *xa-13* gene but multiple genes at different loci affected their resistance. SSR marker RM 21 detected *Xa-4* on chromosome 11. Nep Te Thom, Te Tep, Nang Chi, Trang Hoa Binh Doc, Chet Ran, Mua So 5, Nang Loan Doc, Nep Bo Cau, Nep Mu u, Nang Den, Nang Huong were considered as donors of *Xa-4*.

Similarly, Mua so 54, Nep Ao Gia, Mua so 61, Mua so 55, Vo Do, nho Do, Gie Noi, SG Giai Phong, Chet Ran, Tran gong Bay were considered as donors of *xa-5*.

Landraces were detected *Xa-4* gene as more cited: Nep Tuong, Lun Kien Giang, Than Nong Mua, nep mong ngua, Trang Tep Doc, Nep Mo doc, Nep mu U Doc, Lem Bui Doc.

Soi Da, Nang Hương, Tai nguyen, Trang phieu, Trang tep, Nep do, Lun Tuyen, Mot bui Mua were considered as donors of *Xa-10* gene

Similarly, *Xa-11* was found in Nep ruoi Xanh, *xa-13* was found in Mong chim Roi, then *Xa-21* was found in Nang Tra, Tram Doc, Mua So 24.

Table 3. Reaction to bacterial blight among 13 races of 100 landraces in Mekong Delta

Reaction	Race 01	Race 02	Race 03	Race 04	Race 05	Race 06	Race 07	Race 08	Race 09	Race 10	Race 11	Race 12	Race 13
R	86	91	85	90	86	90	91	87	90	85	67	65	62
S	12	7	14	10	12	8	7	12	10	15	29	34	33
M	2	2	1	0	2	2	2	1	0	0	4	1	5

Notes: race 1 (Kien Giang), race 2 (An Giang), race 3 (Can Tho), race 4 (Dong Thap), race 5 (Long An), race 6 (Tien Giang), race 7 (Ben Tre), race 8 (Tra Vinh, race 9 (VinhLong), race 10 (BacLieu), race 11 (Soc Trang), race 12 (CaMau), race 13 (HauGiang).
R: resistance, S: susceptibility, M: moderately

Blast disease

Blast, caused by *Pyricularia grisea* Cav., is one of the major fungal diseases infected rice (*Oryza sativa* L.) in Vietnam. Local varieties have been considered as genetic sources of disease resistance. Susceptible, moderate resistant and resistant reactions of rice by IRRI's protocol (blast nursery), using 16 races with 32 lines from IRRI and 11 lines from CLRRI were carried out. Almost of these resistance genes were confirmed with their given differentials. Almost races were compatible to the monogenic lines carrying the resistance genes *Pi-a, Pik-s, IRBLta-CT2, Pi-12 (t) and Pi(t)*. Almost lines compatibles with two races originated from Central Vietnam (OMP 0015). Other *Pi-b* was incompatible with all races except OM P003, OMP 008, OMP 0014, OMP 0015 and 0016). The results give 40 to 17 varieties becoming susceptible to new races in Vietnam. Race OMP 0014 was found resistance action only by ***IRBL11-Zh***, race OMP 002 reacted to 21 varieties, which showed their resistance**.** The 43 kinds of resistance genes were differentiated among 16 isolates.

Characterization of local rice varieties against the 13 selected standard blast isolates revealed: these varieties classified into 11 clusters namely a, b, c, d, e, f, g, h, i, j and k. Each clusters showed unique reactions and were differentiated from each other groups (table 4).

Table 4. Classification of rice varieties in Vietnam based on reaction patterns to 13 selected standard differential blast isolates.

Cluster	Designation		
	IRRI variety	Landrace	Improved genotype
A	LTH		
		Ngoc nu	
		Nang huong	
		Ut Luom	
		Nang huong	
		Nang thom	
		Nang loan	
B	IRBLt-K59		
		Trang tep doc	
	IRBLta2-Pi		
		Nang thom doc	
		Lun Kien Giang 1	
			OM 9996
		Nang loan doc	
		Soi da doc	
		Ba ruong gam	
			OM 4559
	IRBLta2-Re		
			OM 10028
	IRBLta2-K1		
		Nang gao	
	IRBLta-CP1		
		Nang tho moc	
		Trang lon	
		Nang quot	
		Duoi chau	
			OM 6387
		Nep phu	
			OM 7364
		Chet xanh	
		Chip le	
			OM 6599
			OM 5756
		Nep ao vang	
		C10	
		504 mua	
		Mot bui	
		Biet ca tron	
			OM 10011
		Lua thom	
		Ba bui	
		Nang tay	
		Ba thiet	

Cluster	Designation		
	IRRI variety	Landrace	Improved genotype
B		Nep nhung	
		Nang huong	
		Mua so 62	
		Hoa lai	
		Nep tuong	
		Nep tau huong	
		Gang xe mua	
		Vang lua	
		Nep mong chim	
		Nang thom muon	
	IRBLta-CT2		
			OM 10029
			Jasmine 33
			OM 9997
	IRBL12-M		
	IRBL19-A		
		Lun do	
			OM 4488
			OM 2395
			OM 10030
			OM 7253
		Nang huong	
		Nep ruoi xanh doc	
			OM 3536
		Nang huong cho dao	
			OM 5740
		Nep mo	
			OM 10040
			OM 5890
			Jasmine 6
		Lem bui	
			OM 10010
		Gia lu	
		Mot bui lun	
		Tra bieu thach	
			OM 6730
		Trang tep	
		Thanh tra	
		Nang thom CD	
		Bong sen	
		Lun thong	
			OM 6627
		Nang nhen	
C		Nep nghe	
		PCR92111-B-2	
		Tieu so da	

Cluster	Designation		
	IRRI variety	Landrace	Improved genotype
		Re hanh vang	
		Trang tep	
		Nang huong doc	
		Nang loan doc	
		Ba co	
		So ri do	
D	IRBL20-IR24		
		Nang thom thanh tra	
			OM 4900
			OM 8928
			OM 4498
			OM 10037
			OM 6020
			OM 5886
			OM 6403
			OM 6797
		KT15	
		Mao chao	
			OM 5756
			OM 6778
		Nanh chon	
		Tau huong	
			OM 10012
E			OM 6886
F		Bang nu	
G		NTCD doc	
H		Tam vuot	
		Hanh lua	
		Nang thom	
		Tau huong	
I	IRBLsh-S		
	IRBLsh-B		
	IRBLb-B		
		Nong nghiep chum doc	
		Trang bo cau	
			Jasmine 35
		Nang huong	
		Nep mu u doc	
	IRBL1a-A		
		Nho thom	
		Trang nho	
		Cu lua	
	IRBLa-C		
		Nang den	
		Tieu chum	
	IRBLks-F5		

Cluster	Designation		
	IRRI variety	Landrace	Improved genotype
		Tai nguyen	
			OM 10031
J	IRBL3-CP4		
		Lun can	
	IRBLks-S		
		Mua so 43	
		Tam cao 9A	
		Nop rum	
			OM 6089
	IRBL5-M		
		Nep chuot che	
	IRBLk-Ka		
		Nep mong ngua	
			Jasmine 13
	IRBLkp-K60		
		Than nong lun	
		Nang huong	
			OM 6161
			OM 5953
	IRBLkh-K3		
		Mong chim roi	
		Nep ruoi xanh	
	IRBL1-CL		
	IRBL7-M		
	IRBLkm-Ts		
		Nho thom	
		Te tep	
			OM 6084
K	IRBLz-Fu		
	IRBLz5-CA		
	IRBLz5-CA®		
	IRBLzt-T		
	IRBL9-W		
			Can Tho 1
			MNR1
	IRBL11-Zh		
	IRBLi-F5		

The varieties in cluster "a" belonged to rice genotypes mostly susceptible to various blast isolates, including S check as LTH (IRRI). Among five Vietnam resistant landraces as Ngoc Nu, Nang huong, Gia Lu, Nang Loan, were clustered in "b" and "c".

The results suggested that the blast resistance of rice varieties from Vietnam was widely varied. It means that genetic diversity to blast resistance is abundant in the gene pool.

Abiotic stress assessment

Drought tolerance

While genetic resources provide an invaluable gene pool for crop breeding, the majority of accessions in germplasm collections remain

uncharacterized and their potential to improve stress adaptation is not quantified. A selection of 114 elite genetic resources for rice were characterized for agronomic and physiological trait expression in drought tolerance (Lang et al. 2009). Under drought stress, the physiological traits best associated with yield were canopy temperature, water uptake, and carbon isotope discrimination, adaptability to the abiotic stresses of a target environment is the main objective of national breeding programs. Breeders utilized traditional germplasm collected from their target environments. They attempted to improve and enrich the gene pool through national programs such as drought stress. Although traditional varieties collected from the target area are considered to have good adaptability, we have screened 125 entries in the CLRRI gene bank for submergence tolerance during the three recent years. Outstanding entries have been used in the breeding programs of Mekong delta. Most deepwater rices in the collection have been evaluated for internode elongation ability. Screening methods developed at CLRRI for submergence tolerance and elongation ability are being used by national programs to evaluate their genetic materials. Evaluation of the germplasm for salt tolerance is more complicated. Screening under controlled drought tolerance also is more difficult in national programs. It may be needed at different growth stages, especially flowering stage among various genotypes. Challenges are still ahead.

Submergence tolerance

In 2007-2009, it was yet another exciting year, filled with significant scientific achievements and valuable products, all thanks to the skills and commitment of the IRRI - Japan projects. Through two years, our projects continued processing, we expanded our network of partners, and we worked more closely with the plant breeding community. To enhance and sustain productivity of these soils, we adopt an integrated approach involving the development of adapted high yielding and submergence tolerant varieties developed via novel breeding methods, proper management of resources and introduction of effective cropping patterns that can meet farmers' needs and market demands. Development of submergence tolerance varieties is generally considered the most effective entry point for improving productivity of submergence affected for production damage by typhoon and flash flood. It is also the cheapest option for farmers. Some varieties such as OM4900, IR64-Sub 1, Swana- Sub1, Br 11 Sub 1, IR82355-5-2-3, IR84194-9 and IR66876-11NDR-1-1-1-1 were developed. They can yield 4-5 ton ha^{-1} under deep water from 0.8-1.0 meter during 20- 25 days under complete submerge, and are being out-scaled. The success of new varieties is assured through eventual testing and selection in target sites in partnership with farmers and under their own management to guarantee relevance and adoption.

Acid sulfate toxicity tolerance

Acid sulfate soil tolerance screening at different growth stages being conducted in collaboration between IAS and CLRRI in the periode of 2008-2010.

170 test entries as varieties for commercial production in 50 countries. Several lines have also been utilized as parents in the breeding programs of different countries as well as those of the international centers concerned with rice. Through differential varietal reactions in multi-locational screening tests, various biotypes and races of major insects and pathogens that attack the rice crop have been identified.

AS996, a well-known derivative from IR64 x *Oryza rufipogon* (collected in Tram Chim, Dong Thap Muoi) has become a leading variety and a donor for rice breeding. It well adapted to acid sulfate soil conditions. It became a leading variety in Bangladesh namely BRRI Dhan 55 since February 2011.

GERMPLASM UTILIZATION IN RICE BREEDING

The conservation efforts and seed dissemination service have provided rice breeders a convenient and ready source of breeding materials for use in varietal improvement. High yield and good grain quality (to meet export requirements) are met the demand of our goal.The accessions were screened for adaptability under local field conditions. A few vigorous selections were crossed and tested in Mekong delta to have the ideal genotypes with

short-duration, high-yielding to enhance significantly rice production here up to 4 times as compared to 1975 (from 4 ton.year^{-1} to 20 ton.year^{-1}). By the end of 2005-2010, a number of promising genotypes had been identified for further observation and selection. Many valuable exotic rice lines and varieties of different agroecotypes were provided through rice breeding. Almost 12,000 of these lines were tested for adaptability in 2005-2010 (Lang et al. 2010). The best selections released directly as commercial varieties included OM4498, OM5930, OM6073, OM4900, OM6161 (lowland and good quality); OM 6162, OM 6840 (drought tolerance); and OM5629 (salt tolerance), OM5981 (acid sulfate soil), OM6071 and OM6877 (BPH resistance).

DNA technologies and rice germplasm.

Setting up a core collection for rice may increase the efficiency of evaluation and increase the information on selected accessions. SSR markers can be used as molecular genetic markers to characterize the accessions, and in the process eliminate obvious redundancies as well as provide the data needed to implement effective hierarchical sampling. Molecular biology, by generating new technologies and methods of analysis that either provide new approaches or supplement classical methods of analysis, has contributed significantly to increased understanding of many aspects of plant biology. In recent years, people who deal with plant genetic resources and other researchers have become increasingly aware of the potential applications and benefits of new technologies to plant germplasm conservation activities and researches. Promising areas of biotechnology that may serve plant genetic resources activities and research are shown in more comprehensive discussions on the technical aspects of these new technologies and their applications in plant germplasm conservation in general. They have been presented elsewhere. MAS and transgenes will be increasingly used for disease control, especially virus diseases. Although biotechnology is becoming increasingly important in agriculture, the fact that over 50% of the agricultural productivity in the world has been achieved through traditional plant breeding should not be ignored. While DNA marker technology cannot replace plant breeding, it will certainly augment the efforts of plant breeders by providing new tools to ease the many problems faced by breeders.

***In vitro* technology**

Hybrid embryos that would otherwise abort prematurely can be rescued by culturing them in vitro. Sterility in the F_1 hybrid can be overcome by chromosome doubling through the use of colchicines. Using chemicals such as growth regulators and immuno-suppressants also increases the chance of getting hybrid plants. Advances in protoplast technology can lead to somatic hybridization.

In the new wide hybridization, we have crossed several seed and embryo culture techniques are currently being utilized development new germplasm such as OM5930 released in 2008 (development by mutation from somaclonal variation of OM3536). Research to identify the most efficient media and culture conditions for a wide range of genotypes and species must continue.

Anther culture ability of rice is significantly different between crosses rice varieties. A doubled haploid (DH) population was established via anther culture of some crossing from F_1 on N6 medium, which had been shown particularly suitable for anther culture of indica hybrids. Among these factors, the most important one is the genotypic difference. The results found that different rice species, or crosses quite differently in response to anther culture. On the other hand, culture medium also strongly influences the anther culture response. Induction of calli showed that formation of embryogenic calli of rice was strongly influenced by both hormone concentration and genotype as well as by germplasm. These findings thus the medium MS + 2mg/L 2,4D+1mg/L kinetin+10% coconut water good for increases in callus induction. The results emphasized that OM4495/ MTL 474, OM6486/MTL474 and OM3536/MTL474 exhibited high callus information rate (Lang et al. 2010). These observations combined together with the quantitative data on plant regeneration obtained in this study. An efficient plant from OM1490/Jasmine 85 and OMCS2000/KDM105 has been developed to improve amylose content

and gel consistency, properly aroma. The results may be useful in the selection of parents with high response to anther culture for rice haploid breeding and in the establishment of permanent DH populations.

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Bảo tồn và sử dụng nguồn tài nguyên di truyền cây lúa ở đồng bằng sông Cửu Long

Trong khoảng thời gian từ năm 2000 đến 2010, Bộ Môn Di truyền và chọn giống thuộc Viện lúa ĐBSCL đã thu thập mẫu để bổ sung vào ngân hàng gen lúa của vùng đồng bằng sông Cửu Long. Hơn 90% giống được thu thập từ vùng Đồng bằng sông Cửu Long là giống indica. Sự khác biệt đáng kể giữa những tính trạng khác nhau ở 196 giống lúa mùa đã thu thập là về chiều dài hạt, chiều rộng hạt, tỷ lệ chắc và trọng lượng 1000 hạt. Số lượng bông/bụi không có sự khác biệt có ý nghĩa về mặt thống kê. Trung bình số allen trên locus và trên mỗi nhiễm sắc thể chứng minh rằng các giống cải tiến đã được cải thiện hơn so với các giống lúa địa phương. Các giống tốt nhất được phóng thích trực tiếp vào thị trường thương mại là các giống: OM4498, OM5930, OM6073, OM4900, OM6161 (thích hợp vùng đất thấp và phẩm chất tốt), OM 6162, OM 6840 (chống chịu khô hạn); và giống OM5629 (chống chịu mặn); OM5981 (chống chịu điều kiện đất phèn), OM6071 và OM6877 (kháng rầy nâu).

Từ khóa: Bảo tồn , nguồn gen , Chỉ thị hình thái, Chỉ thị SSR