2015
National Rice R&D
Highlights

Plant Breeding and Biotechnology Division

Department of Agriculture
PHILRICE
PHILIPPINE RICE RESEARCH INSTITUTE

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PLANT BREEDING AND BIOTECHNOLOGY DIVISION

Division Head: NL Manigbas

Executive Summary

Rice is the most important staple food consumed by more than half of the world's population. Majority of Filipinos and several Asian countries depend on rice as primary economy food. Rice can be grown in different ecosystems, one of which is the irrigated lowland system where inbred and hybrid rice can be direct seeded or transplanted. The others are rain fed, saline prone, cool elevated, flood prone, and upland areas. Aromatic, glutinous, pigmented and japonica rice are some of the specialty types that commands higher price in the market. Recently, the demand is increasing in accordance with the continuous increase in human population; hence, there is a need to improve the yield potential and resistance of the existing varieties. One of the essential keys is the utilization of breeding goals and objectives of conventional and organic rice systems. Basically, the breeding is directed to achieve desired traits such as high grain yield, resistance to biotic and abiotic stresses, and grain qualities acceptable to consumers. The main differences are the selection environment and the expression of these traits on these environments. Some of the important traits to be considered in organic rice breeding system are not often addressed in conventional breeding systems particularly on traits such as nutrient uptake efficiency, weed competitiveness, high total biomass yield, tolerance to mechanical weed control, root plasticity and others and so integration and improved strategies are needed in addressing all these concerns.

In terms of the environmental conditions, there are a lot of challenges to face with varietal improvement. Restricting factors affects rice growth and development under different environmental conditions. These factors greatly affect yield which in turn affects the ability to cater the continual increase in rice. Under these complex and variable environments, breeding objectives must shift to developing varieties which are adapted to specific target environment such as drought, submergence, high temperature, low temperature and under rain-fed conditions. To address this constraints and challenges, different breeding strategies, which include integrated management technologies, marker-assisted selection, classical hybridization and selection, in vitro culture, in vitro mutagenesis, anther culture, root plasticity development, and incorporation of tungro and bacterial blight disease resistance genes are employed to generate and develop improved breeding lines for the target ecosystem.

Dealing at the molecular level, identifying good donors at the pre-breeding phase is a prerequisite in any breeding programs. Varieties and wild types are being screened for particular traits in search for genes or donors useful in breeding programs. But natural variations for important traits, such as resistance to various biotic and abiotic stresses, are limited. Relying solely on natural genetic variation may not be enough to address the needs in the future thus tapping other alternatives methods of increasing genetic diversity may also be very important.

The increasing role of hybrid rice technology in augmenting domestic rice supply, additional higher-yielding rice varieties need to be developed through a more-focused and market-oriented outlook. Hybrid rice breeding at CES has been adaptive to need by streamlining activities to be more output-oriented and resource efficient. Consequently, new parent lines with good combining potential have been developed, good-performing testcrosses have been generated and performance testing of promising hybrids in the breeding pipeline made more comprehensive. In addition, recognizing that seed yield is important is as much as grain yield is; seed production studies have been optimized to be cross-combination appropriate. Corresponding breeding activities at branch stations have also been successful. The continuous development of high-yielding hybrid varieties that are resistant to pests and diseases and possess excellent grain qualities is also one of essential solutions to keep up with the increasing demand for rice and the changing environment. As such, there is a need for a strong national public breeding and research on hybrid rice.

Conventional and advance breeding programs and techniques are being used to develop improved rice varieties at the shortest possible time. Under conventional rice breeding system, selection is a very important tool in plant breeding. This depends on the precision and accuracy of the sets of selection criteria and the ability of the breeder to employ this breeding set. Advance system utilizes the identification of good donors at pre-breeding phase. Particular traits are being screened in search for genes that are useful in breeding programs. Both programs' ultimate goal is to develop new resilient varieties that address the criteria and suited to the target and changing environment.

I. Pre-Breeding and Germplasm Enhancement

Project Leader: AA dela Cruz

Identifying good donors at the pre-breeding phase is a prerequisite in any breeding programs. In rice, varieties and wild types are being screened for particular traits in search for genes or donors useful in breeding programs. But natural variations for important traits, such as resistance to various biotic and abiotic stresses, are limited. Relying solely on natural genetic variation may not be enough to address the needs in the future thus tapping other alternatives methods of increasing genetic diversity may also be very important. This project aims to broaden the base of germplasm resources by identifying new gene sources or by developing new sources, and eventually increase the access and utilization of desirable traits and/or genes existing in the rice germplasm.

Induced mutations for rice quality

TF Padolina, RC Braceros, LR Pautin, and APP Tuaño

In 2015, advanced mutant lines from modern and traditional backgrounds were generated. These lines had improved yields and other morpho-agronomic traits and were advanced according to appropriate breeding nurseries. Different grain quality parameters on physical and milling potentials, physico-chemical traits and some value-adding traits have been preliminary screened while ensuring higher productivity and resistance over their parent stock. Modern varieties such as PSB Rc10, NSIC Rc152, NSIC Rc150 and MS16 were targeted to reduce chalkiness, improve physico-chemical properties and milling quality, respectively. Promising mutant lines converted from the hybrid Mestizo 1 were selected with acceptable yield and better bacterial leaf blight resistance while retaining its aroma and excellent grain quality. Traditional varieties like Azucena, Dinorado and Ballatinaw were also chosen to improve yield while retaining good grain quality and also being screened for other value traits like higher nutrient content, anti-oxidant properties and some tolerance to abiotic stress like drought.

Highlights:

- In 2015, 73 promising mutant lines derived from gamma irradiation with various radiation dose ranging from 20 to 35 kR were selected from 8 parent materials; 4 modern varieties MS16, PSB Rc10, NSIC Rc150, and NSIC Rc152, three traditional varieties Ballatinaw, Dinorado, and Azucena, and lastly, mutants derived from the irradiated F1 seeds of Mestizo 1. (Table 1 and 2)

- Continuing performance evaluation in 2015 DS resulted to the selection of the most promising materials. These were the mutants of Dinorado, Ballatinaw, Azucena, and Mestizo 1 such as Dinorado5kR-38-3-2-3, PR39490-Ballatinaw30kR-7-2-1-1, PR39483-Azucena30kR-62-52-1, and PR37913-Rc72H20kR-1-18-1, respectively. They are currently in the MET stages 1 and 2 Another important mutant line derived from Mestizo 1, PR37913-Rc72H20kR-6-19-1 has been nominated to Plant Variety Protection Board while those promising mutants, one to two best lines each derived from PSB Rc10, MS16, PSB Rc150, and PSB Rc152 showed consistent improved performance against their original parent stock. For the confirmation of the target yield level and grain quality traits, they will be advanced to the multi-location yield trials in the succeeding season. Selected lines with confirmed mutated traits were also nominated in the crossing block as donor germplasm.

- The results of 2015 WS performance trials were affected by two consecutive typhoons and cannot be presented. Moreover, seed samples for the grain quality analysis were likewise affected and cannot be a good source for confirmation analysis. Based on the result of trials, three lines of mutant were also elevated and evaluate this 2016DS in NCT and NCT-Heat Tolerance trial in Mindanao, Iguig Cagayan and PhilRice–CES (namely Azucena, Meztiso Mutant and Nipponbare mutant), also 1 line of Dinorado mutant elevated to NCT phase I of irrigated lowland trials

Table 1. Most advanced mutant lines from various background, their yield ranges, and breeding status. PhilRice CES, 2015.

Background	Dose	range (tons/ha)	of lines	STATUS	HIGHLIGHTED ENTRY
S16	25Kr	6.8 to 10.0	10	PYT	MS16(Early)-25Kr-1-4, MS16(Early)-25Kr-1-22
rig parent		4.5			
B Rc10	25 Kr	7.3 to 9.8	8	PYT	PSB Rc10-25Kr-1-13, PSB Rc10-25Kr-1-25, PSB Rc10-25Kr-1-16
rig parent		3.3			
SIC Rc150	20Kr	7.8 to 9.0	10	PYT	NSIC Rc150-20Kr-2-15, NSIC Rc150-20Kr-2-25
rig parent		6.9			
SIC Rc152	25Kr	6.7 to 9.0	10	PYT	NSIC Rc152-25Kr-8 , NSIC Rc152-25Kr-19
rig parent		6.7			
inorado	25Kr	6.1 to 8.2	10	MET stage 2	Dinorado5kR-38-3-2-3
rig parent		5.8			
llatinaw	30 to 35 kR	4.7 to 6.1	10	MET STAGE 1, NCT-HT	PR39490-Ballatinaw30kR-7-2-1-1
rig parent		3.1	10		
zucena	30kR	4.6 to 6.4	6	AON, DRT, HT	PR39483-Azucena30kR-62-52-1
rig parent		3.7			
estizo 1	20kR	4.8-6.5	9	PVP, MET, HT	PR-37913-Rc72H20kR-1-18-1 (MET) PR37913-Rc72H20kR-6-19-1(PVP)
rig parent		3.7			

Table 2. Number of mutant entries per genotype.

Genotype Background	No. of Mutant lines evaluated
NSIC Rc144	10
NSIC Rc192	38
NSIC Rc272	8
NSIC Rc288	2

Development of herbicide-tolerant and disease-resistant rice through induced mutations

R Miranda, CFS Te, and NR Sevilla

The genetic variation of modern rice varieties has narrowed as a result of decades of breeding. To be able to continue to make gains from rice breeding, access to a diverse natural germplasm is essential. Induced mutation is one strategy to produce novel genetic variation that can be exploited for varietal improvement. Among the important factors that adversely affect yield are diseases and weeds, especially with the changing climatic patterns. This study, therefore, aims to enhance the genetic variation in the PhilRice rice varietal development program specifically for disease resistance and tolerance to herbicide.

Highlights:

- M2 seeds of 3 popular varieties were generated: NSIC Rc222 (8.56kg irradiated; 4 plants and 1910 seeds, EMS-treated and sodium azide treated (52 plants); NSIC Rc240-irradiated (9.95kg), EMS mutated (24 plants) and sodium azide (2 plants); NSIC Rc298-EMS mutated (2181 seeds).

- For the second cycle screening for herbicide tolerance of 13 promising mutants, no plants survived in 2% Round-up herbicide. In the next screening, the herbicide concentration will be reduced to 1%, which was initially used when the 13 putative herbicide mutants were selected. Optimization of leaf assay method is on-going.

- In screening for reactions to tungro, 87 promising resistant plants (from M9 of NSIC Rc192) were selected.

- For the selection for BLB resistance and other traits in the field, Xoo race 3 (PXO 79-Maligaya strain) was used to screen the 58 different mutant lines from four different genotype backgrounds (Table 2). The yield performances were also evaluated. Results were validated based on the expected reactions of differential varieties, resistant and susceptible checks (Table 3).

- For NSIC Rc144 background, 10 entries were rated resistant to Xoo race 3 with lesion lengths ranged from 1.71 - 3.73 cm. Its wild type recorded 11.25cm lesion length. Moreover, 2 promising entries were selected with yield advantages of 8.7% and 16% increase over the wild type (Figure 1A).

- For NSIC Rc272 and NSIC Rc288 backgrounds, no BB-resistant entries were identified however 5 entries were selected based on yield advantages of 6.8-17.73% over their respective wild types (Figure 1B).

- For NSIC Rc192 background, 1 BB-resistant and 5 intermediate BB-resistant entries were selected while 24 entries were identified with good yield performance (with 6.1-56.6% yield advantage over its wild type). Mutants with long grain and red pericarp were also identified (Figure 1C).

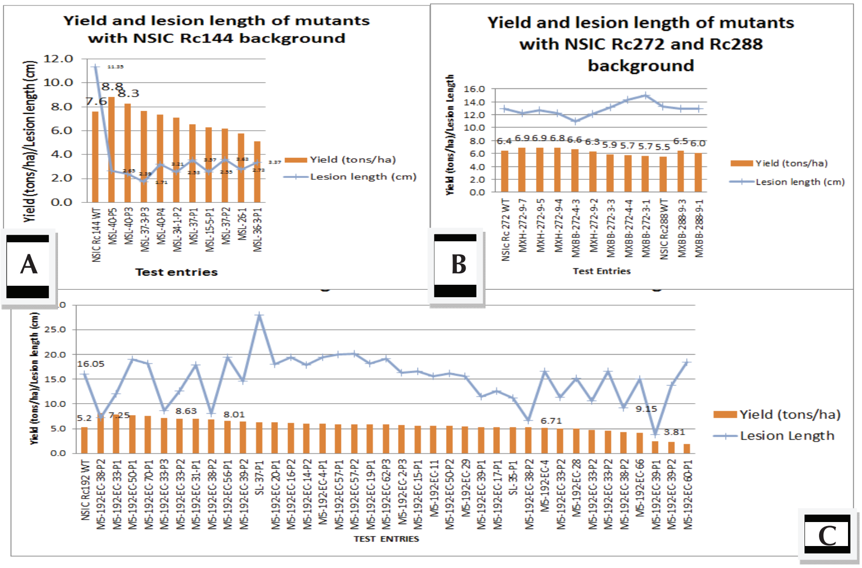


Figure 1. Graphical presentation of lesion length and yield performance of different mutant lines compared to wild types.

Table 3. Lesion length and BLB infection rating of resistant and susceptible checks against Race3.

2015DS Index No.	Entry Code	Line Designation	Yield (tons/ha)	Lesion length (cm)	BLB RATING
14	15DS-MSL-ON-14	IRBB4	5.3	3.42	R
15	15DS-MSL-ON-15	IRBB5	4.7	3.09	R
16	15DS-MSL-ON-16	IRBB7	6.8	7.59	I
17	15DS-MSL-ON-17	IRBB21	7.9	3.13	R
18	15DS-MSL-ON-18	IRBB61	6	1.98	R
19	15DS-MSL-ON-19	IRBB62	7.3	1.29	R
13	15DS-MSL-ON-13	TN1 (Susceptible)	5.7	23.73	S
12	15DS-MSL-ON-12	IR24 (Susceptible)	3.1	11.31	S

Breeding for ultra-early maturing rice varieties with high yield

TF Padolina and LR Pautin

The breeding and development of highly productive lines that are ultra-early or those which mature in less than 100 days (some farmers even clamor for 75-day varieties of rice) is not only a fascinating challenge to plant breeders. It is an important and timely breeding objective to pursue. The government through the Department of Agriculture has recently crafted an intensified campaign to increase our rice production further and attain rice self-sufficiency in the process. Ultra-early maturing (UEM) varieties offer sustainable breakthrough interventions not only to increase total productivity under favorable conditions but under the less favorable environments that are more vulnerable to limited land and water availability for rice cultivation, as well as to climate change impacts on the timing and length of production seasons.

The practice of a shorter production cycle using UEM varieties promotes higher efficiency of fertilization and even reduces the production costs since it also shortens the vulnerable time of the crop to pest attacks in the field and thereby minimizes the application of pesticide inputs. In well-irrigated fields, UEM varieties could provide the soil with a longer “rest” period (fallow) for dry matter incorporation. Another advantage is it can help break the pest cycle.

Highlights:

- Five most advanced and promising UEM lines are under evaluation. Two lines PR40348-7-5-1 and PR40346-4-2-1 in the MET stage 1 showed potential as compared to PSB Rc10 (Table 4) while among the F5 generations 3 lines PR4751-B-2-1, PR45757-B-3-1, and PR45765-B-5-1 were selected based on uniformity, high yield and good agronomic traits.

- Most promising among them, PR40346-4-2-1 produced yield in the range of 3.94 to 7.90 t/ha as compared to PSB Rc10 with only 1.81 to 5.88t/ha across 6 contrasting MET sites. This line ranked better in terms of yield and stability. It has a premium milling quality with long and slender grains, intermediate amylose content which was rated an overall excellent score (Table 5).

- Continuous evaluation on the segregating generations is being done.

Table 4. Yield performance (t/ha) of promising UEM line in the MET stage 1 across 6 sites.

FIXED LINE	Muñ	SM	RTR	LB	Ubay	Mid	ACROSS	GY Rank	YSI
PR40346-4-2-1	7.9	6.53	5.5	7.73	3.94	5.07	6.11	86	163
PR40348-7-5-1	5.58	4.81	3.64	5.88	1.81	3.1	4.15	156	252
IRRI 104 (Rc10)	7.45	5.96	5.16	7.37	3.6	3.63	5.53	143	184

Mun- Munoz, Nueva Ecija, SM-San Mateo Isabela, RTR- Agusan del Sur; LB- Los Banos, Laguna, Ubay- Bohol; Mid- Midsayap, North Cotabato ; GY- grain yield; YSI- yield stability index

Table 5. Grain Quality parameters of UEM lines evaluated in the MET stage 1, 2015DS.

	MILLING RECOVERY						PHYSICAL ATTRIBUTES						PHYSICOCHEMICAL PROPERITES				GQ SCORE
romising Lines	Brown Rice (%, Class)		Milled Rice (%, Class)		Head Rice (%, Class)		Chalky Grains (%, Class)		Grain Shape (L/W)		Grain Length (mm)		Amylose (%, Class)		Gel. Temp. (ASV, Class)		(based on actual parameters tested)
40348-7-1	76.5	F	70.3	Pr	61	Pr	1.6	Pr	6.9	L	3.3	S	20.1	I	6.3	L	Excellent
40346-4-1	77.5	F	70.4	Pr	63	Pr	0.4	Pr	6.8	L	3.1	S	20.1	I	7	L	Excellent
40366-2-1	78	F	71.7	Pr	65	Pr	1.5	Pr	7.1	L	3.3	S	21.3	I	6.9	L	Excellent
40356-1-3	77.5	F	70.4	Pr	61	Pr	2.5	G1	6.9	L	3	I	17.8	I	3.5	HI	Excellent
40356-5-2	78.2	F	71.4	Pr	63	Pr	0.7	Pr	6.7	L	3.1	S	17.2	I	2.7	HI/H	Excellent
40366-2-1	78.3	F	70.4	Pr	58	Pr	5.7	G2	6.9	L	3.3	S	20.3	I	3.8	I/HI	Very Good
40408-6-1	77.3	F	69.5	G1	61	Pr	1.3	Pr	6.8	L	3.1	S	15.8	L	3	HI	Excellent
40364-4-1	79.5	F	72.2	Pr	69	Pr	0.7	Pr	6.6	L	3	I	19.9	I	6.2	L/HI	Excellent

F-fair; Pr- premium; G1-grade 1; L- long grain ; S- slender; I- intermediate; L- low amylose; low gel temp; H/HI- High/high intermediate

Finding durable and novel blast resistance genes effective against Philippine's Magnaporthe grisea pathogen population

JM Niones, TE Mananghaya, LM Perez, JT Niones, JP Rillon, ML Palma, TF Padolina

Rice blast is one of the most devastating diseases of rice causing great loss in rice production. One of the practical and effective strategies to manage the disease is to use resistant cultivars. Currently, approximately 50 blast resistance genes have been identified. As the pathotypic diversity of the rice blast fungus is enormous, the functional responses of these blast resistance genes relative to specific pathogen population have not been reported in the Philippines. In addition, we observed resistances of released Philippine rice varieties break down after a few years of utilization in the farmers' field. The event of broken resistances is then probably due to lack of knowledge on the population structure of the pathogen at the site where a variety is deployed or due to the emergence of new pathogen race.

This study aims to establish information on the structure of rice blast pathogen population in major rice growing areas in the Philippines. From this knowledge, effective resistance genes against the population will be identified. Furthermore, this study also aims to discover novel and durable resistance genes from traditional varieties as well as released varieties.

Highlights:

Genetic and Phenotypic analysis of resistance BC1F2 of US2/Malay 2

- A total of 306 BC1F1 plants of US2*2/Malay 2 were generated in 2015WS, to be used in the identification of putative quantitative trait loci (QTL) associated to blast resistance of Malay 2. Out of 310 SSR markers used in polymorphism survey of both parents, 128 (41.3%) were found polymorphic and 40 SSR markers were already used in DNA analysis of 306 BC1F1 plants. Graphical genotype map was generated to locate chromosome distribution of polymorphic markers across rice genome (Figure 2).

- The 88 BC1F2 seeds of US2/Malay 2 generated were established for blast resistance evaluation. Three replications were made, two resistant checks (SHZ-2, IR65482-4-136-2-2) and two susceptible controls (US2, CO39) were planted for every 10 test entries of BC1F2 materials. Out of 88 entries, 28 (32%) BC1F2 were found resistant, 36 (41%) for intermediate response and 24 (27%) exhibited susceptible reaction to the rice blast pathogen present in PhilRice blast nursery using the National Cooperative Testing (NCT) manual in scoring of leaf blast lesion (Table 6).

Genetic improvement of popular varieties using different blast resistant genes

- Selected released rice cultivars were used for crop improvement by pyramiding of two different blast resistant genes to increase the resistance to rice blast disease. Four derivative lines of cross between NSIC Rc9 and IRBLz5-CA, showed consistent resistant reaction to the rice blast disease in three consecutive seasons (Table 7). Most of the entries evaluated have an intermediate response to the pathogen in 2014 dry season while conferred resistant phenotype in 2014 wet season and 2015 dry season. Few susceptible reactions were detected to advanced lines introgressed with effective blast resistance genes to the rice blast isolate present in blast nursery.

- Introgression of blast resistance gene on the following varieties: PSB Rc10, PSB Rc14, PSB Rc82, NSIC Rc128, NSIC Rc154 NSIC Rc160, NSIC Rc224, NSIC Rc238, NSIC Rc240 and NSIC Rc300 for genetic improvement using marker aided backcrossing. Differential lines with single effective blast resistance gene were used as potential donor (Table 8). Due to two typhoons consecutively hit Nueva Ecija in last quarter of 2015, the field experimental area was heavily damaged and the test entries were lodged and submerged in water.

- A total of 490 F2 test entries were evaluated for rice blast disease resistance in Crop Protection Division blast nursery in 2015 wet season. Out of 490 materials, 235 were found resistant, 124 for intermediate and 131 test entries showed susceptible reaction to rice blast pathogen present in blast nursery (Table 9). Out of 11 F2 cross combinations introduced, 4 F2 segregating populations (NSIC Rc160/IRBLsh-S (CO), NSICRc224/SHZ-2 9, NSIC Rc240/ Dacca 6-1-18, NSIC Rc298/ SHZ-2-11) showed resistant reaction to rice blast disease with a range of 69-81% from the total entries of each cross evaluated. Two resistant checks (IR65482-4-136-2-2 and SHZ-2) and two susceptible checks (US 2 and CO39) were used in rice blast screening. Test entries found resistant were transplanted for advanced generation and harvested seeds will be introduced again in blast resistance evaluation in 2016 dry season.

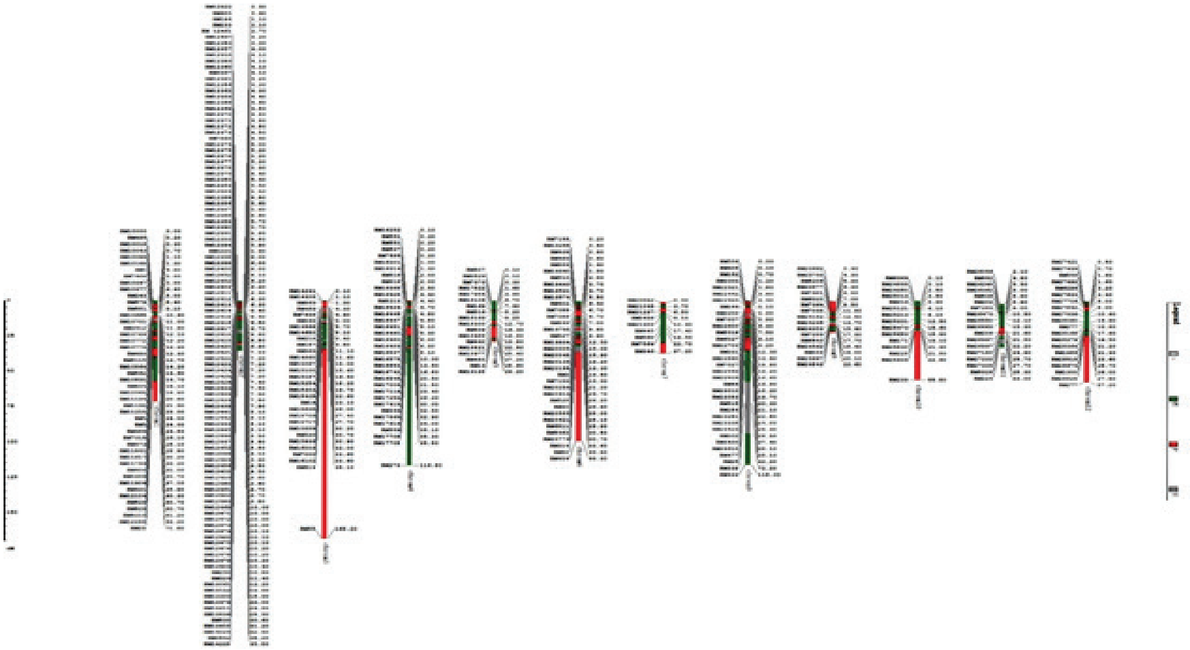


Figure 2. Graphical map and distribution of polymorphic SSR markers in US2 and Malay 2 cross

Table 6. Phenotypic screening of 88 BC1F2 of US2/Malay 2 in CPD-PhilRice CES blast nursery in 2015 DS.

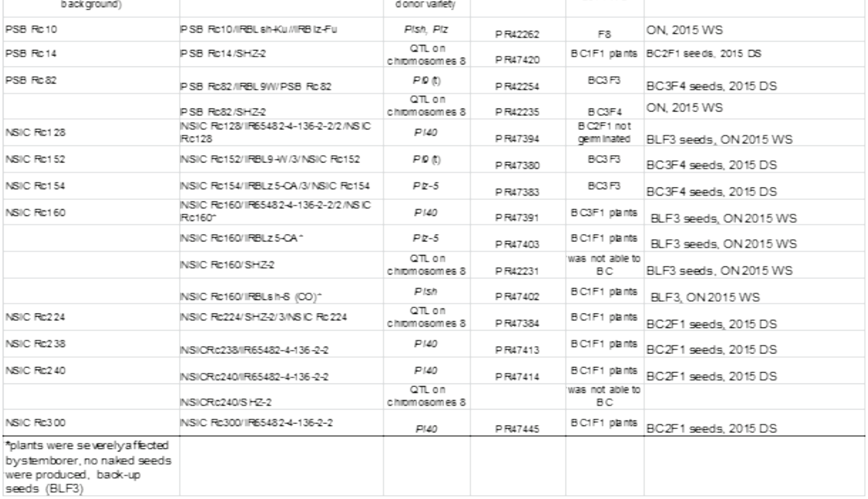
Entry Name	Blast Reaction	Entry Name	Blast Reaction	Entry Name	Blast Reaction	Entry Name	Blast Reaction
IR65482-4-136-2-2	2 (R)	IR65482-4-136-2-2	2 (R)	IR65482-4-136-2-2	2 (R)	IR65482-4-136-2-2	2 (R)
US-2	8 (S)	US-2	9 (S)	US-2	8 (S)	US-2	8 (S)
SHZ-2	1 (R)	SHZ-2	1 (R)	SHZ-2	1 (R)	SHZ-2	1 (R)
CO-39	9 (S)	CO-39	9 (S)	CO-39	8 (S)	CO-39	9 (S)
BLUM-1	4 (I)	BLUM-23	4 (I)	BLUM-45	3 (R)	BLUM-67	1 (R)
BLUM-2	6 (I)	BLUM-24	3 (R)	BLUM-46	9 (S)	BLUM-68	2 (R)
BLUM-3	4 (I)	BLUM-25	7 (S)	BLUM-47	4 (I)	BLUM-69	3 (R)
BLUM-4	3 (R)	BLUM-26	7 (S)	BLUM-48	6 (I)	BLUM-70	3 (R)
BLUM-5	4 (I)	BLUM-27	6 (I)	BLUM-49	6 (I)	BLUM-71	3 (R)
BLUM-6	4 (I)	BLUM-28	5 (I)	BLUM-50	6 (I)	BLUM-72	7 (S)
BLUM-7	6 (I)	BLUM-29	2 (R)	BLUM-51	3 (R)	BLUM-73	2 (R)
BLUM-8	5 (I)	BLUM-30	3 (R)	BLUM-52	9 (S)	BLUM-74	4 (I)
BLUM-9	7 (S)	BLUM-31	9 (S)	BLUM-53	3 (R)	BLUM-75	6 (I)
BLUM-10	8 (S)	BLUM-32	5 (I)	BLUM-54	4 (I)	BLUM-76	1 (R)
BLUM-11	9 (S)	BLUM-33	4 (I)	BLUM-55	7 (S)	BLUM-77	4 (I)
BLUM-12	9 (S)	BLUM-34	6 (I)	BLUM-56	5 (I)	BLUM-78	8 (S)
BLUM-13	9 (S)	BLUM-35	7 (S)	BLUM-57	3 (R)	BLUM-79	8 (S)
BLUM-14	4 (I)	BLUM-36	3 (R)	BLUM-58	9 (S)	BLUM-80	6 (I)
BLUM-15	4 (I)	BLUM-37	3 (R)	BLUM-59	2 (R)	BLUM-81	8 (S)
BLUM-16	7 (S)	BLUM-38	4 (I)	BLUM-60	5 (I)	BLUM-82	5 (I)
BLUM-17	9 (S)	BLUM-39	4 (I)	BLUM-61	4 (I)	BLUM-83	5 (I)
BLUM-18	5 (I)	BLUM-40	3 (R)	BLUM-62	7 (S)	BLUM-84	5 (I)
BLUM-19	3 (R)	BLUM-41	4 (I)	BLUM-63	2 (R)	BLUM-85	4 (I)
BLUM-20	6 (I)	BLUM-42	5 (I)	BLUM-64	3 (R)	BLUM-86	7 (S)
BLUM-21	6 (I)	BLUM-43	3 (R)	BLUM-65	1 (R)	BLUM-87	3 (R)
BLUM-22	9 (S)	BLUM-44	8 (S)	BLUM-66	2 (R)	BLUM-88	2 (R)
						Malay 2	1 (R)

Table 7. Blast resistance evaluation of advanced lines with blast resistant genes in PhilRice CES blast nursery.

Parentage	*Pi gene*	*Generation*	Disease reaction		
			2014 DS	2014 WS	2015 DS
NSIC Rc9/SHZ-2//IRBLzFu	QTL, Piz	F7	I	R	R
NSIC Rc9/SHZ-2//IRBLzFu	QTL, Piz	F7	I	S	R
NSIC Rc9/SHZ-2//IRBLzFu	QTL, Piz	F7		S	R
NSIC Rc9/IRBLzFu//SHZ-2	QTL, Piz	F7		S	R
NSIC Rc9/IRBLzFu//SHZ-2	QTL, Piz	F7		R	R
NSIC Rc9/IRBLzFu//SHZ-2	QTL, Piz	F7	S	R	R
NSIC Rc9/IRBLzFu//SHZ-2	QTL, Piz	F7	I	R	R
NSIC Rc226/SHZ-2	QTL	F7	I	R	R
NSIC Rc226/SHZ-2	QTL	F7		R	
NSIC Rc226/SHZ-2	QTL	F7	S	R	
PSB Rc10/IRBLsh-Ku//IRBLz-Fu	Pish,Piz	F7	S	S	
PSB Rc10/IRBLsh-Ku//IRBLz-Fu	Pish,Piz	F7		R	
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	I	R	R
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	I	R	R
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	I	R	R
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	I	R	R
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	I	R	R
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	R	R	R
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	R	R	R
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	R	R	R
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	I	R	R
NSIC Rc9/IRBLz5-CA	Piz5	BC3F3	R	R	R
NSIC Rc226/SHZ-2	QTL	BC3F3	I	R	
NSIC Rc194/SHZ-2	QTL	BC3F3	I	R	
NSIC Rc194/SHZ-2	QTL	BC3F3	I	R	R
NSIC Rc194/SHZ-2	QTL	BC3F3	I	S	R
NSIC Rc194/SHZ-2	QTL	BC3F3	I	S	R
NSIC Rc194/SHZ-2	QTL	BC3F3	I	S	R
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	R	
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	S	
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	R	
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	R	
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	R	
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	R	
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	S	
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	R	
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	R	
PSB Rc82/IRBL9W	Pi-9	BC3F3	I	R	R
PSB Rc82/SHZ-2	QTL	BC3F3	I	R	R
PSB Rc82/SHZ-2	QTL	BC3F3	I	R	R

Legend: R-Resistant; I-Intermediate; S-Susceptible

Table 8. Genetic improvement of promising variety by introducing effective resistance gene in the Philippines.



Target variety (Estimated genotype of genetic background)	Cross combination	Resistance gene Introducing from donor variety	Pedigree Name	Generation 2014 WS	Remarks
PSB Rc10	PSB Rc10/IRBLsh-Ku//IRBLz-Fu	*Pish, Piz*	PR42262	F8	ON, 2015 WS
PSB Rc14	PSB Rc14/SHZ-2	QTL on chromosomes 8	PR47420	BC1F1 plants	BC2F1 seeds, 2015 DS
PSB Rc82	PSB Rc82/IRBL9W/PSB Rc82	*Pi9 (t)*	PR42254	BC3F3	BC3F4 seeds, 2015 DS
	PSB Rc82/SHZ-2	QTL on chromosomes 8	PR42235	BC3F4	ON, 2015 WS
NSIC Rc128	NSIC Rc128/IR65482-4-136-2-2/2/NSIC Rc128	*Pi40*	PR47394	BC2F1 not germinated	BLF3 seeds, ON 2015 WS
NSIC Rc152	NSIC Rc152/IRBL9-W/3/NSIC Rc152	*Pi9 (t)*	PR47380	BC3F3	BC3F4 seeds, 2015 DS
NSIC Rc154	NSIC Rc154/IRBLz5-CA/3/NSIC Rc154	*Piz-5*	PR47383	BC3F3	BC3F4 seeds, 2015 DS
NSIC Rc160	NSIC Rc160/IR65482-4-136-2-2/2/NSIC Rc160*	*Pi40*	PR47391	BC3F1 plants	BLF3 seeds, ON 2015 WS
	NSIC Rc160/IRBLz5-CA*	*Piz-5*	PR47403	BC1F1 plants	BLF3 seeds, ON 2015 WS
	NSIC Rc160/SHZ-2	QTL on chromosomes 8	PR42231	was not able to BC	BLF3 seeds, ON 2015 WS
	NSIC Rc160/IRBLsh-S (CO)*	*Pish*	PR47402	BC1F1 plants	BLF3, ON 2015 WS
NSIC Rc224	NSIC Rc224/SHZ-2/3/NSIC Rc224	QTL on chromosomes 8	PR47384	BC1F1 plants	BC2F1 seeds, 2015 DS
NSIC Rc238	NSICRc238/IR65482-4-136-2-2	*Pi40*	PR47413	BC1F1 plants	BC2F1 seeds, 2015 DS
NSIC Rc240	NSICRc240/IR65482-4-136-2-2	*Pi40*	PR47414	BC1F1 plants	BC2F1 seeds, 2015 DS
	NSICRc240/SHZ-2	QTL on chromosomes 8		was not able to BC	
NSIC Rc300	NSIC Rc300/IR65482-4-136-2-2	*Pi40*	PR47445	BC1F1 plants	BC2F1 seeds, 2015 DS
*plants were severely affected by stemborer, no naked seeds were produced, back-up seeds (BLF3)					

Table 9. Summary of test entries evaluated for rice blast resistance evaluation in 2015 WS in PhilRice CES blast nursery.

		Reaction to leaf blast		
Test Entries	**No. of Entries**	**Resistant**	**Intermediate**	**Susceptible**
F_2 population	486	235	123	128
Improved rice cultivar	4	0	1	3
Total	**490**	**235**	**124**	**131**

Development of PhilRice software for predicting physical attributes in milled rice

IG Pacada, EH Bandonill, AM Tuates, TF Padolina, AP Tuaño, and BO Juliano

One of the important considerations in developing new rice varieties is grain quality. However, breeding of rice varieties with the desired quality require intensive evaluation especially for physical attributes. Physical attributes in milled rice consist of four parameters, namely: % chalky grains, % immature grains, grain length, and grain shape. All these traits are manually done by skilled classifiers. The most laborious task for classifier is the determination of chalky grains. They need to evaluate two sets of 30g milled rice of each of candidate elite line using their naked eye. The grain quality evaluation team of the Rice Varietal Improvement Group (RVIG) manually evaluates the physical attributes of 600 to 800 promising elite lines every year. This process is undeniably time consuming and tedious. Thus, automating classification could be the best alternative approach to speed up the conventional classification process. This study aimed to develop image processing software for predicting chalkiness and other physical attributes and to automate the classification process.

Highlights:

- The evaluation of predicting value of the developed software using samples from National Cooperative Testing (NCT) showed inconsistent result. This inconsistency is due to mismatch of training model in the software Artificial Neural Network (ANN) and the evaluated samples.

- The training models are adapted to the established standard protocol for postharvest handling of rough rice, while the samples evaluated has no information if the set protocol was followed.

- Establishment of NCT entries intended for testing the predicting value of the developed software was carried out.

- Preparation of milled rice samples for pilot testing is adapted to the special protocol for the developed software. Analysis is in progress.

General evaluation of donor germplasm

AA dela Cruz, TF Padolina, PAM Cubian

One of the most difficult tasks in carrying out a successful breeding program is the choice of germplasm. Rice breeders need to be sure that the source germplasm has desirable genetic variability to be able to develop a variety with a set of desirable characteristics. Wide variations among genotypes have greater chances to select superior characteristics of agronomic importance. Then again, it is important to have parents that complement each other well, with good specific and general combining abilities. To facilitate the development of economically high-yielding cultivars with various desirable agronomic traits, consideration on other characteristics should there be given when selecting the parent material such as aspects related to difference in grain type and shape, plant height, and resistance to biotic and abiotic stresses. With diverse genetic pool of rice varieties available, makes it useful to develop products that will have an impact at farmers' field level.

Highlights:

- In 2015, a total of 1066 rice germplasm entries were assembled in the crossing block for use in rice breeding. The materials used were selected from available rice germplasm pool composed of varieties (modern and traditional), elite lines, introductions, mutant lines and derivatives of wide hybrids. These are potential sources of traits useful in the development of high-yielding rice with good qualities and resistance to certain biotic and/or abiotic stresses.

- Among the materials assembled, 415 were characterized (177 in DS and 238 in WS) for major yield enhancing traits. Table 10 shows the top rice accessions identified as potential parents based on the standard basis of selection, grain length, grain shape and days to maturity. Several promising rice accessions were identified, however only the top 3 rice accessions (or those belonging in the top 1 to 3 ranks) were presented.

- The standard basis for selection of parents recommends use of rice accessions with ≥ 25g 1000 grain weight, ≥ 150 grains per panicle, and ≥ 85% filled spikelets. During DS, the heaviest 1000 grain weight was recorded in IR10N118 (37.9g), Fermoso tall long grain (37.2g) and IR91896-21-3-1-3 (36.5g), while in Arabel (41g), Mustaqilik (35g) and Nerica 17 (34g) in the WS. The highest number of grains per panicle, on the other hand, was recorded in OM5628 (293), PR36246-HY-1-16-1 (257), PR46840-B-B (241) in the WS. Meanwhile, the highest percent filled spikelets was recorded in C39, NSIC

Rc194 (Submarino 1) and G178 (96%) in DS, and in Malay 2 (96%), Quinizon (95%), PSB Rc3 and Paro Dumbja White (94%) in WS.

- In terms of grain length, most of the rice accessions evaluated were classified with “extra-long grains”: Guyod (11.35mm), IR86385-87-1-1-B (11.43mm), IR77542-520-1-1-1-1-3 (11.64mm), Basmati 370 (11.4) in DS, and Arabel and Basmati short (11.2) in WS. Some of the rice accessions classified with “long grains” in DS were PR29814-B-5-3-1-1 (7.2mm), IRBL11-Zh (7.3mm), IRBLzt-T, and C39 (7.4mm), while IRBLks-S, IRBLta2-Re, ILPUMBYEO and IR81551-2-1-3-3-2-PR (7.4mm) in WS. Meanwhile, only 3 rice accessions were classified with “medium grains” in WS: IRBLt-K59 and SANGJUBYEO (6.3mm), and IRBLsh-B (6.1mm).

- With regards to grain shape (length/width), most of the evaluated rice accessions were “slender” while others were “bold”. There were rice accessions classified with “round” grain shape. The top “slender” rice accessions identified in DS were BR6902-14-4-2-5 (6.55), Guyod (6.4), IR77542-520-1-1-1-1-3 (6.3), while in WS were Basmati 370 (5.6), Aromatic 1 (5.3) and PR46822-B-B-1 (5.2). On the other hand, the top bold rice accessions identified in DS were IRBLks-F5 (3.0), Ballatinao (2.95), and GMET 5 (2.9), while in WS were IRBLkh-K3, Holilber and IRBL5-M (3.0).

- In terms of maturity, the most early-maturing rice accessions identified were with 94 days maturity: DS: IRBL19-A,IRBLa-A, IRBLa-A, IRBLkm-TS, IRBLks-S, IRBLsh-B, IRBLta2-Pi, Liaoling 21 and Ipsala; WS: IRBL7-M, IRBLb-B, IRBLkh-K3, IRBLks-S, IRBLsh-B, IRBLsh-S, IRBLta2-Pi, IRBLta2-Re, IRBLt-K59, IRBLzt-T, Ipsala, Efe, Homsodera.

- A total of 158 rice accessions (targeting traits for high yield, lodging tolerance, resistance to drought, BLB, RTD, SB and blast) were utilized by various groups of breeders for hybridization. In the irrigated lowland breeding program alone, a total of 212 new crosses were generated using the 2015 crossing block materials.

Table 10. Top rice accessions identified as potential parents based on the standard basis of selection, grain length, grain shape and days to maturity.

			2015DS		2015WS	
Yield Components			**Number of qualified rice accessions**	**Top Promising Rice Germplasm**	**Number of qualified rice accessions**	**Top Promising Rice Germplasm**
Standard basis for selection of parents	*1000g wt*	*= 25 g*	128	IR10N118 (37.9g); Fermoso, tall, long grain (37.2g); IR91896-21-3-1-3 (36.5g)	109	Arabel (41g); Mustaqilik (35g); Nerica 17 (34g)
	Grain / panicle	*= 150*	-	-	43	OM5628 (293); PR36246-HY-1-16-1 (257); PR46840-B-B (241)
	%filled spikelets	*= 85%*	53	C39, NSIC Rc194 (Submarino 1) and G178 (96%)	47	Malay 2 (96%); Quinizon (95%); PSB Rc3 and Paro Dumbja White (94%)
Grain length	*extra long*	*>7.4 mm*	161	Guyod (11.35mm); IR86385-87-1-1-B (11.43mm); IR77542-520-1-1-1-1-3 (11.64mm)	214	Basmati 370 (11.4); Arabel and Basmati short (11.2)
	long	*6.4-7.4mm*	16	PR29814-B-5-3-1-1 (7.2mm); IRBL11-Zh (7.3mm); IRBLzt-T and C39 (7.4mm)	21	IRBLks-S, IRBLta2-Re, ILPUMBYEO and IR81551-2-1-3-3-2-PR (7.4mm)
	medium	*5.5-6.3mm*	0	-	3	IRBLt-K59 and SANGJUBYEO (6.3mm); IRBLsh-B (6.1mm)
	short	*<5.5 mm*	0	-	0	-
Grain shape (length / width)	*slender*	*>3.0*	168	BR6902-14-4-2-5 (6.55); Guyod (6.4); IR77542-520-1-1-1-1-3(6.3)	183	Basmati 370 (5.6); Aromatic 1 (5.3); PR46822-B-B-1 (5.2)
	bold	*2.0-3.0*	25	IRBLks-F5 (3.0); Ballatinao (2.95); GMET 5 (2.9)	55	IRBLkh-K3, Holilber and IRBL5-M (3.0)
	round	*<2.0*	0	-	0	-
Maturity	*early*	*=100 days*	16	IRBL19-A,IRBLa-A,IRBLa-A, IRBLkm-TS, IRBLks-S, IRBLsh-B, IRBLta2-Pi, Liaoling 21 and Ipsala (94 days)	19	IRBL7-M, IRBLb-B, IRBLkh-K3, IRBLks-S, IRBLsh-B, IRBLsh-S, IRBLta2-Pi, IRBLta2-Re, IRBLt-K59, IRBLzt-T,

Genetic gain in yield and associated traits of irrigated lowland inbred rice (Oryza sativa L.) varieties developed and released in the Philippines

DB Bastasa, J Hernandez, NL Manigbas

Breeding efforts for improving the yield potential of irrigated lowland (IL) inbred rice varieties in the Philippines has passed almost five decades since the release of IR8 in 1966. IR 8 is the first high-yielding semi-dwarf inbred rice variety developed by IRRI which resulted in remarkable increase in yield potential during the first decade. The following years of rice improvement by IRRI, PhilRice and UPLB focused on incorporation of multiple disease and insect resistance, shortening of growth duration, improvement of grain quality and increasing yield potential by developing hybrid rice and new plant type (Peng and Khush,2003). Periodic evaluation of the rate of genetic gain in grain yield and associated agronomic traits is important to assess the progress of rice genetic improvement (Fufa, et al., 2005).

This study aims to determine the contribution of rice breeding in the Philippines to changes in cultivars released from 1966 to 2013. Current information derived from this study is useful for designing future rice breeding strategies to further optimize gains in selection.

Highlights:

- The 28 rice varieties representing different years of varietal release over the time period 1966 to 2013 showed significant variation in grain yield as well as some of the plant traits measured.

- Figure 3 shows the positive linear relationships between plant height, leaf length, total grains/panicle, total grains/hill, panicle length, % spikelet fertility/hill and both grain yield and year of release.

- Among the plant traits, plant height ($p=0.000$), total grains/hill ($p=0.03$), and leaf length ($p=0.05$) had significant effects on grain yield increase.

- Growth duration, harvest index and 1000-grain weight also had positive linear relationship with grain yield but the result was not significant.

- Traits which are negatively correlated with yield are: total plant biomass, panicles/hill, % filled grains/panicle, % productive tillers/hill and total tillers/hill; while traits which are negatively correlated with both yield and year include panicles/hill, % productive tillers/hill and total number of tillers/hill.

- There were significant differences in grain yield among the rice varieties released in different years of varietal improvement. Significant increase in grain yield over time was noted in all three experimental sites, namely: Agusan del Norte, Agusan del Sur and Bukidnon. Across sites, average yield ranged from 1.8 t/ha to 3.11 t/ha and varietal yield trend was positive (Figure 4). Linear regression analysis of grain yield against year of release indicated an annual yield gain of 20.14kg/ha per year which is equivalent to 1% per year on the basis of the yield of IR8. This agrees with the result of Peng et al (2000) in their experiment conducted in 1996 and 1998 which could mean that annual genetic gain in rice yield in the Philippines remain constant after almost five decades of genetic improvement with respect to irrigated lowland inbred rice. These results need further validation in another cropping season.

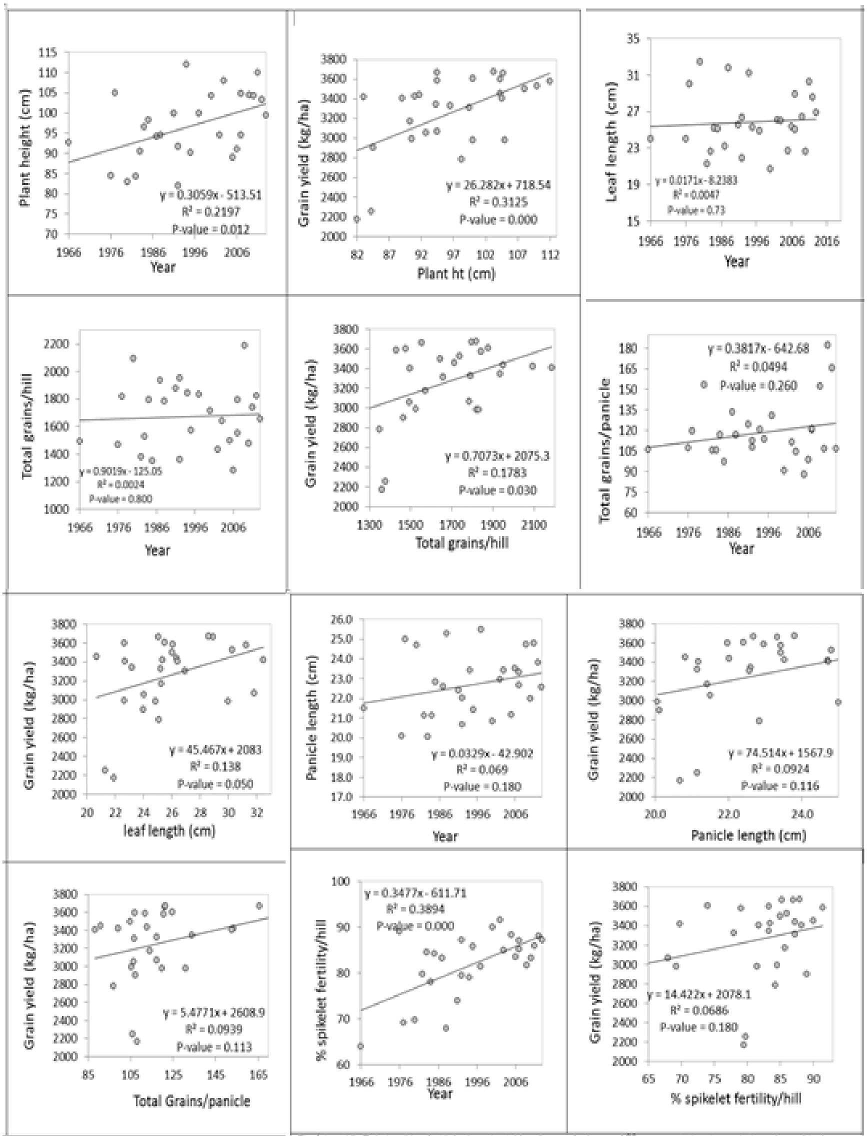


Figure 3. Relationship of plant height, leaf length, total grains/panicle, total grains/hill, panicle length and % spikelet fertility/hill with both grain yield and year of release of 28 representative rice varieties released in the Philippines from 1966 to 2013.

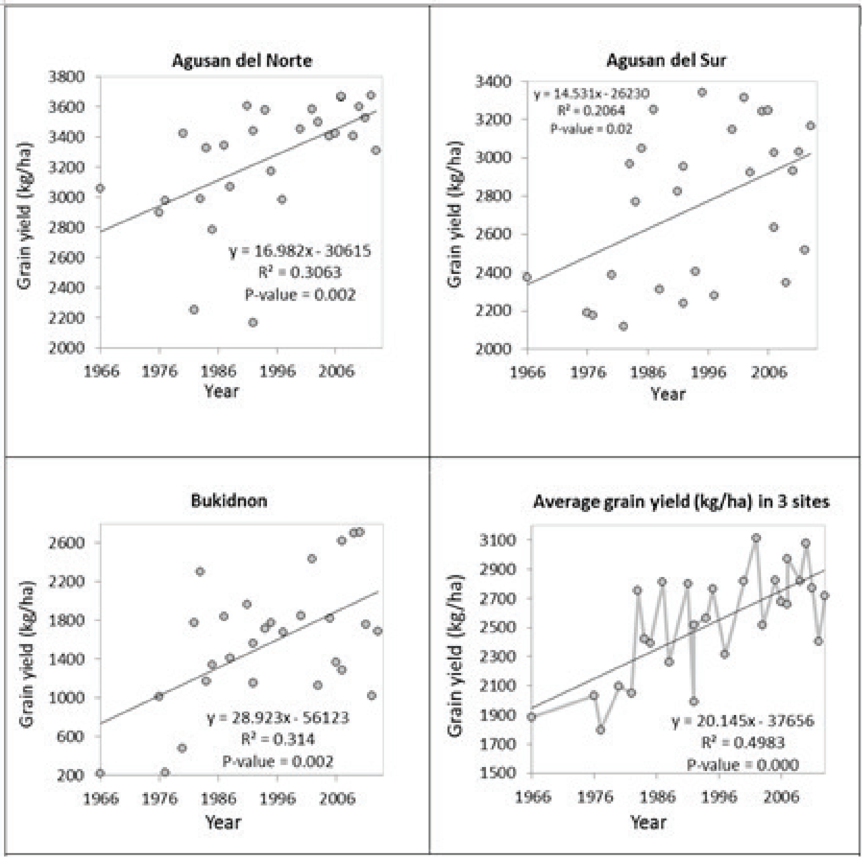


Figure 4. Trends in grain yield of selected rice varieties released from 1966 to 2013 in three sites: Agusan del Sur, Bukidnon and Agusan del Norte.

Genetic improvement and mechanism of resistance to stemborer in rice

IG Pacada, LM Perez, GS Rillon, GDC Santiago.

The GRD conducted a massive screening of traditional varieties (TRVs) for insect resistance, and some of these TRVs showed resistance/ tolerance to stemborer. Verification should be implemented and investigating its mechanism of resistance should also be thoroughly examined. The yellow stem borer emerges in Luzon while the white stem borer occurred in Mindanao. The confirmation and investigation of resistance/tolerance of identified TRVs will validate in these two areas by exposing them on high natural stem borer infestation in the field. Mechanism of resistance classification will be followed, this is to determine if non-preference, antibiosis, tolerance, and avoidance is involved.

Highlights:

- Out of 52 TRVs evaluated, 18 of them verified to have resistance to whitehead, 28 are intermediate, and 6 are susceptible (Figure 5).

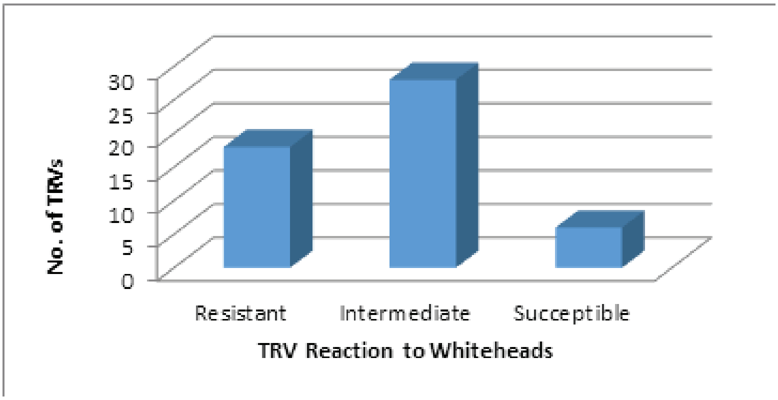


Figure 5. Reaction of 52 TRVs to whiteheads.

Increasing the yield of Gal-ong, a traditional rice variety (special rice), through induced mutation

ES Avellanoza, RT Miranda and JC Yabes

Traditional rice varieties are famous for its good grain, eating quality, and aroma. However, seeds produced from these varieties for commercialization and for export purposes were limited due to their low yield resulting to low productivity. Therefore, satisfying the demands of high grain quality aromatic rice was unsuccessful.

Mutation is defined as sudden heritable change in a characteristic of an organism. Mutation techniques have played a significant role in increasing rice production in the Asia-Pacific Region. According to the recent database (Maluszynski, et al., 2000), 434 mutant varieties of rice have been released with improved characters such as semi-dwarf height, early maturity, improved grain yield, disease and cold-tolerance, and improved grain quality. The development of higher yielding traditional rice varieties through induced mutation method is one of the potential tools for generating more variability which has been successfully exploited for improving several traits in many crop plants including rice (Oryza sativa L). The use of gamma radiation, chemical and several methods for induced mutation has been proven effective means to generate novel alleles. Since, mutagenesis has been proven to be very effective in reducing plant height, it opened new opportunities in developing superior and elite breeding lines or improved rice with better grain and eating quality and higher yield (Balotch, et al. 2003; Chakravarty, 2010). Moreover, to improve the yield potential of such cultivars the plant height shall be reduced and nitrogen responsiveness shall be increased without losing the aroma and other quality characters of the parental variety (Singh and Singh, 2000; Sharma, et al. 2008).

In this study, a traditional rice variety Gal-ong will be used as plant material. It is very popular in Abra and Benguet due to its excellent grain quality and aroma and its produced are utilized for commercialization and for export purposes. However, the yield is very low, which may be attributed to its low tillering ability and have very tall stature. Acquisition of seeds, seed purification and selections for gamma irradiation and chemical treatments will be conducted. Generation and establishment of M2 populations, selections of promising mutant lines, advanced generation of selected mutants and characterization will be conducted especifically for mutant lines observed with higher yield.

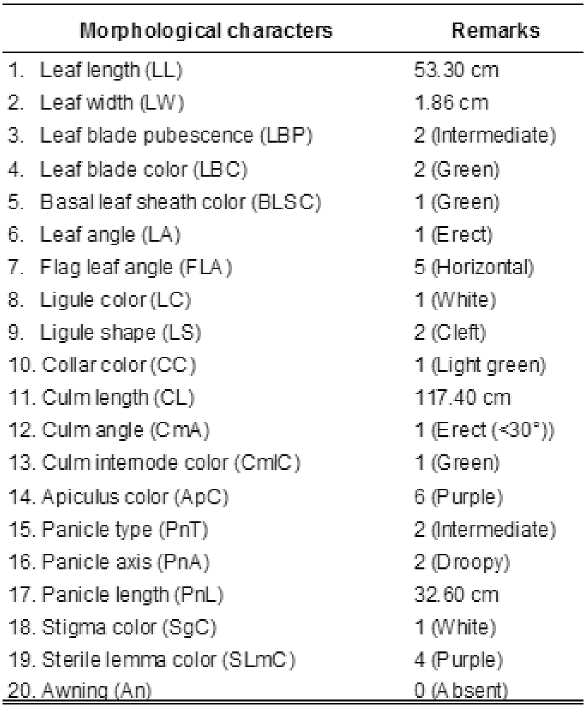
Highlights:

- In July 2015, acquisition of wild type Gal-ong (WTGO) seeds from PhilRice Batac Station was done. These were purified and seed-increased to produce enough quality seeds to be used in the succeeding experiments. Seed bed preparation and sowing of the WTGO (Figure 6) was done in PhilRice Batac Station last July 21, 2015 and were transplanted after 21 days in designated plots, having an area of 1m x 4.2m (5 x 21 hills) with 20cm space between rows and 30cm space between plots.

- Assessment of morphological characters (Table 11) and agronomic traits (Table 12) of WTGO plants based on the standard evaluation system for rice (SES) (IRRI, 2014) was conducted during 2015 wet season. Data on seedling vigor, plant height and tiller number were gathered to serve as baseline information for the subsequent seasons of field experiments. In addition to these, six yield component data such as productive and non-productive tiller counts, panicle length, filled and unfilled spikelets per panicle, average number of grains per panicle, percent spikelet fertility and 1000 grain weight were also gathered. Preliminary yield data was also recorded to have a prior information on the yield of Gal-ong in conducting the experiment.

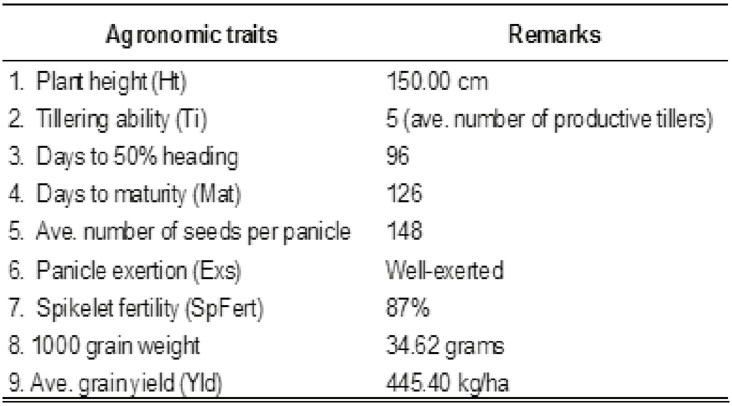
- Alongside the WTGO field experiment set-up, an advanced generation (M2) of irradiated seeds was also sown in the field. Individual plant selection was done at maturity stage of the plants based on the improved characteristics that can be attributed as a result of the induced-mutation method. There were 61 M2 Gal-ong plant selections that were tagged and will be forwarded to M3 advanced generation during the next cropping season.

Table 11. Morphological characteristics of purified WTGO at maturity stage (Standard Evaluation System for Rice, 2014-IRRI).



Morphological characters	Remarks
1. Leaf length (LL)	53.30 cm
2. Leaf width (LW)	1.86 cm
3. Leaf blade pubescence (LBP)	2 (Intermediate)
4. Leaf blade color (LBC)	2 (Green)
5. Basal leaf sheath color (BLSC)	1 (Green)
6. Leaf angle (LA)	1 (Erect)
7. Flag leaf angle (FLA)	5 (Horizontal)
8. Ligule color (LC)	1 (White)
9. Ligule shape (LS)	2 (Cleft)
10. Collar color (CC)	1 (Light green)
11. Culm length (CL)	117.40 cm
12. Culm angle (CmA)	1 (Erect (<30°))
13. Culm internode color (CmIC)	1 (Green)
14. Apiculus color (ApC)	6 (Purple)
15. Panicle type (PnT)	2 (Intermediate)
16. Panicle axis (PnA)	2 (Droopy)
17. Panicle length (PnL)	32.60 cm
18. Stigma color (SgC)	1 (White)
19. Sterile lemma color (SLmC)	4 (Purple)
20. Awning (An)	0 (Absent)

Table 12. Field performance of the WTGO based on the preliminary evaluation of agronomic traits, 2015WS.



Agronomic traits	Remarks
1. Plant height (Ht)	150.00 cm
2. Tillering ability (Ti)	5 (ave. number of productive tillers)
3. Days to 50% heading	96
4. Days to maturity (Mat)	126
5. Ave. number of seeds per panicle	148
6. Panicle exertion (Exs)	Well-exerted
7. Spikelet fertility (SpFert)	87%
8. 1000 grain weight	34.62 grams
9. Ave. grain yield (Yld)	445.40 kg/ha

Figure 6. Sowing of WTGO in PhilRice Batac Experiment Station in July 21, 2015.

II. Development of Irrigated Lowland Rice

Project Leader: JM Niones

Food security in Asia is challenged by increase food demand, threatened by declining rice production area and water availability. Rice is the most important human food consumed by 60% of the world's population every day. Approximately 530 million ton per year rice produced globally, about 90% to 92% is produced and consumed in Asia (IRRI, 1997). The estimated rice production has to be increased by 56% over the next 30 years, to keep up with the population growth and demand for food (IRRI, 1997). In the Philippines, it needs to feed 21 persons per hectare with a small harvest area of only 4.2M hectares. On the other hand, yield growth over the last 10 years is only 1.83% per annum and the challenge to increase this productivity is under pressure. The irrigated lowland areas comprising 71% of the total harvest area is the most reliable ecology of developing new intensive–culture rice crops, be it transplanted or direct seeded. With the advent of modern and innovative technologies, variety development based on genetic enhancement and extensive phenotyping will allow development of future's rice ideotypes.

The primary objective of irrigated lowland breeding project is the development of superior rice varieties with high and stable yield, resistant to RTV, BLB and blast, good grain quality, and resilient to climate change is an economical strategy in increasing farmers' productivity.

Highlights:

- Released varieties: NSIC 2015 Rc394, NSIC 2015 Rc396 and NSIC 2015 Rc403.

- A total of 394 F1 hybrid crosses were generated with high yield traits for transplanted and direct seeding system.

- In segregating generations, a total of 10,618 breeding lines were selected with good phenotypic acceptability and advance for next generation for transplanted and direct seeding.

- A total of 100 homozygous (fix) lines were elevated to Advanced Observational Nursery (AON) and performance yield trial.

- In the AON, PR43367-17-1-2-1 (PR39420-14-10-2-3-1 / TW16) line showed excellent phenotype, plant type and good kernel quality. This line had 112cm plant height and 11 productive tillers. This breeding line matures 124 days after sowing and intermediate field reactions to prevailing diseases.

- PR42333-2B-43 derived from the HUA 565 / PR37126-PB cross showed high yield performance, excellent plant type and good kernel quality among the test entries. This line matured in 125 days with 107 cm plant height and 18 productive tillers. This line showed intermediate field reactions to prevailing diseases.

- PR42592-12-3-1-B-B and PR41951-13-2-1-2-B-B had good AG, fair phenotypic acceptability and very good grain quality.

- PR43374-33-1-2-B (push resistance (PR) of 1.47kgf and PR42529-29-2-1-3-B PR of 1.44kgf) were identified promising lines with lodging resistant lines compared with NSIC Rc240 and PR40589-HY-1 checks varieties.

- One F7 line carrying Xa4, xa5, Xa7, Xa21, Glh14 and tsv1 was identified. The yield component traits of this line, along with other breeding lines with 3-4 BB resistance genes and with Glh14 and/or tsv1, will be evaluated to identify the finest common donor of BB and RTD resistance with high yield potential.

- Eight elite breeding lines were selected with Xa4, xa5, Xa21.

- Selected F7 and elite lines pyramided with 3-4 BB resistance genes were recommended for advancement to preliminary yield trials.

- 335 mutant breeding lines and 33 F2 segregating lines were selected and established for field evaluation.

Hybridization and pedigree nursery for transplanted and direct-seeded irrigated lowland rice varieties

TF padolina, JM Niones

Desirable breeding materials were achieved through continued hybridization, selection, and field screening from large population size resembles greater prospect of selecting promising segregants. The effectiveness of selection depends on the phenotypic evaluation as well as the interaction of the genotypes to different stresses. The basis of selection in the segregating population in bulk method were reactions of genotypes to field stresses and exclusion of undesirable traits such those with high susceptibility to prevailing pests and lodging. Breeding materials in the modified bulk were exposed to zero input to ascertain early generation breeding lines with potential for low input technology. Identified crosses/

derived lines were currently advanced to F4 to F6 generations for further evaluation in the pedigree nursery.

On other hand, direct-seeding is a practical option for rice crop establishment to increase production income because the method reduces labor cost and time. At present, there is only one released variety bred for direct-seeding. Farmers opt to use varieties not bred for direct-seeding because of limited varieties for this method. Selection of parents with traits that counter the negative effect of direct seeded environment (e.g. flooding, lodging, weeds, pests, diseases) is important in the development of direct-seeded varieties superior F1s. Rigid selection base on breeding objectives in the pedigree nurseries result to uniform and acceptable breeding lines for advancement to performance trials.

Highlights:

- A total of 226 crosses were accomplished during the year (Table 13). Single-way cross was used in developing F1 generations which were targeted for high yield and resistance to biotic and abiotic stresses. Of these crosses, 37 were advanced in the Hybrid Population Non-Selection (HPNS) under the Bulk Nursery during the dry season and 119 in the wet season. Discarded crosses were based on poor plant type, high sterility and susceptibility to field pest and diseases.

- There were 76 crosses evaluated in the Hybrid Population Non-Selection. The selection resulted to 19 entries (DS) and 32 entries (WS) advanced to Hybrid Population for Selection (HPS). In the HPS there were 32 crosses evaluated during the dry season and 19 in the wet season, after thorough observation and keen selection, 3,176 derived lines (2256 dl in DS and 920 dl in WS) were advanced to pedigree nursery.

- In the pedigree nursery, a total of 5,893 entries were planted and evaluated during the year. After selection on higher generation there were 74 entries elevated to Advanced Observational Nursery (AON). All other entries on its early generation will be retained due to the inclement weather conditions.

- One hundred Sixty-eight single crosses were generated and will compose the 2015 F1 nursery for direct seeded system.

- Forty-one F1 materials were evaluated and bulk harvested for 2015WS F2 nursery direct seeded system.

- In segregating generations direct seeded system (F2 to F6), 4,725 lines were evaluated. Selection among and within lines were done which generated 2035 lines for advance generation and 26 uniform lines for performance yield trial. Summary of selections per generation is shown in Table 14. Entries in WS (F3-F7) will be re-evaluated in 2016DS due to damage caused by typhoons Kabayan and Lando.

- Two lines with special and desirable traits were nominated in the hybridization block

Table 13. Early generation breeding materials for irrigated lowland transplanted rice during 2015 DS.

NURSERY	Segregating material		Filial Generation	Field Evaluation Result
	2015 DS	2015 WS	2015 DS/WS	for 2016 DS
F_1 NURSERY	70c	156c	F1	75c
HYBRID POPULATION FOR NON-SELECTION (HPNS)	39c	37c	F2	119c
HYBRID POPULATION FOR SELECTION (HPS)	32c	19c	F3-F4	32c
PEDIGREE NURSERY	2,634dl	3259dl	F4-F10	920dl + 3158dl (retained)

Table 14. Selections in pedigree nurseries.

Pedigree Nursery	Entries	Selections
F_2	43	721 plants
F_3	1463	199 Lines (L)
F_4	681	165 L
F_5	249	73 L; 12 Bulk (B)
F_6	156	46L; 14 B

Performance evaluation of transplanted rice breeding lines

TF Padolina, EC Arocena

Advanced uniform lines selected from nurseries will pass through field performance trials. The study evaluates the advanced breeding lines' uniformity, yield and other agronomic characteristics, field reactions to prevailing pests and grain quality for possible multi-location evaluation. Thus, the best entries shall be endorsed to the Multi-Environment Trials (MET) following the sequential evaluation stages and the most promising are eventually nominated to the National Cooperative Trial (NCT).

Highlights:

- There were 270 entries evaluated during the 2015 dry season (DS). Twenty-five entries were elevated to PYT and 46 entries were retained.

- The top 10 AON entries out yielded both checks (PSB Rc82 & PSB Rc18) by 36.5 to 92.47 %. These were 7 to 9 tonners and mostly with maturity similar to PSB Rc18 of 124 days (Figure 7).

- The best line PR43367-17-1-2-1 matured in 124 days; with 112cm plant height, 11 productive tillers, good kernel quality, intermediate field reactions to prevailing diseases and good plant type. This line is a derivative of the cross PR39420-14-10-2-3-1 / TW16.

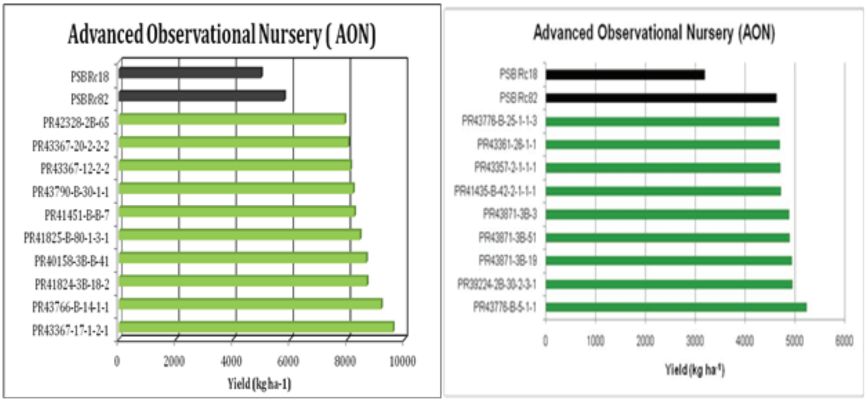
- There were 118 entries evaluated during the WS. The yield performance of the test entries were affected by two typhoons that occurred during the season. Majority of the test entries then were at soft dough and maturity stages, hence, selection was limited. Some entries were identified promising even under such condition. Twenty entries were advanced to PYT with yields ranging from 3.2t/ha to 5.2t/ha. All other entries were retained for further evaluation. The top yielding entries elevated to PYT were also shown in Figure 7.

- Among the 138 entries planted, one entry was elevated to Multi-location Yield Trial (MYT) and simultaneously submitted for seed increase and purification under the study Purification of Outstanding Selection (POS). There were 11 entries elevated in the POS including the MYT candidate. Fifty-six were retained for further evaluation and selection.

- The top 10 PYT entries had exhibited 5.51 to 25.78 % yield advantage over PSB Rc18. Top Entries were 8 to 9 tonners under the medium maturing group ranging 115 to 120 days as compared to PSB Rc18 of 123 days (Figure 8).

- The best line PR42333-2B-43 from the cross HUA 565 / PR37126-PB matured in 125 days; with 107cm plant height, 18 productive tillers, good kernel quality, intermediate field reactions to prevailing diseases and have well to excellent plant type.

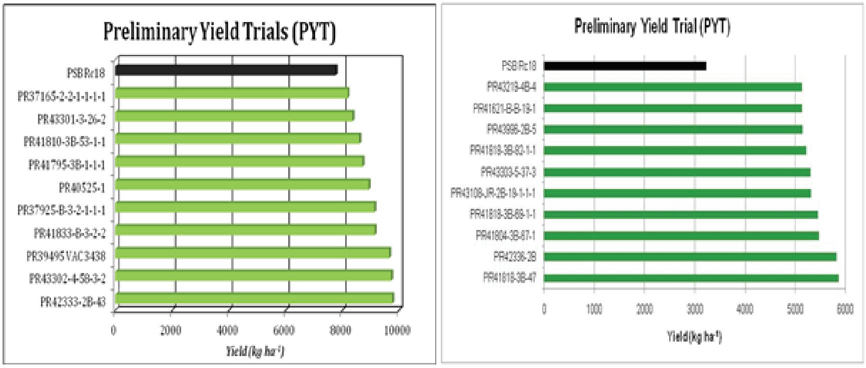
- The WS trial had 150 test entries evaluated. Similarly, the trial was affected by two typhoons that occurred when the entries are most at soft to hard dough and maturity stages. Sterility, poor grain filling, shattering and severe lodging were observed, hence selection was limited. Despite these conditions, 32 test entries were elevated to MYT. Yields of these entries ranged from 3.6t/ha to 5.9t/ha. All other entries were retained for further evaluation. Top yielding entries elevated to MYT during the WS were also shown in Figure 8.



Dry Season

Wet Season

Figure 7. Yield performance of promising entries in the Advanced Observational Nursery (AON) compared to their respective checks, PhilRice CES, 2015.



Dry Season

Wet Season

Figure 8. Yield performance of promising entries in the Preliminary Yield Trials (PYT) compared to their respective check, PhilRice CES, 2015.

Performance evaluation of direct-seeded breeding lines

OE Manangkil

Performance evaluation of uniform lines from pedigree selections determines the yield, reactions to biotic and abiotic stresses, and over-all acceptability of the breeding lines. Component studies such as screenings for anaerobic and lodging tolerance, multi-location trials, pest, diseases, and grain quality evaluations are done in this stage of variety development.

Highlights:

- One hundred forty-four breeding lines were established in ON. Top 10 high yielding entries is shown in Figure 9. Among the ten high yielding entries, PR 42592-12-3-1-B-B and PR 41951-13-2-1-2-B-B had good AG, fair phenotypic acceptability and very good grain quality based on actual parameters tested.

- Six breeding lines were evaluated in National Cooperative Test (NCT) Phase I and 1 in Multi-Adaptation Trial.

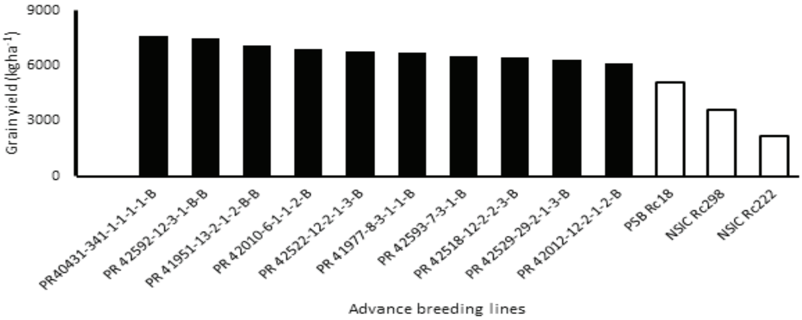


Figure 9. Top 10 high yielding breeding lines in ON.

Multi-location yield trial

EC Arocena

The trial was conducted at PhilRice CES, Bicol, and Negros. At PhilRice CES, 95 test entries with PSB Rc82, NSIC Rc222 and NSIC Rc298 as check varieties for Group I and PSB Rc18 and NSIC Rc240 for Group II were evaluated. A plot size of 5.88 sq. m (1.4m x 4.2m) set in RCBD with three replications was used. Planting distance was set at 20 x 20cm apart and fertilizer rate of 120-60-90kg NPK/ha. Chemical control for weeds, snails and prevalent insects were applied to minimize the damages caused by these pests. Hand weeding and removal of volunteer plants were done during the implementation of the study. Uniformity, heading date, plant height, tillering ability, phenotypic acceptability, field reactions to pests and diseases, and yielding ability were observed.

Highlights:

- During the DS at PhilRice CES, statistical analysis showed that there were significant differences in yield among test entries and replications in Group I and Group II with percent cv of 14.1 and 15.4, respectively. In Group I, most of the test entries were comparable to PSB Rc82 (8837kg/ha), the highest yielding check. However, four test entries PR37942-3B-5-1-2 (8902kg/ha), PR39870-2B-4 (8932kg/ha), PR38963-2B-2-1-1-1 (8996kg/ha), and PR38169-2B-11-2-3-2-2-1 (9378 kg/ha) numerically out-yielded PSB Rc82 with yield advantage (YA) of 0.7 to 6.1%.

- These top four test entries showed significantly higher yield when compared to NSIC Rc222 (7066kg/ha) and with comparable performance to NSIC Rc298 (7800kg/ha). Maturity of the test entries ranged from 111 to 128 DAS with PA scores ranged from 3 to 6. In Group II, one test entry

PR38992 (Fe)-B-1-4-3 (8752kg/ha) numerically out-yielded the highest yielding check variety PSB Rc18 (8707kg/ha) with 0.5% YA.

- For Group II, 37 test entries showed comparable performance to PSB Rc18 while the rest were either significantly lower at 0.5 or 1.0% probability level. Nine test entries including PSB Rc18 (8334 to 8752kg/ha) showed significantly higher yield than NSIC Rc240 (6466kg/ha) while the rest showed comparable performance. Maturity of the test entries ranged from 119 to 137 DAS with PA scores ranged from 3 to 6.

- Some entries in both groups exhibited moderate infection/ infestation to bacterial leaf blight and stemborer. Lodging incidence from 3 to 5 was also observed on some entries.

- The WS trial at CES was affected by typhoon Kabayan (soft dough stage) and typhoon Lando (hard dough to maturity stage), hence, the yielding ability of the entries were affected. In Group I, PSB Rc82 (5669kg/ha) numerically out-yielded all the test entries including the two other check varieties. However, seven test entries: PR38154-B-1-4-2-4-2-1, PR36914-B-9-4-1-8-1-2-1-2 (A), PR38873-2B-24, PR38169-2B-11-2-3-2-2-1, PR40778-5-2-2-3-B, PR39226-2B-55-1-3, and PR38948-B-35-3-4-1 numerically out-yielded the other check varieties NSIC Rc222 (4702kg/ha) and NSIC Rc298 (4867kg/ha)with yields ranged from 4929kg/ha to 5606kg/ha and YA of 1.3 to15.2%. Maturity of the test entries ranged from 107 to 126 DAS with PA scores ranged from 3 to 5.
- In Group II, 19 test entries with yields ranged from 4510kg/ha to 5580kg/ha numerically out-yielded the highest yielding check, NSIC Rc240 (4502kg/ha) with YA ranged from 0.2 to 23.9%. Maturity of the test entries ranged from 107 to 128 DAS with PA scores ranged from 3 to 5.

- Forty-two (42) entries were elevated to MET 0 for irrigated lowland 2016DS. These were selected based on the 2014WS and 2015DS performance.

- In Bicol, the DS trial showed that there were significant differences in yield among test entries and replications in Group I and Group II with percent cv of 19.6% and 21.6%, respectively. In Group I, 10 test entries with yields ranged from 5567kg/ha to 6467kg/ha numerically out-yielded the highest yielding check variety PSB Rc298 (4400kg/ha) with YA of 27 to 47%. Two test entries, PR38963-(Fe)-B-5-1-3 (6467kg/ha) and PR38963-2B-2-1-1-1-1 (6400kg/ha) showed significantly higher yield than PSB Rc82 (3833kg/ha). Maturity of the test entries ranged from 117 to 132 DAS. Some entries were observed with moderate stemborer infestation.

- In Group II, 10 test entries with yield ranged from 4267kg/ha to 5367kg/ha numerically out-yielded the highest yielding check, PSB Rc18 (3267kg/ha) with 31% to 64% YA. Maturity of the test entries ranged from 120 to 132 DAS. Some entries also exhibited moderate reaction to stemborer infestation.

- Problems encountered during the conduct of the experiment were low germination which resulted to insufficient seedlings, and occurrence of typhoon at seedling stage before transplanting which resulted to missing entries.

- During the WS, similarly, the trial was affected by typhoons which affected the yield performance of the entries. Statistical analysis showed significant differences in yield among replications in Group I and Group II with percent cv of 19.1 and 23.9%, respectively. In Group I, 16 test entries numerically out-yielded PSB Rc82 (2976kg/ha) with yields ranged from 3018kg/ha to 3647kg/ha with YA ranged from 1.4 to 22.6%. Maturity of the test entries ranged from 108 to 116 days after seeding. In Group II, seven test entries (PR40526-13-2-1-1, PR38963-2B-2-1-1-1, PR37912-1B-3-1-1, PR40526-13-2-2-3, PR40518-7-6-1, PR43345-B-32-1-1, and PR37557-3B-11-1-1) numerically out-yielded PSB Rc18 (2834kg/ha) with yields ranged from 2849kg/ha to 3397kg/ha and with YA ranged from 0.5 to 19.9%. Maturity of the test entries ranged from 109 to 116 days after seeding.

- In Negros, statistical analysis for DS data showed that there were significant differences in yield among test entries in Group I and Group II with percent cv of 32.8 and 30.6%, respectively. In Group I, 10 test entries with yields ranged from 4949kg/ha to 6750kg/ha numerically out-yielded the highest yielding check, NSIC Rc298 (4515 kg/ha) with YA of 9.6 to 49.5%. Maturity of the test entries ranged from 111 to 116 DAS. In Group II, three test entries (PR40517-17-6-5-1, PR38963-2B-2-1-1-1, and PR40539-B-B-30-1-1) with yields ranged from 5817kg/ha to 6800kg/ha numerically out-yielded the highest yielding check, PSB Rc18 (5421kg/ha) with 7.3 to 25.4% YA. Maturity of the test entries ranged from 110 to 116 DAS.

- Overall DS performance across three locations in Group I showed that there were 20 test entries that numerically out-yielded the highest yielding check, PSB Rc82 (5582 kg/ha) with yields ranged from 5855 kg/ha to 6979 kg/ha and with YA ranged from 5% to 25%. In Group II, the 10 test entries that numerically out-yielded the highest yielding check, PSB Rc18 (5798 kg/ha) had yields ranged from 6144 kg/ha to 6576 kg/ha and with YA ranged from 6.0% to 13.4%. There were 10 promising lines identified which performed best in at least two locations with yields ranged from 5000kg/ha to 9378kg/ha (Table 15).

Table 15. Top 10 yield performance of advance breeding lines at least two locations under MYT, 2015DS.

DESIGNATION	PhilRice-CES		PhilRice-BICOL		PhilRice-NEGROS	
	Yield (kg/ha)	Rank	Yield (kg/ha)	Rank	Yield (kg/ha)	Rank
GROUP I						
PR38036-2B-2-2-1-3-3-2	7371	33	5567	10	5533	7
PR38963-2B-2-1-1-1	8996	2	5567	11	6375	2
PR381698-2B-3-1-3-1-1-2-1	7191	38	5900	7	5929	4
PR38963(Fe)-B-5-1-3	7912	21	6467	1	6047	3
PR38963-(Fe)-B-5-4-2	7430	32	6267	4	5654	5
PR38169-2B-11-2-3-2-2-1	9378	1	5767	9	2956	42
PR38963-2B-2-1-1-1-1	5769	48	6400	2	5000	9
PSB Rc82	8837	5	3833	42	4077	22
NSIC Rc222	7066	41	4167	38	4011	24
NSIC Rc298	7800	23	4400	35	4515	16
GROUP II						
PR39206-2B-47-1-2-2	8454	6	5000	7	4531	17
PR40517-17-6-5-1	7349	29	5267	3	5817	3
PR38963-2B-2-1-1-1	7441	26	5000	5	6014	2
PSB Rc18	8707	2	3267	27	5421	4
NSIC Rc240	6466	44	-	-	3885	32

Early seedling vigor, anaerobic tolerance and lodging resistance evaluation

OE Manangkil

Subsurface seeding or seeding under soil or water (anaerobic condition) could categorically control weeds and pests problems in direct seeded system. Varieties that are intolerant to anaerobic conditions and have low seedling vigor would result in high seedling mortality owing to low germination and slow seedling growth. Susceptibility to lodging at flowering to maturity affects yield and grain quality.

In line development, evaluations of anaerobic tolerance and early seedling vigor are done in F2 and in ON. Tolerant F2 and ON lines are advanced to pedigree nurseries or nominated to yield trials and hybridization block. Lodging resistance is done in advance breeding lines. Anaerobic tolerant and lodging resistant lines are also included in crossing works.

Highlights:

- Advanced breeding lines and F2 populations were evaluated for anaerobic germination tolerance and seedling vigor. Forty-three F2 populations and 49 breeding lines from ON were dry seeded with 5cm water level for 10 days to evaluate anaerobic germination and early seedling vigor. Six populations and 3 breeding lines had excellent anaerobic germination and seedling vigor while 5 populations and breeding lines had good rating.

- One hundred forty-four breeding lines and checks in the ON were measured for pushing resistance (PR) using push gauge. Comparing with checks NSIC Rc240 and PR40589-HY-1, PR43374-33-1-2-B and PR42529-29-2-1-3-B were identified promising lodging resistant lines with PR of 1.47 and 1.44kgf respectively.

Marker-assisted selection for pest and disease resistance genes in inbred variety development

AA Dela Cruz

Recognizing the economic importance of bacterial leaf blight (BB) and rice tungro disease (RTD), the Irrigated Lowland Breeding Program of PhilRice incorporated routine marker-assisted selection (MAS) to facilitate introgression and pyramiding of various BB and RTD resistance genes into promising PhilRice breeding lines and selected popular rice varieties. Molecular markers for BB resistance genes (Xa4, xa5, Xa7 and Xa21) and RTD resistance locus/gene (Glh14, GLH resistance locus; tsv1, RTSV resistance) are used to facilitate selection of important breeding materials. These markers have been proven effective in increasing selection efficiency most especially for traits that are simply inherited. The utilization of high-yielding rice varieties with durable pest and disease resistance will eventually help prevent crop failures and alleviate rice productivity, particularly in endemic areas, by providing opportunity for effective disease control.

Highlights:

- Table 16 shows the composition of the breeding materials established in 2015DS for marker-assisted selection and the number of plants/lines selected based on presence of 3-4 BB resistance genes, Glh14 and/or tsv1.

- Among the 250 F2 plants generated, 65 were pyramided with 3-4 BB resistance genes: 8 with Xa4, xa5, Xa7, Xa21; 56 with Xa4, xa5, Xa21; 1 with Xa4, Xa7, and Xa21.

- Among the 23 F3 lines, 18 lines were pyramided with 3 BB resistance gene: 4 with Xa4,xa5,Xa7; 5 with Xa4,xa5,Xa21; 9 lines with Xa4,Xa7,Xa21.

- Among the 267 F5 lines, 12 were selected with 3 BB resistance genes: 8 with Xa4,xa5,Xa7; 3 with Xa4,xa5,Xa21; 1 with Xa5,Xa7,Xa21; 1 with Xa4,xa5,Xa7, Xa21.

- Among the 51 F6 lines, 4 were selected with Xa4, xa5, Xa21 while 5 were with Xa4, Xa7, and Xa21.

- Among the 28 F7 lines, 4 were selected with 4 BB resistance genes, while 22 have various combinations of 3 BB resistance genes.

- Among the 91 elite lines, 8 were selected with Xa4, xa5, Xa21.

- Selected F7 and elite lines pyramided with 3-4 BB resistance genes were recommended for advancement to preliminary yield trials.

- 1 F7 line carrying Xa4, xa5, Xa7, Xa21, Glh14 and tsv1 was identified. The yield component traits of this line, along with other breeding lines with 3-4 BB resistance genes and with Glh14 and/or tsv1, will be evaluated to identify the finest common donor of BB and RTD resistance with high yield potential.

- In 2015WS, additional F2 plants derived from 4 elite lines (1 for direct seeding and 3 for transplanting) were pyramided with 3 BB resistance genes, Glh14 and/or tsv1.

- Important breeding lines were purified and seed-increased in 2015WS.

Table 16. Important rice breeding lines selected through marker-assisted selection (MAS), 2015DS.

Pedigree Nursery	Total number of lines	*Xa4,xa5,Xa7, Xa21, Glh14,tsv1*	*Xa4,xa5,Xa7, Xa21*	*Xa4,xa5,Xa7*	*Xa4,xa5,Xa21*	*Xa4,Xa7, Xa21*	*xa5,Xa7,Xa21*	**Total number of lines***
F_2	250**	0	8	0	56	1	0	**65****
F_3	23	0	0	4	5	9	0	**18**
F_5	267	0	1	8	3	0	1	**13**
F_6	51	0	0	0	4	5	0	**9**
F_7	28	1	4	5	5	12	0	**27**
Elite	91	0	0	0	8	0	0	**8**
Total	**710**	**1**	**10**	**17**	**62**	**27**	**0**	**117**

Development of next generation rice plant type to break yield plateau

JM Niones, SE Abdula, AY Cantila and JL Balos

Increasing productivity is always one of the main goal of rice breeding program. Rice varieties with higher yield potential are necessary to meet the incresing demands of the population. Several approaches are being explored to break the yield barrier. These include development of a new plant type (NPT) with low tillering capacity and large panicles from tropical japonica germplasm and the supercharged C4 rice. But until this time, the potential of these approaches have not been realized. Another approach is the exploration of hybrid vigor (hybrid rice) with progress in increasing yield up to 15% relative to the inbred rice. Seed production of F1 hybrid seeds however, is still very challenging (low yield). With these approaches, the yield plateau remains the same for four decade. Developing next generation rice varieties with yield potential of 15 to 20t/ha (or yield advantage of 40 to 70%), is therefore needed. With the present plant architecture of most breeding program which is dwarf to semi-dwarf and early maturing, this yield could not be achieved given the thermodynamic and biological limits of the crop. To increase the yield potential further, a conceptualized next generation plant to raise the harvest index to around 0.6 and the biomass to 30t/ha. Such plant type is expected to have a yield potential of about 15t/ha. Biomass can be increased by developing plants with sturdier stems, a plant height of 1.2 to 1.8 meter, and erect leaves to accommodate more photosynthesis.

The general objective of the study is to develop inbred rice lines with yield advantage of 50 to 100% relative to the current highest yield of 10t/ha (as reference check). Specifically, it aims to evaluate potential germplasm with more than 500 spikelets per panicle and develop segregating plants with architecture height of 1.2 to 1.8 meters, erect leaves and resilient to major biotic and abiotic condition for the irrigated ecosystems.

Highlights:

- 335 Mutants and 33 F2 entries were established in the field for evaluation.
- Two batches of plants (tradvars and Inbreed) were planted in pots in the screen house for this season's crossing, with 2 weeks gap.
- 240 F1 plants were planted in the screen house along with its female parent for phenotypic evaluation.
- The development of lines was through Gamma and Colchicine (chromosome doubling or polyploidy) and extensive conventional crossing. The initial selection criteria were based on plants with height range from 1.2 to 1.8m, productive tillers of 10 tillers or more and having semi-erect to erect leaves for the entries totaling to 720 (Figure 10). A total of 113 plants were selected for further selection and trials on 2017.
- Entries of 250GY gave above 20 productive tillers (PT) such as entries 273 with 23, 512 with 27, 511 with 24, 290 with 31 and 252 with 30. In the same way, ten plants were recorded with 140cm or much taller while having 10 PT or more. In all, 40 mutant lines were selected along with erect to semi-erect leaf orientation, 133.6cm mean plant height (PH) (14 plants with ≤150cm), 12 mean PT (8 plants with ≤19 tillers).
- For conventional breeding derived lines, 56 plants were selected with 131.2cm mean PH, 11 mean PT at F3 generation while 17 plants with 127cm mean PH and 9 mean at F4 generation. These lines were planted December 2015 and pre-selection is still ongoing.

Figure 10. Seven hundred twenty (720) entries planted under Midsayap condition, 2015 DS.

III. Hybrid Rice Breeding and Genetics

Project Leader: JD Caguiat

The success of hybrid rice technology lies mainly in the development of high yielding varieties adapted to local conditions. Between 1994 and 2011, the National Seed Industry Council has approved a total of 44 hybrid varieties for commercial cultivation in the Philippines. Seventeen of these varieties were bred and developed by the public sector, of which six were bred by PhilRice together with its partners UPLB and PhilSCAT. To date, PhilRice breeders at its Central Experiment Station, and branch stations in Los Baños (in collaboration with UPLB) and San Mateo, have maintained specialized breeding activities despite the steady rise of private sector participation in this particular enterprise.

The continuous development of high-yielding hybrid varieties that are resistant to pests and diseases and possesses excellent grain qualities is essential to keep up with the increasing demand for rice and the changing environment. As such, there is a need for a strong national public breeding and research on hybrid rice.

The main purpose of this project is to increase rice productivity in the irrigated lowland ecosystem. This project covers the development of parent lines and F1 hybrids, breeding methodology and seed production research, and screening and testing of hybrids in various target environments.

The project was composed of 11 studies namely; Development of hybrid parent lines (PBD-006-001), Evaluation of experimental hybrids and prospecting of new maintainer and restorer lines (PBD-006-002), Performance tests of experimental hybrids (PBD-006-003), Seed production of experimental hybrids (PBD-006-004), Incorporating stress resistance genes through molecular markers (PBD-006-005), Generating useful variation in hybrid parent lines through induced mutagenesis (PBD-006-006), Screening and evaluation of parent lines and hybrids (PBD-006-007), Yield prediction of single cross hybrids and combining ability analysis of parent lines (PBD-006-008), Genetic improvement of parent lines for abiotic stress (PBD-006-009), Development of parent lines and hybrids at PhilRice Isabela (PBD-006-010), Identification and use of wide compatibility genes (s5n) for enhancing heterosis (PBD-006-011).

In 2015, among the project`s accomplishments for the development and improvement of parent lines include ten usable developed maintainer (CMS) and restorer lines and 10 prospected potential parent lines; three BC1F1, five BC1F2, and four BC2F1 populations developed and advanced with Xa23 gene for BLB resistance. We have also generated four experimental CMS lines with high outcrosing rate, five lines with exerted stigma, one maintainer and one restorer line with salinity tolerance. For generation and screening of new parent lines and hybrids, 16 parent lines were subjected to in-vitro mutagenesis (IVM), gamma irradiation and anther culture while 90 lines were assembled and screened for biotic tolerance (blast, tungro, BB, BPH, and GLH) and ten lines for drought tolerance. The combining ability (CA) estimates of 19 parents and 48 hybrids were analyzed and four clusters of heterotic block of elite parent lines were determined. For the development and seed production of experimental and advanced elite hybrids, two hybrids with ≥15% standard heterosis entered in the NCT, 179 promising hybrids selected from testcross nursery (TCN), observational nursery (ON), preliminary yield trial (PYT), multi-location yield trial (MYT) out of 1,234 entries evaluated, 412 A×B paired crosses produced for CMS nucleus, 100kg CMS breeder/foundation seeds, and 50kg F1 seeds produced.

Development of hybrid parent lines

RA Millas, MSF Ablaza, , KA Garcia, MM Rosario, VP Luciano, FP Waing, and JD Caguiat

One of the challenges in hybrid breeding is the selection, development and improvement of suitable parental lines that can be used for developing hybrids. In hybrid rice breeding, the cytoplasmic male sterile (CMS) line is considered as the heart in the development of F1 hybrids because failure in purity of this will result to poor hybrid. Therefore, CMS line development is a very essential component in the development of hybrid rice. Because of its great role and importance, diverse CMS lines with good qualitative and quantitative traits must be developed. Introduced CMS lines often are not adapted to local conditions, with very low resistance to biotic stresses and poor grain quality.

Maintainer and restorer lines are very essential components in the development of hybrid rice as well. Without maintainer and restorer lines, multiplication of CMS lines and production of F1 are not possible. Continuous research on the identification of inbred cultivars that can either maintain the sterility or restore the fertility of CMS lines plays an important role in developing high-yielding germplasm pools. Therefore, there is a need to develop new maintainer and restorer lines and improve existing ones.

The study aimed to: (1) develop new and diverse hybrid parent lines, male sterile lines (A- and S- lines), and pollen parents (R- and P-lines); (2) improve morpho-agronomic characteristics of parent lines; and (3) convert potential B lines into new A lines and utilize potential R lines to further enhance the restorer line genepool of hybrid breeding program of PhilRice

Highlights:

- Established in the restorer line improvement and development nursery in 2015 were 2734 lines for the dry season and 1852 for the wet season from F1 to F8. Bases for selection were good phenotypic acceptability and agro-morphological characteristics. Lines in the F8 generation were evaluated for grain yield potential during the dry season. A total of 58 test entries including two check varieties, namely PSB Rc82 and PSB Rc18, were established following Alpha lattice design. Grain yield estimates (kg ha-1) ranged from 727.47 (PR36641HY-8-3-12-1-2-3) to 7,310.98 (PR36622HY-5-1-3-3-1-3). The checks obtained 5,461.43 (PSB Rc82) and 4,292.84 (PSB Rc18). The top 20% selection with yields ranging from 5,007.43 to 7,310.98 will be included in the Source Nursery for development of experimental hybrids in the succeeding season.

- The maintainer line nursery was composed of 23 lines for improvement during the dry season, 24 lines for the wet season, and 81 selected lines with desirable morphological traits. Through hybridization, 63 new BxB crosses were generated during the dry season and 74 new crosses during the wet season. Sixty three F1 populations, 17 F2 populations, 16 F3 entries, 142 F4 entries, and 92 F5 entries were selected and established based on good phenotypic acceptability and response to naturally occurring pests and diseases during the wet season. Eight F5 and twelve F6 populations will be subjected to the maintainer line yield trial in the next cropping season. Twelve F7 cross combinations were testcrossed to CMS lines for conversion.

- Twelve F6 and 12 F7 lines were established in the maintainer line yield trial with two check varieties; PSB Rc18 and PSB Rc82. The trials were set-up in 2 sq.m. plots in augmented design for F6 lines and RCBD with three replications for F7 lines. Among the F6 entries, only one line designated as PR46164-HY-5-1-1-1 consistently out-yielded both checks by 5.46% (PSB Rc18) and 38.79% (PSB Rc82). For the F7 trial, none yielded higher than PSB Rc18. However, PR45969-HY-18-1-1-1-1 significantly out-yielded PSB Rc82 by 63.26%. The trial set-up during the wet season was devastated by typhoon Lando, hence data was invalid. The trial will be repeated in the next cropping season.

- For CMS conversion, 37 inbred lines with the desired traits were assembled during the dry season and 56 lines during the wet season. These potential maintainer lines were obtained from plant selections from elite breeding materials of the maintainer development nursery. Thirty three lines were used for re-testcrossing to CMS lines and included in the backcross nursery to further evaluate their maintaining ability. Boots were collected for pollen sterility evaluation under the microscope before backcrossing. Pollen sterility of the F1 was evaluated in the following season. During the wet season, 21 plants from 11 F1 entries, 14 plants from 23 BC1F1 entries, 30 plants from 41 BC3F1, and 43 plants from 71 BC4F1 entries were found to be completely sterile and will be further evaluated. One BC6F1 line, PR46131HY, will be characterized according to PVP standards (Table 18). Progeny lines are to be repeatedly backcrossed up to the fifth generation. New CMS lines with stable sterility and good agronomic characters will then be declared and used as new testers in the Source Nursery.

- A recombinant inbred population, PR47221-G038 F6 (PR34641-2B-19-1-1/Leuang IRGC 22761), with 200 lines was established in replicated yield trial at Philice CES for an initial yield trial evaluation. Phenotypic data such as panicles number per plant, grain yield (harvested from 5 hills) and plant height was gathered. Grain yield data of PR47221-G038 ranged from 5.5 to 9.8 t/ha with an average yield of 7.2t/ha. In addition, a new set of recombinant inbred populations: G066 F2 (NSIC Rc240/NSIC Rc238), G073 F2 (Piling-piling/NSIC Rc240) and intermated G021 was also established.

- The consistent top performing PR40614-AC, PR40613-AB, PR40615-AD, PR47236-GB-13, PR47239-G028, PR47222-G007, PR47234-G019, PR47238-G027 and

PR40853 lines were selected and further evaluated in replicated yield trials. Phenotypic data such as panicles number per plant, grain yield and plant height were gathered. Grain yield data ranged from 5.0 to 8.7t/ha with an average yield of 7.2t/ha. The predicted yield data of the top performing lines with genotype considered as random effects factor, and replication and block considered as fixed effects factor are shown in Table 19. Sample entry is shown in Figure 11.

- An initial replicated yield trial evaluation was done in 100 F8 lines composed of six populations denoted as G015-G020. Phenotypic data such as panicles number per plant, grain yield (harvested from 5 hills) and plant height was gathered. Grain yield data in DS ranged from 3.3 to 9.3t/ha with an average yield of 7.0 t/ha. The predicted yield data of the top performing F8 lines for both seasons with genotype considered as random effects factor, and replication and block considered as fixed effects factor are shown in Table 20. In 2015WS, a replicated yield trial was done in the 100 top performing lines selected based on 2015 DS yield performance and phenotypic acceptability data. Grain yield data ranged from 1.8 to 5.0 t/ha with an average yield of 3.3t/ha. As observed, MD17-7-3-3-1-1 line top performed in both dry and wet season. This will be seed increased and will be advanced for MET-O trial.

- Field establishment of various selected populations were done. Selections based on phenotypic acceptability were also done for the F3 to F7 populations. The selected lines were comprised of: 33 populations in F3 generation; four populations in F4 generation denoted as G064, G070, G090, and IG006; six populations in F5 generation denoted as G054, G055, G059, G060, G061, and G068; five populations in F6 generation denoted as G044, G046, G047, G051, and G053; seven populations in F7 generation denoted as G032, G035, G036, G037, G039, G040, and G042. Selection was carried out based on phenotypic acceptability among populations. The number of lines selected per generation was 448 for F3, 95 for F4, 127 for F5 and 58 for F6. The per-se performance of prospected restorer lines ranged from 5667.99 – 8920.76 kg/ha with yield advantage of 6.66 – 67.86% compared to the checks, PSB Rc82 (5314.30kg/ha) and PSB Rc18 (3466.90 kg/ha) (Table 21). These selected restorer lines will be further evaluated in the testcross nursery and to be forwarded to the seed production for observational nursery.

Table 17. Yield of advanced restorer lines and checks in the male parent yield trial nursery.

Designation	Grain yield (kg/ha)
PR36622HY-5-1-3-3-1-3	7310.98
PR43304HY-1-2-3-1-3-2	6409.84
PR36502HY-1-1-8-1-2-2	6111.12
PR36622HY-5-1-3-2-1-1	5820.53
PR43315HY-2-1-3-1-1-3	5732.69
PR36642HY-8-4-5-2-3-3	5649.21
PR43324HY-1-3-3-3-2-1	5411.13
PR43315HY-2-1-1-1-1-2	5408.20
PR36502HY-1-1-8-1-1-4	5243.39
PR43324HY-1-3-3-2-1-3	5206.69
PR36620C-HY-4-1-9-1-1-1	5007.43
PR36620C-HY-4-1-9-1-2-1	4984.21
PR43324HY-1-3-3-1-2-3	4962.27
PR36622HY-5-1-3-3-3-3	4933.60
PR36502HY-1-1-8-1-3-2	4909.05
PR36502HY-1-1-8-1-1-2	4903.61
PR42437HY-53-1-1-1-1-2	4890.25
PR42437HY-44-1-1-2-1-2	4816.58
PR36620C-HY-4-1-9-1-2-3	4768.17
PR36642HY-8-4-5-2-3-1	4715.41
PR36502HY-1-1-8-1-3-3	4686.90
PR43304HY-1-2-3-1-3-3	4674.86
PR36502HY-1-1-8-1-2-1	4623.47
PR42444HY-4-1-2-1-2-3	4569.86
PR43324HY-1-3-3-1-2-1	4544.71
PR36622HY-5-1-3-3-2-1	4496.17
PR43324HY-1-3-3-2-3-3	4361.32
PR43324HY-1-3-3-1-1-3	4303.12
PSB Rc18	4292.84
PSB Rc82	5461.43

Table 18. Cross combination of entries in the CMS conversion nursery.

Generation	Designation	2015 DS	2015 WS		2016 DS
		Entries Evaluated	Entries Evaluated	Crosses Generated	Plants Selected
F1	PR48305-HY		2	1	1
	PR48307-HY		3	2	2
	PR48308-HY		2	14	14
	PR48309-HY		2	2	2
	PR48310-HY		1	1	1
	PR48312-HY		1	1	1
BC1F1	PR47620-HY	4	12	11	11
	PR47621-HY	3	6	1	1
	PR47622-HY	2	5	2	2
BC3F1	PR46622-HY	3	16	35	12
	PR46619-HY	6	25	81	18
BC4F1	PR46157-HY	19	25	6	6
	PR46155-HY	35	28	85	19
	PR46147-HY	12	18	48	18
BC6F1	PR46131-HY	6	22	77	for PVP
TOTAL		90	168	367	108

Table 19. Predicted yield performance of the top performing GYT lines evaluated in replicated yield trials at PhilRice Central Experiment Station during 2015 DS.

Designation	Grain yield (kg/ha)
PR47236-GB-13-16-1-1-1	8,706.23
PR40614-AC3-4-1	8,628.05
PR40615-AD-10-16	8,612.65
PR40614-AC8-10-1	8,362.97
PR47239-G028-18-1-2	8,150.67
PR40614-AC1-9-2	8,144.33
PR40614-AC8-3-3	8,140.22
PR40614-AC3-5-1	8,087.76
PR47226-G011-10-2-3-1	8,086.48
PR40614-AC5-11-1	8,082.93
PR47234-G019-1-2-1-1	8,034.46
PR40614-AC1-5-1	7,999.95
PR40613-AB-58	7,996.90
PR47222-G007-7-3-3-1	7,989.68
PR40614-AC3-1-1	7,975.02
PR40615-AD-10-14	7,971.02
PR40613-AB-98	7,870.97
PR40615-AD10-1-2	7,837.41
PR40615-AD-4-18	7,778.18
PR40615-AD4-9-7	7,757.21
PR40614-AC1-6-3	7,753.75
PR47234-G019-9-3-1-1	7,744.84
PR40615-AD-4-3	7,714.60
PR47234-G019-20-1-3-1	7,692.40
PR40614-AC4-8-2	7,656.39
PR47238-G027-56-1-2	7,615.61
PR40615-AD-4-7	7,591.12
PR40614-AC8-7-1	7,548.45
PR47222-G007-3-3-3-1	7,548.06
PR47237-MD1-2-2-3-1	7,542.80
PR40853-7-2-2	7,542.07
PR40629-G021-113	7,521.97
PR40613-AB-66	7,512.20
PR40614-AC7-1-1	7,503.82
PR40614-AC5-4-2	7,498.90
PR40615-AD-10-11	7,485.32
PR40615-AD4-5-8	7,471.25
NSIC Rc238	7,979.07
NSIC Rc240	7,975.96
NSIC Rc222	6,813.75

Table 20. Predicted yield performance of the top performing GF8 lines evaluated in replicated yield trials at PhilRice Central Experiment Station during 2015 DS.

Designation	Grain yield (kg/ha)
PR47237-MD17-7-3-3-1-1	9,330.17
PR47234-G019-1-2-2-1-2	9,123.07
PR47237-MD14-1-2-2-1-1	8,741.20
PR47237-MD23-4-3-1-2-1	8,686.44
PR47234-G019-16-3-1-1-1	8,674.39
PR47234-G019-12-1-1-1-2	8,642.45
PR47234-G019-4-2-1-1-1	8,525.52
PR47237-MD12-3-1-1-1-1	8,451.69
PR47234-G019-12-3-1-1-1	8,422.56
PR47236-GB-8-33-1-2-1-2	8,369.21
PR47234-G019-12-1-1-1-1	8,312.63
PR47232-G017-44-1-1-1-1	8,299.75
PR47234-G019-19-2-1-1-1	8,252.87
PR47233-G018-15-1-1-1-1	8,239.67
PR47237-MD23-6-3-1-1-1	8,135.09
PR47234-G019-1-2-2-1-1	8,059.84
PR47236-GB-13-16-1-1-1-1	8,054.49
PR47234-G019-1-3-1-1-1	8,031.63
PR47237-MD12-3-3-1-1-1	8,017.15
PR47234-G019-20-1-2-1-1	7,949.79
PR47235-G020-13-3-1-1-1	7,921.12

Table 20. Predicted yield performance of the top performing GF8 lines evaluated in replicated yield trials at PhilRice Central Experiment Station during 2015 DS. (Con't)

PR47233-G018-4-2-1-1-1	7,817.32
PR47233-G018-10-1-1-1-3	7,788.56
PR47236-GB-10-24-1-2-1-1	7,725.25
PR47234-G019-20-1-3-1-1	7,687.01
PR47233-G018-14-1-2-1-2	7,595.30
PR47237-MD12-3-1-1-1-2	7,496.86
PR47236-GB-10-24-1-3-1-1	7,486.90
PR47234-G019-19-2-1-1-2	7,460.17
PR47234-G019-18-3-1-1-1	7,435.41
PR47234-G019-1-2-1-1-1	7,393.52
PR47237-MD23-4-3-3-1-2	7,364.29
NSIC Rc222	8,594.70
NSIC Rc240	7,126.00
NSIC Rc216	7,116.93
PSB Rc82	5,834.07

Table 21. Per-se performance of prospected restorer lines of three-line hybrids in the testcross nursery, PhilRice-CES, 2015 WS.

	Restorer lines	Grain yield (kg/ha)	Yield advantage (%)	
			PSB Rc82	PSB Rc18
1	TCN 150211	8920.76	67.86	157.31
2	TCN 150221	8077.18	51.99	132.98
3	TCN 150024	7706.78	45.02	122.30
4	TCN 150696	7612.65	43.25	119.58
5	TCN 150245	7274.54	36.89	109.83
6	TCN 150188	7205.67	35.59	107.84
7	TCN 150267	7200.22	35.49	107.68
8	TCN 150222	6957.09	30.91	100.67
9	TCN 150103	6844.47	28.79	97.42
10	TCN 150194	6829.47	28.51	96.99
11	TCN 150217	6813.43	28.21	96.53
12	TCN 150695	6798.75	27.93	96.10
13	TCN 150292	6627.91	24.72	91.18
14	TCN 150077	6616.40	24.50	90.84
15	TCN 150469	6567.61	23.58	89.44
16	TCN 150298	6477.22	21.88	86.83
17	TCN 150449	6418.60	20.78	85.14
18	TCN 150178	6367.29	19.81	83.66
19	TCN 150084	6302.35	18.59	81.79
20	TCN 150358	6226.74	17.17	79.61
21	TCN 150257	6114.04	15.05	76.35
22	TCN 150256	6088.08	14.56	75.61
23	TCN 150699	6052.44	13.89	74.58
24	TCN 150693	6048.00	13.81	74.45
25	TCN 150299	6036.28	13.59	74.11
26	TCN 150004	5862.71	10.32	69.11
27	TCN 150625	5782.73	8.81	66.80
28	TCN 150065	5746.47	8.13	65.75
29	TCN 150303	5733.24	7.88	65.37
30	TCN 150058	5667.99	6.66	63.49
	PSB Rc18	3466.90		
	PSB Rc82	5314.30		

Figure 11. Sample GYT entries for grain yield trial evaluation in replicated alpha-lattice design (PhilRice CES, 2015 DS).

Development of experimental hybrids and prospecting of new maintainer and restorer lines

VP Luciano, MM Rosario, MSF Ablaza, JD Caguiat

The three-line system in hybrid breeding is a key approach to help attain rice self-sufficiency in the country. Hybrid rice is one technology with a lot of promise to contribute greatly to this goal because of its 15 to 20% yield advantage over inbreds. Heterotic hybrids also offer high income opportunities to the farmers. This is either through F1 cultivation or parental seed production. The success of hybrid rice breeding depends to a great extent on the quality and diversity of elite lines used as parents in developing new hybrids. New approaches such as the use of excellent inbreds and promising lines from Optimum Plant Morphology (OPM), Tropical Japonica (TJ) breeding, and doubled haploid (DH), are essential in discovering promising new hybrid combinations.

The main goal of the study was to identify superior F1 combinations as well as to determine the combining ability of newly developed parent lines. Specifically, the study aimed to (1) identify potential maintainer lines (B) or restorer lines (R) from the early generation and elite breeding lines of irrigated lowland inbred rice breeding project, (2) to develop F1 hybrids from a cross between cytoplasmic male sterile (CMS) lines, DH, OPM and TJ lines from the inbred rice breeding project, (3) to convert potential B lines into new A lines and utilize potential R lines in further enhancing the restorer line genepool of hybrid breeding program of PhilRice.

Highlights:

- There were 80 (2015 DS) and 124 parent lines (2015 WS) composed of entries generated from double haploids (DH), tropical japonica (TJ), optimized plant morphology (OPM), marker assisted recurrent selection (MARS) and hybrid marker assisted selection (HMAS) established in the source nursery. These parent lines were crossed with seven CMS lines (PR2A, IR68897A, IR58025A, PR15A, PRH1A, PR28A and PR20A) and one TGMS line (TG101S) generating 624 F1 during 2015 DS and 444 F1 during 2015 WS. Generated F1 hybrid entries including parent lines were evaluated in the testcross nursery (TCN) (Figure 12).

- Among the experimental hybrids evaluated in the TCN during 2015 DS, 20 entries (TCN 333, TCN 412, TCN 535, TCN 493, TCN 411, TCN 545, TCN 426, TCN 526, TCN 534, TCN 129, TCN 221, TCN 220, TCN 42, TCN 290, TCN 446, TCN 441, TCN 37, TCN 516, TCN 487 and TCN 289) showed 31.08% to 177.67% yield advantage against the check varieties (Mestiso 19, Mestiso 20, PSB Rc18 and PSB Rc82). The best combination was PR20A x TCN329 with 95.29 to 177.67% yield advantage over the four checks varieties (Table 22). Evaluated in the TCN during 2015 WS, 20 F1 (TCN 150211, TCN 150221, TCN 150024, TCN 150696, TCN 150245, TCN 150188, TCN 150267, TCN 150222, TCN 150103, TCN 150194, TCN 150217, TCN 150695, TCN 150292, TCN 150077, TCN 150469, TCN 150298, TCN 150449, TCN 150178, TCN 150084 and TCN 150358) showed 17.17% to 157.31% yield advantage over the check varieties (Mestizo 1, Mestiso 19, PSB Rc18, PSB Rc82).

- To evaluate the performance of new improved (with BLB resistance) CMS lines, fifteen potential restorer lines were testcrossed with IR68897A, and improved IR68897A (PR28A, PR29A and PR30A). Using improved CMS lines, PR30A x PR35749-HY-R has the highest yield of 13955.94 followed by PR28A x PR31559-AR32-4-3-2R with 14078.75 kg/ha yield, and PR29A x Matatag2-25Kr-263-4-23R with 13404.07 kg/ha yield. Among entries testcrossed using the original CMS line, the cross combination IR68897A x PR31559-AR32-4-3-2R has the highest yield of 13141.82 kg/ha (Table 23).

- Among the top high yielding male parents, 19 entries were completely crossed with 8 CMS lines in 2015WS. PR2A has the highest testcross variance of 10097529.66 followed by PR15A with 5421585.77. TGMS 71 has the highest tester means of 5210.04 followed by PR2A with 41332.90. Among the testers used, PR2A showed the highest testcross variance and with the second highest tester means which implies that it has good combining ability and a potential female parent to be used in testcrossing.

- There were 40 (2015 DS) and 45 (2015 WS) parent lines identified as potential restorer while 30 lines (2015 DS) and 71 (2015 WS) identified as potential maintainer lines. The potential restorer lines will be advanced to restorer line development for further evaluation while the potential maintainer lines will be elevated to the backcross nursery for the conversion of new CMS line.

Table 22. Yield and yield advantage of F1 hybrids against check varieties evaluated in the TCN on 2015 DS.

F1 CODE	FEMALE	MALE PARENT	F1 YIELD (kg)	Yield Advantage (%)			
				Mestiso 19	Mestiso 20	PSBRc18	PSBRc82
TCN333	PR20A	TCN 329	17378.05	95.29	146.48	177.67	150.95
TCN412	IR73328A	TCN 409	14613.44	64.22	107.27	133.50	111.03
TCN535	PR28A	TCN 533	14078.57	58.21	99.68	124.95	103.30
TCN493	PR30A	TCN 489	13955.94	56.83	97.95	122.99	101.53
TCN411	PR20A	TCN 409	13569.08	52.49	92.46	116.81	95.94
TCN545	PR28A	TCN 543	13562.77	52.42	92.37	116.71	95.85
TCN426	PR20A	TCN 419	13526.16	52.00	91.85	116.13	95.32
TCN526	PR29A	TCN 523	13404.07	50.63	90.12	114.18	93.56
TCN534	IR68897A	TCN 533	13141.82	47.69	86.40	109.99	89.77
TCN129	IR58025A	TCN 128	13114.73	47.38	86.01	109.55	89.38
TCN221	IR73328A	TCN 216	12891.82	44.88	82.85	105.99	86.16
TCN220	IR58025A	TCN 216	12850.42	44.41	82.26	105.33	85.57
TCN42	PRH1A	TCN 36	12477.26	40.22	76.97	99.37	80.18
TCN290	PR2A	TCN 287	12185.82	36.94	72.84	94.71	75.97
TCN446	IR73328A	TCN 445	12111.63	36.11	71.79	93.52	74.90
TCN441	IR72079A	TCN 440	11999.92	34.85	70.20	91.74	73.28
TCN37	IR72079A	TCN 36	11841.28	33.07	67.95	89.20	70.99
TCN516	PR28A	TCN 509	11785.37	32.44	67.16	88.31	70.19
TCN487	PR29A	TCN 484	11712.12	31.62	66.12	87.14	69.13
TCN289	PR24A	TCN 287	11664.56	31.08	65.45	86.38	68.44
Check		Mestizo 19	8898.51				

Table 23. Yield of testcrosses and male parents using CMS lines IR68897A (original) and improved IR68897A (PR28A, PR29A and PR30A).

Code	Male Parent	Yield (kg/ha)	Yield (kg/ha)			
			IR68897A	PR28A	PR29A	PR30A
TCN479	RB100	6747.46	7818.22	7924.83	7675.92	7300.38
TCN484	SRT-3R	6683.37	10032.73	7042.97	11712.12	8456.80
TCN489	PR35749-HY-R	7790.54	9030.72	9643.60	7824.85	**13955.94**
TCN523	Matatag2-25Kr-263-4-23R	6738.96	9655.27	8956.59	**13404.07**	10417.44
TCN499	PR34142-5-3-2R	8210.30	8282.38	8419.33	7292.09	7494.48
TCN504	PR36244-HY-1-10-3R	4634.65	8243.71	9051.82	7847.33	5093.62
TCN509	C7324WH-13-1-1-3-2-1R	8088.42	8181.05	8390.47	8080.05	9925.66
TCN514	PJ23R	8787.60	9563.46	11785.37	10330.35	11058.43
TCN494	IR60819-34-2R	7064.22	8838.60	8465.12	8963.22	10717.98
TCN528	PR34302R	8323.11	9034.53	10177.46	-	8679.27
TCN533	PR31559-AR32-4-3-2R	6936.63	**13141.82**	**14078.57**	10720.85	9676.74
TCN538	PR72889-69-2-2-2R	8932.33	9657.91	8631.06	9853.11	8335.16
TCN543	PR36248-HY-2-5-1R	7475.68	7325.85	13562.77	9457.50	9176.28
TCN548	PR26134-10-1-1-3-1-2R	8066.88	8326.48	10782.00	6236.05	7884.36
TCN553	PR31885-3-1R	-	5013.31	5318.53	5431.78	7800.39

- No data

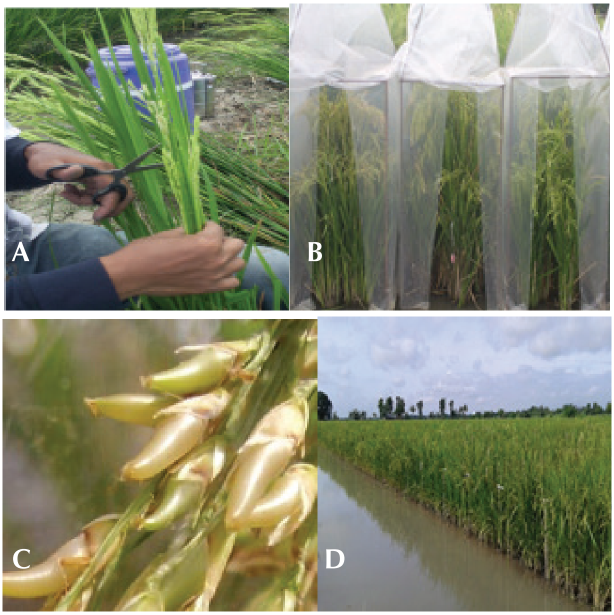


Figure 12. Generation of testcrosses in the source nursery and evaluation of F1 in the testcross nursery. A.) Leaf clipping B.) Isolation barrier C.) Testcrosses D.) Evaluation of testcrosses in the TCN.

Performance tests of experimental hybrids

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Heterosis breeding is one complementary strategy to negate the growing rice shortage in the country. Utilization of heterosis had contributed tremendously to the increased productivity in many crops specifically in rice as it promises a 15% yield advantage compared to conventional varieties under the same input levels. The increase in grain yield is a result of hybrid vigor that breeders aim to exploit.

Evaluating experimental hybrids, which is an essential segment of variety development, supports in identifying the ones with superior performance in terms of grain yield, level of heterosis and resistance to pest and diseases, over designated check cultivars under local conditions, to be released for public use. A series of tests composed of the observation nursery (ON), preliminary yield trial (PYT) and multi-location yield trial (MYT) serve this purpose. Information collected from these trials become basis for advancing particular entries for the national cooperative tests of hybrid materials (NCT-Hyb). This study aimed to (1) evaluate the performance of promising hybrids in different nurseries for grain yield, and other important morpho-agronomic traits, (2) identify hybrids with wide range of adaptation and stable performance across environments, and (3) identify location/season specific hybrids.

Highlights:

- In 2015, 53 experimental hybrids developed from crosses involving nine female parents (eight CMS lines and one TGMS line) and 53 male parents in the DS, and 59 experimental hybrids developed from crosses involving 13 female parents (12 CMS lines and 1 TGMS line), and 39 male parents in the WS were evaluated in the observational nursery for morpho-agronomic traits and grain yield against three inbred (NSIC Rc222 (WS only),PSB Rc18, PSB Rc82) and two hybrid (Mestiso 19, Mestiso 20) check varieties. The trial was laid out in augmented design using 105-hill plots, with the test entries assigned randomly without replication into incomplete blocks each with complete sets of checks. For the DS, Maturity (DAS) of the test hybrids ranged from 110 (PR47575H) to 126 (PR47569H, PR47613, PR47589H) with a mean of 118.30, while those of the checks were 110 (PSB Rc82, Mestiso 19), 111 (Mestiso 20) and 123 (PSB Rc18). Plant height (cm) of the checks were 94.8 (PSB Rc82), 100 (PSB Rc18), 105.8 (Mestiso 20) and 108.6 (Mestiso 19), while those of the test hybrids ranged from 67.0 (PR47603H) to 119.6 (PR47599H) with a mean of 95.14. Tiller numbers for checks were 11 (Mestiso 20), 13 (Mestiso 19), 14 (PSB Rc18) and 16 (PSB Rc82) while those of the test hybrids ranged from 9 (PR47578H, PR47612H) to 16 (PR47589H, PR47591H, PR47590H, PR47567H, PR47606) with a mean of 12.64. Yield (kg ha-1) data were collected from 2.1-m2 crop cuts and corrected to a moisture factor value of 1.0. Grain yield of the test hybrids ranged from 1752.16 (PR47618H) to 6411.53 (PR47580H) with a mean of 3775.92 (Table 24).

- Top 15% of the hybrids recorded grain yields ranging from 5151.46 (PR47586H) to 6411.53 (PR47580H). Based on computed yield advantage values (YA,%), and by a 15% yield advantage cutoff, about 25% of the test hybrids out-yielded PSB Rc18 and PSB Rc82 ranging from 18.9% (PR47574H) to 60.6 (PR47580H) for PSB Rc18, and from 16.0 (PR47606H) to 52.6 (PR47580H) for PSB Rc82. By a 5% advantage cutoff against hybrid check varieties, 32% out-yielded Mestiso 19 ranging from 15.8 (PR47606H) to 52.3 (PR47580H), while only two entries out-yielded Mestiso 20 with values of 9.1 (PR47567H) and 21.7 (PR47580H). Duncan`s Multiple Range Test identified 17 grain yield mean groupings significantly different at $\alpha=0.05$. Top 15% selection will be forwarded for further evaluation in the PYT in the succeeding seasons (Figure 13).

- For the WS, Maturity (DAS) of the test hybrids ranged from 108 (PR48795H, PR48799H, PR48804H) to 124 (PR48803H), with mean of 116. Plant height (cm) ranged from 94.15 (PR48754H) to 143.55 (PR48764H) with mean of 116.86. Tiller number ranged from 6 (PR48766H) to 15 (PR48754H, PR48765H) with mean of 10. Trait measurements for check varieties are also indicated in Table 8. Grain yield (t ha-1) data were collected from 2.1-m2 crop cuts and corrected to a moisture factor value of 1.0. Grain yield of the test hybrids ranged from 1.71 (PR48754H) to 10.31 (PR48765H) with mean of 5.56. Eleven entries recorded yield of >7000 kg ha-1, ranging from 7211 (PR48800H) to 10314 (PR48765H). With thresholds of 15% for inbred check comparison and 5% for hybrid check comparison, 11 entries out-yielded PSB Rc82 (6.21), 14 entries out-yielded PSB Rc18 (5.77), 40 entries out-yielded Mestiso 19 (4.97), and 15 entries out-yielded Mestiso 20. Top selection will be forwarded to SPPYT 2016 DS.

- The preliminary yield trial in 2015 evaluated 22 experimental hybrids developed from crosses between 12 female parents (eight CMS lines and four TGMS lines) and 21 male parents in the DS, and 17 experimental hybrids developed from crosses between five female parents (one TGMS line and four CMS lines), and 16 male parents in the WS against three inbred (NSIC Rc222 (WS only), PSB Rc18, PSB Rc82) and two hybrid (Mestiso 19, Mestiso 20) check varieties to evaluate morpho-agronomic traits and grain yield potential. The trial was laid out in Randomized Complete Blocks with three replications using 200-hill plots. Morpho-agronomic traits measured were maturity (Mat,DAS), plant height (Ht,cm), and productive tiller count (Tn). For the DS, morpho-agronomic measurement values of the checks were 123 (Mat), 102.13 (Ht) and 14 (Tn) for PSB Rc18, 110 (Mat), 93.67 (Ht) and 14 (Tn) for PSB Rc82, 110 (Mat), 115.13 (Ht) and 13 (Tn) for Mestiso 19, and 111 (Mat), 111.87 (Ht) and 13 (Tn) for Mestiso 20. Among the test hybrids, maturity ranged from 118 (PR45671H) to 130 (PR45661H) with a mean of 124; plant height ranged from 88.77 (PR47786H) to 112.27 (PR47792H) with a mean of 99.65; productive tiller count ranged from ten (PR45655H) to 16 (PR47790H, PR47771H, PR47786H) with a mean of 13.27. Grain yield (kg ha-1) data were collected from 5.76-m2 crop cuts and corrected to a moisture factor value of 1.0. Yield among test hybrids ranged from 4299.05 (PR45655H) to 10184.06 (PR47771H) with a mean of 6874.39. Yield for checks were 5609.89 (PSB Rc18), 7305.10 (PSB Rc82), 7580.14 (Mestiso 19), and 10362.38 (Mestiso 20). Based on computed yield advantage values (YA, %), and by a 15% yield advantage cutoff over inbred checks, 14 hybrids out-yielded PSB Rc18 with YA ranging from 15.41 (PR45671H) to 81.55 (PR47771H), and four hybrids out-yielded PSB Rc82 with YA ranging from 17.60 (PR47992H) to 39.41 (PR47771H). By a 5% yield advantage cutoff over hybrid checks, 5 hybrids out-yielded Mestiso 19 with YA ranging from 4.59 (PR47795H) to 34.35 (PR47771H), and no hybrid attained positive YA over Mestiso 20 (Table 20). Duncan`s Multiple Range Test identified four grain yield mean groupings significantly different at $\alpha=0.05$. Top 50% selections will be nominated for multi-location advanced testing in the succeeding seasons (Figure 14).

- For the WS, morpho-agronomic measurement values of the check varieties were 117 (Mat), 118 (Ht), 12 (Tn) for NSIC Rc222, 123 (Mat), 116 (Ht), 12 (Tn) for PSB Rc18, 114 (Mat), 115 (Ht), 12 (Tn) for PBS Rc82, 117 (Mat), 113 (Ht), 12 (Tn) for Mestiso 19, and 114 (Mat), 122 (Ht), 13 (Tn) for Mestiso 20. Among the test hybrids, maturity ranged from 111 (PR46957H, PR46956) to 119 (PR46987H) with a mean of 114.24. Plant height ranged from 113.87 (PR46958H) to

Grain yield (kg ha-1) data were collected from 5.76-m2 crop cuts and corrected to a moisture factor value of 1.0. Yield of the test entries ranged from 3623.047 (PR46981H) to 5937.42 (PR46951H) with mean of 5059.95. With thresholds of 15% for inbred check comparison and 5% for hybrid check comparison, three entries out-yielded PSB Rc18, 12 entries out-yielded Mestiso 19, and six entries out-yielded Mestiso 20 (Table 24).

- The multi-location yield trial at PhilRice CES in 2015 DS was heavily affected by stem borer infestation, causing the failure of the trial. Test entries will be re-evaluated in succeeding seasons. Fifteen promising hybrids were evaluated in the multi-location yield trial against five check varieties in 2015 WS. The trial was laid out in RCBD with three replications. For the trial at PhilRice CES, maturity of the hybrids ranged from 111 (PR39375H, PR35118H) to 119 (PR46990H) with mean of 114.82. Plant height ranged from 109.47 (PR35118H) to 127.60 (PR46988H) with mean of 122.66. Tiller number ranged from 10 (PR46958H) to 15 (PR46987H) with mean of 13.With thresholds of 15% for inbred check comparison and 5% for hybrid check comparison, one entry out-yielded Mestiso 19, six entries out-yielded Mestiso 20, four entries out-yielded Mestiso 48, eleven entries out-yielded Mestiso 55. Data from other test sites are still pending return (Table 26).

Table 24. Maturity, height, productive tiller number, grain yield, and computed yield advantage over check varieties of observational nursery entries in 2015 WS.

Entry	Maturity (DAS)	Height (cm)	Tiller number	Grain yield (kg ha^{-1})	Yield Advantage (%)			
					PSB Rc18	PSB Rc82	Mestiso 19	Mestiso 20
PR48765H	123.13	128.55	15.20	10314.67	78.82	66.08	107.59	68.23
PR48796H	119.33	130.43	9.20	9222.07	59.87	48.49	85.60	50.41
PR47220H	111.33	121.43	8.20	8985.07	55.77	44.67	80.83	46.54
PR46837H	121.33	107.03	8.20	8439.07	46.30	35.88	69.85	37.64
PR48768H	120.13	130.35	12.20	7972.67	38.21	28.37	60.46	30.03
PR48769H	123.13	123.95	13.20	7918.67	37.28	27.50	59.37	29.15
PR48755H	120.13	114.35	9.20	7649.67	32.61	23.17	53.96	24.76
PR48794H	111.33	115.63	9.20	7579.07	31.39	22.03	52.54	23.61
PR48775H	123.53	125.43	10.60	7423.27	28.69	19.52	49.40	21.07
PR36474H	119.33	125.43	11.20	7322.07	26.94	17.90	47.36	19.42
PR48800H	111.33	109.43	12.20	7211.07	25.01	16.11	45.13	17.61
PR48776H	123.53	132.23	11.60	6734.27	16.75	8.43	35.53	9.83
PR48806H	122.33	114.83	11.20	6723.07	16.55	8.25	35.31	9.65
PR48791H	113.53	109.83	10.60	6716.27	16.43	8.14	35.17	9.54
PR48805H	111.33	109.03	10.20	6619.07	14.75	6.58	33.22	7.95
Mestiso 19	112.00	110.60	9.33	4968.67				
PSB Rc82	116.67	112.93	10.67	6210.67				
PSB Rc18	117.00	117.53	11.00	5768.33				
Mestiso 20	121.00	127.60	11.67	6131.33				

Table 25. Maturity, height, productive tiller number, grain yield, and computed yield advantage values over check varieties of preliminary yield trial entries in 2015 WS.

Entry	Maturity (DAS)	Height (cm)	Tiller number	Grain yield (kg ha^{-1})	Yield Advantage (%)			
					PSB Rc18	PSB Rc82	Mestiso 19	Mestiso 20
PR46958H	113.00	114.00	16.27	5937.42	18.88	−5.47	37.61	18.16
PR46981H	113.00	115.60	12.00	5830.08	16.73	−7.18	35.13	16.02
PR46951H	113.33	117.20	11.73	5824.35	16.62	−7.27	34.99	15.91
PR46966H	115.00	115.20	10.60	5692.97	13.98	−9.37	31.95	13.29
PR46955H	112.00	120.73	10.33	5649.53	13.11	−10.06	30.94	12.43
PR46957H	113.00	113.87	10.60	5431.86	8.76	−13.52	25.90	8.09
PR46967H	112.67	122.20	12.47	5233.64	4.79	−16.68	21.30	4.15
PR46971H	112.00	122.93	9.67	5197.84	4.07	−17.25	20.47	3.44
PR46956H	115.67	128.73	12.47	5197.55	4.07	−17.25	20.47	3.43
PR46988H	112.00	120.27	11.93	5111.60	2.34	−18.62	18.47	1.72
PR46989H	113.00	123.73	12.87	5023.44	0.58	−20.02	16.43	−0.03
PR46960H	114.00	116.20	12.00	4636.52	−7.17	−26.18	7.46	−7.73
PR46990H	114.00	118.40	9.40	4530.12	−9.30	−27.88	5.00	−9.85
PR46962H	111.00	117.53	12.73	4138.80	−17.13	−34.11	−4.07	−17.64
PR46949H	111.00	115.87	10.67	4107.45	−17.76	−34.61	−4.80	−18.26
PR46969H	119.00	128.27	10.73	3690.48	−26.11	−41.25	−14.46	−26.56
PR46987H	114.33	113.93	10.67	3623.07	−27.46	−42.32	−16.03	−27.90
Mestiso 19	117.33	113.40	11.53	4314.52				
Mestiso 20	113.67	122.40	13.27	5025.08				
PSB Rc18	123.00	115.60	12.07	4994.51				
PSB Rc82	114.00	115.47	12.40	6281.23				

Table 26. Maturity, height, productive tiller number, grain yield, and computed yield advantage values over check varieties of multi-location yield trial entries in 2015 WS, PhilRice CES.

Entry	Maturity (DAS)	Height (cm)	Tiller number	Grain yield (kg ha^{-1})	Yield Advantage (%)			
					Mestiso 19	Mestiso 20	Mestiso 48	Mestiso 55
PR46960H	114.67	121.07	11.93	5674.93	24.18	39.89	35.02	59.46
PR46958H	113.67	116.20	10.53	4664.75	2.08	14.99	10.99	31.07
PR46989H	115.00	123.67	11.93	4644.94	1.64	14.50	10.51	30.52
PR46969H	116.33	123.67	13.73	4444.10	-2.75	9.55	5.74	24.87
PR46962H	115.00	123.27	13.33	4293.83	-6.04	5.85	2.16	20.65
PR46990H	119.33	124.33	13.47	4292.23	-6.08	5.81	2.12	20.61
PR39375H	111.00	115.87	13.80	4181.24	-8.50	3.07	-0.52	17.49
PR46971H	118.00	124.33	13.53	4130.12	-9.62	1.81	-1.73	16.05
PR39391H	111.02	115.79	12.88	4112.76	-10.00	1.38	-2.15	15.56
PR46988H	113.33	127.60	12.73	4080.71	-10.70	0.59	-2.91	14.66
PR35118H	111.00	109.47	14.73	3958.16	-13.39	-2.43	-5.83	11.22
PR46981H	114.02	116.39	11.88	3379.84	-26.04	-16.68	-19.59	-5.03
PR46987H	119.00	127.33	15.47	3158.27	-30.89	-22.15	-24.86	-11.26
PR39019H	111.67	119.60	13.87	3062.30	-32.99	-24.51	-27.14	-13.95
PR42208H	116.00	127.33	14.67	2884.48	-36.88	-28.89	-31.37	-18.95
Mestiso 19	115.67	126.40	14.53	4569.89				
Mestiso 55	119.00	124.33	10.40	3558.90				
Mestiso 48	114.67	127.80	15.67	4203.03				
Mestiso 20	111.00	126.07	14.60	4056.64				

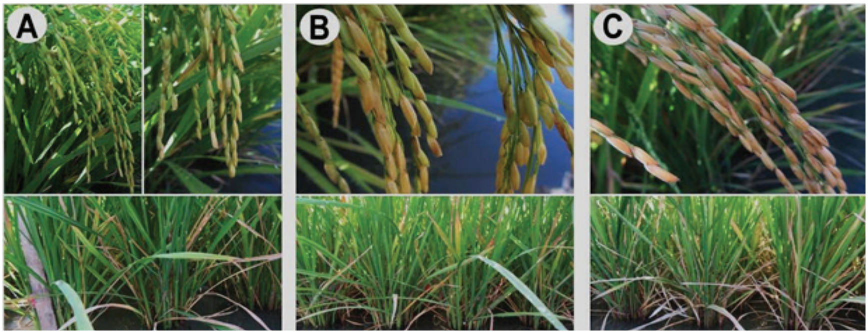

Figure 13. Top performing entries in the ON 2015 DS (A) PR47567H, (B) PR47570H, (C) PR47568H

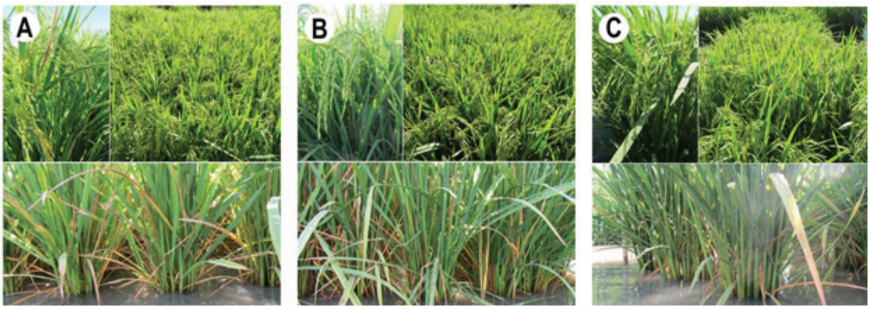

Figure 14. Top performing entries in the PYT 2015 DS (A) PR47216H, (B) PR47570H, (C) PR47771H

Seed production of experimental hybrids

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Hybrid rice cultivation is one of the key approaches through which the country can attain food staples sufficiency. A very crucial component of the hybrid rice technology is seed production, which involves three parents: the cytoplasmic male sterile line (CMS or A line), maintainer line (B) and restorer line (R). Widespread adoption of this technology necessitates the availability of ample quality seeds needed in large-scale cultivation.

The production of hybrid seeds differs from that of inbred rice seeds. It involves two steps, the multiplication of CMS lines (A × B) and the production of F1 seeds (A × R), both done alongside seed increase of maintainer and restorer lines. High quality in terms of physical purity and genetic trueness to type must be maintained. The genetic purity of the hybrid parents is essential in the development and commercialization of hybrid varieties since the yield of hybrid rice will decrease by 0.1 t ha-1 when the purity of hybrid seeds decrease by 1%. This study aimed to (1) to produce sufficient physically and genetically pure hybrid parent lines, and experimental and newly released hybrids for various yield trials and demonstration nurseries (2) evaluate and monitor important traits of the A, B and R lines of each hybrid, and (3) subject selected entries to in-house and external seed quality control.

Highlights:

- The seed production activities catering the various studies under the hybrid rice breeding project include CMS line multiplication, F1 seed production for the observational nursery (SPON), preliminary yield trial (SPPYT) and the national cooperative tests for hybrids (SPNCT).

- To produce breeder/nucleus seeds of 15 CMS lines, 15 A × B cross combinations were established in row crossing plots with row ratio of 10 A: four B lines (Figure 15). Seed yield (kg ha-1) measurements were obtained from seven 50-hill crop cut samples and averaged across samples plots (Table 27). Seed yield in the DS ranged from 459.59 (PR29A) to 2165.77 (PR30A). Seed yield in the WS ranged from 102.75 to 1694.8. Total weight of CMS line seeds produced was 305599.8g.

- The SPON in 2015 produced seeds of 60 hybrids to be used in the observational nursery for hybrids in 2015 WS and 2016 DS. Hill-to-hill crossing of female and male parents in crossing cages was done at a ratio of 2 male hills: 6 female hills. The target number of seeds to be produced was 300, but a number of cross combinations generated less than 300 due to high stem borer infestation in the DS. Sufficient number of seeds for 39 cross combinations was generated in the WS (Figure 16).

- Thirty-four cross combinations were seed produced for the preliminary yield trial in 2015. Out of 20 cross combinations included in the SPPYT in 2015 DS, only 13 successfully produced relatively enough F1 seeds to be used in the F1 evaluation in the following season (Table 22). The hybrids were developed from cross combinations between four female parent lines (three CMS lines and one TGMS line) and 11 male parents. Seed yield measurements were recorded from a crop cut of at least 660 hills of CMS lines. Computed seed yield (kg ha-1) ranged from 97.57 (PR46957H) to 2206.25 (PR46960H). Total weight of F1 seeds produced was 28306g. In the WS, low seed yields were obtained due to two typhoons that affected the setup during the ripening stage. For 21 cross combinations, the seed yield ranged from 10.04 (PR47002H) to 386.14 (PR46565H). Total F1 seeds produced which will be forwarded to PYT in 2016 DS weighed 5317.1g.

- F1 seeds of ten promising hybrids to augment current seed stock under testing in the NCT-HYB were produced in 2015 under F1 SPNCT. Seed yield measurements (kg ha-1) in the DS were obtained from seven 50-hill crop cut samples and averaged across samples plots (Table 22). Seed yield (kg ha-1) of the four entries were 1673.51 (PR42208H), 1332.11 (PR39091H), 42.87 (PR36577H) and 18.43 (PR36578H). Total weight of F1 seeds produced was 23458.10. Six cross combinations were seed produced in the WS. Seed yield ranged from 53.5 (PR39391H) to 1220.56 (PR35726H), with a bulk seeds produce which weighed 9572.90g.

Table 27. Seed yield (kg ha-1) and bulk yield of seeds produced in 2015.

Entry	Female parent	Male parent	Seed yield (kg ha^{-1})	Seed yield (t ha^{-1})	Bulk yield (g)
CMS Line Multiplication					
2015 DS					
PR30A	PR30A	PR30B	2165.77	2.17	35643.00
PR28A	PR28A	PR28B	1830.55	1.83	21972.00
PR27A	PR27A	PR27B	808.56	0.81	25988.00
PR2A	PR2A	PR2B	758.21	0.76	6036.00
IR68897A	IR68897A	IR68897B	3654.86	3.65	26356.00
PR20A	PR20A	PR20B	859.55	0.86	14788.00
IR73328A	IR73328A	IR73328B	1297.88	1.30	60029.00
PR15A	PR15A	PR15B	501.92	0.50	5558.00
PR24A	PR24A	PR24B	472.75	0.47	8526.00
PR29A	PR29A	PR29B	831.04	0.83	15555.00
IR79156A	IR79156A	IR79156B	2847.88	2.85	7787.00
PR21A	PR21A	PR21B	464.66	0.46	1233.00
IR79128A	IR79128A	IR79128B	862.65	0.86	25378.00
IR80156A	IR80156A	IR80156B	1036.02	1.04	6903.00
2015 WS					
PR15A	PR15A	PR15B	683.11	0.68	555.6
PR20A	PR20A	PR20B	223.05	0.22	268
PR24A	PR24A	PR24B	431.88	0.43	3163.1
PR21A	PR21A	PR21B	831.59	0.83	3795.2
PR28A	PR28A	PR28B	106.75	0.11	67.3

Table 27. Seed yield (kg ha-1) and bulk yield of seeds produced in 2015. Con't.

PR29A	PR29A	PR29B	102.75	0.10	321.5
PR30A	PR30A	PR30B	141.25	0.14	201.8
IR68897A	IR68897A	IR68897B	280.76	0.28	771.5
IR58025A	IR58025A	IR58025B	1694.80	1.69	3153.5
IR79156A	IR79156A	IR79156B	589.61	0.59	3122.7
Seed Production for the Preliminary Yield Trial					
2015 DS					
PR46958H	IR68897A	PR37988-B-20-6-1-1	1250.69	1.25	3602.00
PR46960H	IR68897A	PR34126-B-10	2206.25	2.21	6354.00
PR46962H	IR68897A	PR41804-3R	1100.35	1.10	3169.00
PR46957H	IR68897A	PR27598-135-1-2	97.57	0.10	281.00
PR46987H	TGMS 71	PR41093-24-1-3	1070.08	1.07	2825.00
PR46690H	TGMS 71	PR41185-88-1-3	873.48	0.87	2306.00
PR46988H	TGMS 71	PR3-1-4	826.89	0.83	2183.00
PR46989H	TGMS 71	PR37918-3B-21-1-2-1	1131.06	1.13	2986.00
PR46966H	PRH1A	Matatag2-25kr-263-4-3-2	342.42	0.34	904.00
PR46967H	PRH1A	SRT 76	291.29	0.29	769.00
PR46971H	PRH1A	PR4-2-21	492.42	0.49	1300.00
PR46969H	PRH1A	PR37988-B-20-6-1-1	378.03	0.38	998.00
PR46995H	PR15A	PR41804-3R	238.26	0.24	629.00

Table 27. Seed yield (kg ha-1) and bulk yield of seeds produced in 2015. Con't.

2015 WS					
PR46565H	IR58025A	AB2	386.14	0.39	1019.4
PR47570H	IR68897A	PR34302R	235.98	0.24	623
PR47589H	IR68897A	MB-324	227.46	0.23	600.5
PR47591H	IR68897A	PR45595HY-AC	128.18	0.13	338.4
PR47611H	IR68897A	PR45583HY-AC	111.97	0.11	295.6
PR45650H	PR41919S	Azucene-M5-R-1	108.83	0.11	287.3
PR46996H	PR41918S	C1812-B-4-3-1-1	104.58	0.10	276.1
PR46564H	PRH1A	PR36641-HY-7-5	95.11	0.10	251.1
PR47567H	PR15A	IR73885-1-4-3-2-10R	82.35	0.08	217.4
PR47592H	IR68897A	PR45606HY-AC	79.66	0.08	210.3
PR47577H	PRH1A	PR36620C-HY-19-7-4	73.86	0.07	195
PR47586H	IR68897A	AB-37	66.4	0.07	175.3
PR47604H	PRH1A	AB-60	64.89	0.06	171.3
PR46997H	PR41917S	IR79242-28-3-2-8	62.69	0.06	165.5
PR47606H	PR28A	AB-94	61.14	0.06	161.4
PR46992H	PR41917S	38NSIC RC138-4-1	43.45	0.04	114.7
PR45648H	PR41918S	Raeline 10	25.95	0.03	68.5
PR47594H	IR68897A	PR45597HY-AC	19.43	0.02	51.3
PR47574H	IR68897A	PR36620HY-AC-20-3-9	15.34	0.02	40.5
PR47572H	PR2A	PR35749HY	10.61	0.01	28
PR47002H	PR41917S	PSB RC28	10.04	0.01	26.5

Table 27. Seed yield (kg ha-1) and bulk yield of seeds produced in 2015. Con't.

Seed Production for the NCT-HYB					
2015 DS					
PR42208H	IR73328A	AC-66R	1673.51	1.67	18570.00
PR39091H	PRH1A	PR36244HY	1332.11	1.33	4562.00
PR36577H	IR58025A	SN 159	42.87	0.04	280.50
PR36578H	PR3A	PSB Rc8	18.43	0.02	45.60
2015 WS					
PR35726H	IR58025A	PR36246-1-19-2-2	1220.56	1.22	3005
PR42208H	PRH1 A	PR36244-HY-1-10-3	1000.5	1.00	1905.8
PR36577H	IR58025A	SN 159	630.49	0.63	1604.5
PR42214H	S78	PR37246-52-6-1-1	491.33	0.49	2391.5
PR39324H	PR19A	PR36248-HY-3-6-4	456.5	0.46	426.6
PR39391H	PR2A	PR34142-5-1-3-3	53.5	0.05	239.5

Figure 15. Row crossing plots of PR27A multiplication, PhilRice CES, 2015 DS.

Figure 16. Paired crossing to produce F1 seeds for the observational nursery. PhilRice CES, 2015 WS.

Incorporating stress resistance genes through molecular markers

JOS Enriquez, FP Waing, RA Millas, and JD Caguiat

Hybrid rice, because of higher yield potential, has been envisioned as one of the technologies that will bring the Philippines closer to self-sufficiency. The first-ever hybrid rice variety in the Philippines was released in 1994. To date, there are now 42 varieties of hybrid rice that have been approved by the government for commercial cultivation. Of this number, 12 are considered public hybrids because they have been developed by IRRI, PhilRice, and UPLB. The success of hybrid rice cultivation however, is continually being threatened by its susceptibility to many diseases. Most if not all of these hybrids are susceptible to bacterial blight, tungro and blast, the three most important diseases of irrigated lowland rice in the country. Among the major prevalent diseases, bacterial leaf blight caused by Xanthomonas oryzae pv. oryzae (Xoo), is one of the most devastating diseases of rice throughout the world, especially in tropical Asia (Zhou et al. 2010). The disease is characterized by water-soaked and yellowish lesions, starting from leaf tips that later increase in length and width. Lesions usually have a wavy margin but later coalesce during severe infection to totally occupy the leaf blades. When the disease occurs at young seedlings (called kresek or seedling wilt) it may lead to severe crop damage. The disease was reported to reduce yield ranging from 20 to 50% in severe cases (Mew 1987; Ou 1985). In the Philippines, Xoo has been classified into 12 strains representing 10 races based on differential reaction of different cultivars (Hifni and Kardin 1998)

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A different R gene, Xa21 from a wild rice species, O. longistaminata has a broad resistance-spectrum to BB races (Khush et al. 1990). This R gene was cloned (Song et al. 1995) and thus been widely used in rice breeding programs by conventional breeding approach, marker-assisted selection (MAS) and genetic transformation. Unfortunately, Xa21 was again broken down recently by new virulent races in Philippines, Korea, India and China (Lee et al. 1999; Marella et al. 2001; Zeng et al. 2002). Through continuous searching for new R gene, a novel bacterial blight (BB) resistance gene from Oryza rufipogon (RBB16) was identified and designated as Xa23 (Zhang et al. 1998). The near-isogenic lines (NILs) introgressed with Xa23 gene were highly resistant to all strains of Xanthomonas oryzae pv. oryzae from the Philippines, China, and Japan, and the gene was expressed at all growth stages (Zhang et al., 2001). The broad-spectrum resistance of Xa23 makes it a potential donor in hybrid parental lines for hybrid rice production where BB is a major constraint.

This study aimed to: (1) evaluate published and functional markers of Xa23 gene for applicability in marker-assisted selection (MAS), (2) incorporate Xa23 gene in the elite hybrid parent lines by MAS, (3) introgress bacterial blight resistance gene to popular but susceptible public hybrid parent lines, and (4) assess the recurrent parent genome recovery, morpho-agronomic traits and reaction to bacterial blight of improved hybrid parent lines.

Highlights:

- In 2015 DS, 225 F1 plants and two F2 populations (~200 plants) generated from the hybridization of hybrid parent lines and modern varieties (NSIC Rc160, NSIC Rc222, and NSIC Rc224) with the Xa23 donor, IRBB23, were established in the field (Figure 17). Twenty one days after transplanting, leaf samples were collected individually from each plant for DNA extraction. Using the extracted genomic DNA as template, target gene assay was performed using two expressed-sequence tag (EST) markers, C189 and O3STS1 (Figure 18). Heterozygosity test was also conducted in order to select for true F1 plants (Figure 19).

- At maximum tillering stage, the two F2 populations (~200 plants) were inoculated with Xoo Race 3. Two weeks after inoculation, the resistance of each entry was visually evaluated through their lesion patterns. Entries showing BLB resistance in the field, good plant type, and found to have the Xa23 resistant allele through target gene assay were selected. There were 24 selected plants having the Xa23 resistant allele, BLB resistance in the field, and good phenotypic acceptability. For the true F1 plants, selection was based on molecular genotyping data. Based on the heterozygosity test, 184 true F1 plants were selected. Selected plants were backcrossed to their corresponding recurrent parent to increase the recovery of desirable characters. Entries that were not used for backcrossing were harvested into bulk for establishment in 2015 WS.

- In 2015 WS, 183 F1 plants, ten F2 populations, and 32 F3 lines generated in 2015 DS were established in the field. Table 12 contains the entries established and activities performed in 2015 WS. A total of 1231 leaf samples were collected from the F1 plants and F2 populations 21 days after transplanting and were used to extract high quality genomic DNA. EST markers, O3STS1 and C189, were used for marker-based genotyping in order to detect the presence of the resistant allele of Xa23 gene in each entry. Heterozygosity test was also conducted in order to determine true F1 plants.

- The resistance of ten F2 populations to Xoo race 3 in the field was evaluated in 2015 WS. The entries were inoculated with the pathogen at maximum tillering stage and resistance was evaluated based on lesion patterns after two weeks. Phenotypic acceptability of each F2 populations was also evaluated. A total of 173 F2 BLB resistant plants having the resistant allele of Xa23 and good phenotypic acceptability were selected. Also, based on molecular marker genotyping data, 134 plants were selected as true F1. Selected entries were used for backcrossing and entries that were not used for backcrossing were harvested into bulk. There were no selections in F3 lines due to the accumulated damage brought by Typhoon Kabayan and Typhoon Lando. Thus, field evaluation and selection for the F3 lines will be repeated in 2016 DS.

- The study will be terminated this 2015. Since the study only aims to introgress the Xa23 gene, it was decided by the whole project to incorporate the study to (1) Development of Hybrid Parent Lines (PBD-006-001) and (2) Accelerating the Development and Adoption of Next-Generation (NextGen) Rice Varieties for Major Ecosystems in the Philippines (173-A-RTF-022). The activities of the NextGen project include the introgression and pyramiding of various resistance genes and PBD-006-001 encompasses this study's objectives as it generally aims to develop superior hybrid parent lines with disease resistance.

Table 28. Entries with corresponding generation and activities performed in 2015 WS.

DESIGNATION	Gene	Generation	Activity
PR48414	Xa23	BC1F2	TG, Disease scn; BC
PR48411	Xa23	BC1F1	TG, Disease scn; BC
PR48412	Xa23	BC1F1	TG, Disease scn; BC
PR48413	Xa23	BC1F1	TG, Disease scn; BC
PR48417	Xa23	BC1F1	TG, Disease scn; BC
H0150	Xa23	BC1F1	TG, Disease scn; BC
PR47063	Xa23	F3	Disease scn
PR47099	Xa23	F3	Disease scn
PR48404	Xa23	F2	TG, Disease scn
PR48405	Xa23	F2	TG, Disease scn
PR48406	Xa23	F2	TG, Disease scn
PR48407	Xa23	F2	TG, Disease scn
PR48408	Xa23	F2	TG, Disease scn
PR48409	Xa23	F2	TG, Disease scn
PR48410	Xa23	F2	TG, Disease scn
PR48415	Xa23	F2	TG, Disease scn
PR48416	Xa23	F2	TG, Disease scn

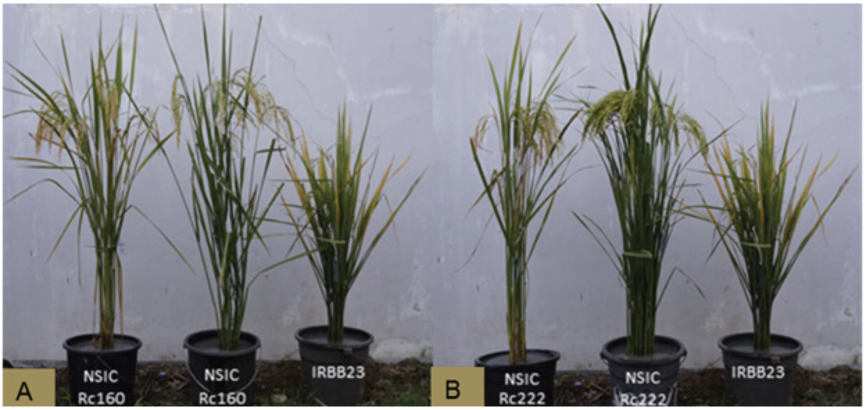


Figure 17. Introgression of Xa23 into popular but susceptible varieties (A) NSIC Rc222 and (B) NSIC Rc160 (From left to right: Recurrent parent, Improved offspring, Xa23 donor).

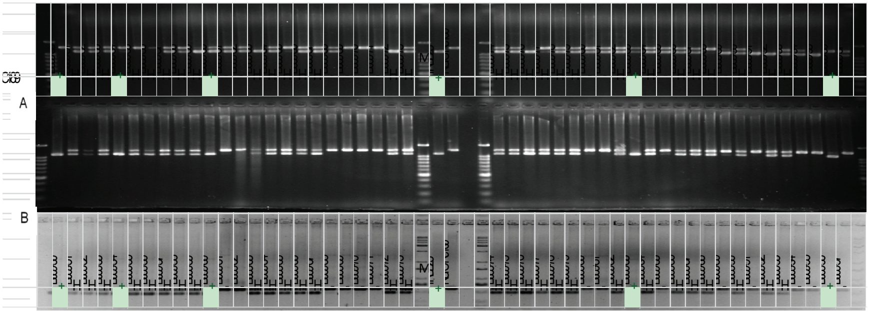


Figure 18. Target gene assay for Xa23 using (A) O3STS1 (R allele= ~1.1 kb; S allele = 1.2 kb) and (B) C189 (R allele= 800 bp; S allele= 900 bp) with IRBB23 (R) and NSIC Rc160 (S) as checks. Highlighted entries having the resistant Xa23 allele for both O3STS1 and C189 markers were selected.

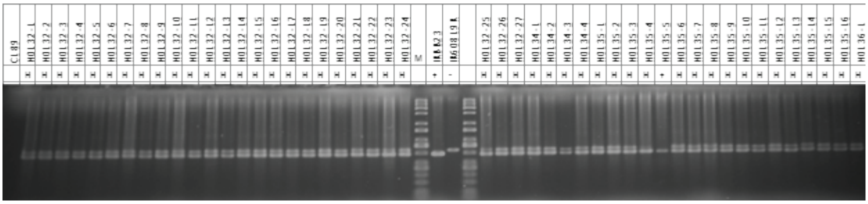


Figure 19. Heterozygosity test for true F1 plants using the C189 marker with IRBB23 (+) and IR60819R (-) as checks. Heterozygotes showing double bands (scored as H) were selected as true F1.

Generating useful variation in hybrid parent lines through induced mutagenesis

MM Rosario, VP Luciano, MF Ablaza, KA Garcia, JD Caguiat

To meet the demand of rice needed by the rapidly growing human population with decreasing land and water resources, rice yields have to be significantly increased. Hybrid rice is one technology with a lot of promise to contribute greatly to this goal because of its 15-20% yield advantage over inbreds. The success of hybrid rice breeding depends to a great extent on the quality and diversity of elite lines used as parents in developing new hybrids. Techniques such as In vitro mutagenesis (IVM) and In vitro culture (IVC) are essential in discovering promising new hybrid parent lines. Mutation breeding can be considered successful in obtaining new cultivars and broadening the genetic base of rice crop. In addition, it generates enhanced variant of extensively adapted cultivars through the use of agents that increase the chances of gene mutations. The induced rice mutants have proved to be useful research tools in genetic and physiological assessment on yield-limiting factors in rice. Moreover, induced mutation can aid isolation of new genes that are not obtainable in the germplasm. In vitro culture (IVC), likewise, induces mutation generating gametoclonal or somaclonal variants which may be exploited to improve or develop new varieties. Doubled haploid (DH) via Anther culture (AC) is one of the most exploited IVC system. DH technology has recently changed the way inbreds are developed in breeding programs. It greatly reduces the time required to obtain inbreds compared with six or more generations of selfing.

The study aimed to: (1) induce mutation in hybrid parent lines using sodium azide/ethyl methane sulfonate (EMS) or gamma irradiation (2) utilize in-vitro culture and in-vitro mutagenesis in hybrid parent line development, and (3) generate mutant hybrid parent lines with drought tolerance.

Highlights:

In vitro culture (IVC)

- A total of 97 entries (26 in dry season and 71 in wet season) which comprised of 45 BxB, 30 RxR, 14 traditional rice varieties along with four M1 entries and their wild types (WT) were subjected to anther culture. Of these, 37 (38.14%) exhibited callus formation and were transferred to regeneration media for plant development. For dry season (DS), cross from HY-16 achieved the highest % callus formation (%CF) of 8.44 generating 4 DH plants, while WT 5999 produced the greatest number (9) of DH plants with 5.81%CF. Overall, 18 DH plants were generated from six test entries. On the other hand, of the 71 crosses subjected to anther culture, 21 (29.6%) exhibited callus formation four weeks after dark incubation (Table 29). Calli were sub-cultured in regeneration media (MSK2) and incubated in the lighted room for plant development.

In vitro mutagenesis (IVM)

- Mature seeds from five maintainer lines were evaluated for their response to tissue culture. Five hundred seeds were inoculated to callus induction media (CIM). After four weeks of dark incubation, seed-derived calli were then transferred to regeneration media (RM). All entries exhibited calli formation, but only PR9B generated green plants with a total of 353. Plants were still in the lighted room for further root development (Figure 20) and will be established in the screenhouse until plant maturity.

- Based on tissue culturability result, PR9B was found to be responsive. Hence, another set of 600 matured seeds were inoculated to CIM and calli were excised after four weeks of dark incubation prior to induce mutation. A total of 540 seed derived-calli were irradiated with 60Co at 40Gy dosage. Irradiated calli were subjected to regeneration media (MSK2) and incubated in the lighted room until plant development (Figure 21). Generated putative mutants along with 353 plants from tissue culturability will be established in the screenhouse until plant maturity, and seeds will be harvested and screen for drought tolerance under in vitro condition using three different concentrations (0%, 5% and 10%) of polyethylene glycol (PEG).

Seed Mutation (SM)

- Seeds from three (3) tungro breeding lines (Matatag 11, 5999 and 21473) and one (1) hybrid maintainer line (PRH1B) were subjected to mutation via gamma irradiation. One hundred grams of seeds were irradiated with 250Gy dosage. Treated seeds (M0) were sown along with their WT and grown at PhilRice-CES field. M2 seeds were harvested for abiotic and biotic screening purposes. On the other hand, 10 M2 populations along with their WT were established, a total of 287 individual plants were selected based on their phenotype. Selected plants (M3 seeds) will be established for generation advance.

AC-derived restorer lines

- A total of 38 test hybrids with AC-derived restorer lines were evaluated and selected in different hybrid nurseries. Eighteen (18) were assessed in testcross nursery (TCN) and twenty (20) for observational nursery (ON). Selected outstanding hybrids in TCN will be advanced to Seed Production for Observational Nursery (SPON) prior for ON evaluation. On the other hand, superior crosses in the ON will be forwarded to Seed Production for Preliminary Yield Trial (SPPYT) preceding PYT evaluation.

Table 29. Crosses with corresponding number of plated anthers, callused anthers and callus formation.

Field code	Total number of anthers plated (AP)	Total number of callused anthers (CA)	% callus formation (CF)
BxB crosses			
HY-1	3600	17	0.47
HY-2	3300	51	1.55
HY-3	1950	1	0.05
HY-6	4150	53	1.28
HY-7	3750	53	1.41
HY-11	10650	80	0.75
HY-22	6750	182	2.70
RxR crosses			
RF1-20	2700	5	0.19
RF1-24	5850	52	0.89
RF1-31	3600	7	0.19
Traditional rice varieties			
G-140	7200	110	1.53
G-141	15600	801	5.13
G-142	2400	36	1.50
G-145	8700	519	6.00
G-146	7500	192	2.56
G-147	18300	141	0.22
G-148	6750	18	0.27
G-149	1050	35	3.33
G-151	7800	162	2.08
G-152	8400	57	0.68
G-154	4950	5	0.10

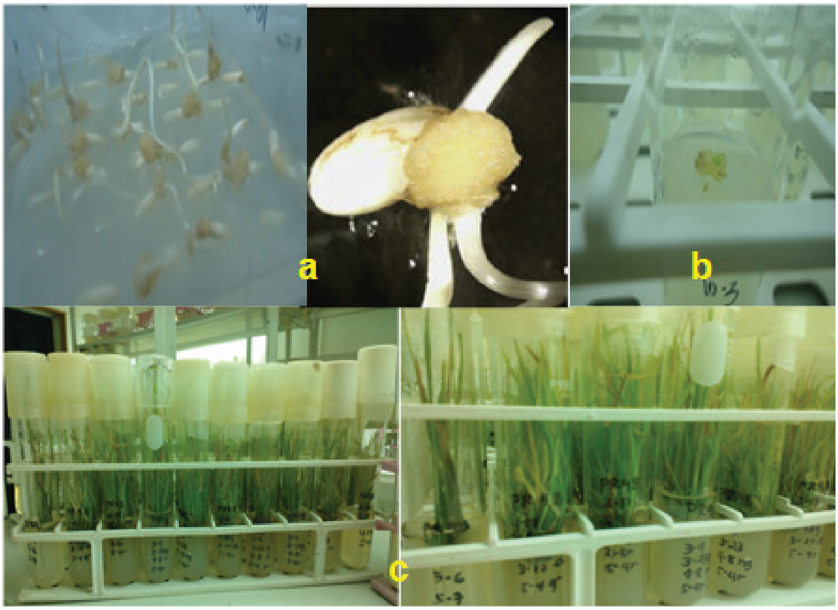


Figure 20. (a) Mature seeds with calli in CIM (b) callus in RM (c) Generated PR9B plants from seed derived-calli.

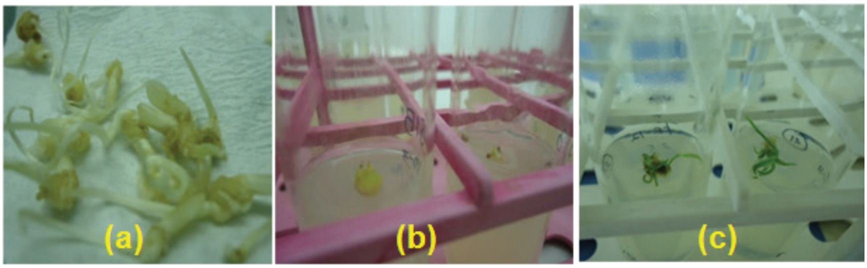


Figure 21. (a) Seed derived- calli prior to gamma irradiation (b) irradiated calli in RM (c) irradiated calli with shoots.

Screening and evaluation of parent lines and hybrids

FP Waing, JOS Enriquez and JD Caguiat

The continuous development of high-yielding hybrid varieties that possess resistance to pests and diseases and excellent grain qualities is essential to keep up with the increasing demand for rice and the changing environment. As such, there is a need for the development and improvement of maintainer and restorer lines, which are very essential components in the development of hybrid rice, for biotic and abiotic stress resistance.

Bacterial blight (BB) caused by Xanthomonas oryzae pv. oryzae (Xoo) is the most important bacterial disease of rice in irrigated and rainfed rice environment causing as high as 20-50% yield reduction in severe epidemics. To date, thirty (30) major genes have been reported to confer resistance against the rice bacterial pathogen Xoo, which included 21 dominant and 9 recessive R genes (Chu et al 2006). These include a series of genes with marker tags that have been proven to be useful for MAS: Xa4, xa5 (Garris et al. 2003), Xa7 (Chen et al 2008), xa13 (Chu et al 2006), and Xa21 (Song et. al., 1995).

Rice blast is among the most widespread and damaging diseases of rice in upland and rainfed areas causing more than 50% losses in yield. The disease has two commonly recognized phases: leaf blast (seedling) and neck blast (mature plant). The pathogen causing blast Magnaporthe oryzae, consisted of 18 lineages in the Philippines. In the case of tungro, the most important viral disease in the country, flanking markers are available for rtv, the RTSV resistance QTL from ARC11554. In addition, the RTSV resistance gene from Utri Merah, tsv1, has been very recently fine-mapped (Lee et. al., 2010) and markers very close to the gene just need to be evaluated for usefulness in line development.

Abiotic stress is a major limiting factor in the productivity of rice in large areas of the world. Because plants cannot avoid abiotic stress by moving, they have acquired various mechanisms for stress tolerance in the course of their evolution. Enhancing or introducing such mechanisms in rice is one effective way to develop stress-tolerant cultivars. Direct-seeded rice (DSR) cultivation is increasingly being practiced among farmers in both rainfed and irrigated ecosystems (Pandey and Velasco 2002). Labor scarcity, water shortage, and high production cost have become the major driving forces of this shift. Developing high yielding varieties that can withstand flooding during germination and early growth is essential for sustainability of practicing direct seeding for rice crop establishment.

The purpose of the study is to screen parent lines and hybrids for biotic (blast, bacterial blight, tungro, and GLH) and abiotic stress tolerance (submergence); and to develop new and diverse hybrid parent lines and F1 hybrids tolerant to abiotic stress and resistant to pest and diseases.

Highlights:

- A total of 90 parent lines and F1 hybrids comprised of 57 restorer lines, 20 maintainer lines and 13 F1 hybrids were assembled for phenotypic and genotypic characterization in 2015 DS and WS. Some of these entries were released hybrids (three) and test hybrids (10-in the pipeline). These were subjected to screening for blast, brown plant hopper (BPH) and green leaf hopper (GLH) resistance in dry season; and for bacterial leaf blight (BLB) and tungro in both dry and wet season.

- Screening for biotic stress resistance

  Blast Ninety entries (two replication) were evaluated for blast resistance in collaboration with Crop Protection Division (CPD) inside their blast nursery using the induce inoculation method. Among the entries screened, 51 entries showed resistance while 21 showed intermediate resistance and 16 were susceptible. It is interesting to note that most of the promising restorer lines (34 out of 47 lines) were resistant to intermediate resistant blast except for three: PR36502HY-2-3-8-2-1, PR36643HY-1-1-21-2-1 and PR42275-HY-1-2-2-1-1 which exhibited susceptibility to the disease.

  Green Leaf Hopper and Brown Plant Hopper Similar procedure of screening for both GLH and BPH was done. Entries were evaluated following the seed-box method in two replications. One week after seeding, 2nd to 3rd nymph stage of GLH/BPH was allowed to feed on the test plants. Entries were scored, five days after or if the susceptible check TN1 was completely damaged and wilted. For GLH resistance; six entries were found resistant, 24 were moderately resistant, 29 were moderately susceptible and 22 were susceptible (Figure 22A). For BPH resistance screening, 30 entries were found resistant, 19 were moderately resistant, 30 were moderately susceptible and 4 were susceptible (Figure 22B). Interestingly, there were three entries that showed higher level of resistance to both GLH and BPH than the resistant check (IRGC#117285). These include PR36502HY-2-3-5-1-1, PR36645HY-8-1-2-2-2-2 and PR42275-HY-1-2-2-1-1.

  Bacterial Leaf Blight The assembled entries (90 parent lines) were screened for BLB reaction under screenhouse condition at PhilRice CES. The lines were inoculated with PXO79 (race

3) and PXO99 (race 6) in the screenhouse following the leaf clipping method at maximum tillering stage. Approximately 1 to 2cm of the tip of the leaves was cut with sterile scissors previously dipped in bacterial suspension. Assessment of the severity of lesions was done 14 days after inoculation. However, due to unfavorable environmental condition during the period of disease incubation, the symptom occurrence and disease development was not successful. Another screening set-up was established in 2015 wet season with the same protocol. Data gathering is yet to be done.

Rice Tungro Disease Tungro screening was done in both dry and wet season. Greenhouse-reared adult viruliferous GLH were allowed to feed on the seven day old seedlings of the hybrid parent lines for 24 hours. After virus inoculation, GLH were removed from the test plants. Inoculated plants were transferred in pots and were maintained inside the screenhouse for symptom development for 28 days after inoculation (DAI). IRGC#16680, IRGC#16682 and IRGC#21473 were used as tolerant checks and IRGC#105 (Taichung Native 1) as susceptible check. Among the test entries, 40 lines were moderately resistant to the disease (Figure 22). All the remaining entries were susceptible (Figure 23).

- Included in the screening were parent lines and F1 of released hybrids (Mestiso 47, Mestiso 48 and Mestiso 55). Additionally, the parent lines and F1 of test hybrids under NCT and performance trials were also screened. Table 25 enumerates the parent lines of these hybrids and their reactions to the stresses imposed. All the test entries were found resistant to both GLH and BPH. In addition, seven F1 hybrids were moderately resistant to tungro and the remaining entries were susceptible.

- Target gene genotyping was also conducted to confirm the presence of the different resistance genes using markers for tsv1 (RM336 and RM5495), bacterial blight (Xa4, xa5, Xa7 and Xa23), and sub1 (ART5 and SC3). Leaf tissues were collected from each test entries for DNA extraction. Based on the molecular analysis conducted, some of the lines carry resistance genes/putative QTLs but the presence/absence of these resistance genes/putative QTLs did not completely translate to the observed reaction (resistance/ susceptibility) of the lines to the different stresses. Xa4 gene which confers low resistance to BLB was detected in most of the lines. The parent lines carrying various resistance genes were potential source of resistance for hybrid parent line improvement and development.

- From these lines, the known restorer lines will be screened for the presence of fertility restoring (Rf) genes and the cytoplasmic male sterile (CMS) lines will be screened for gene specific marker in 2016DS. This will be done to evaluate the efficiency and applicability of these markers for marker-assisted breeding.

- Document change request (DCR) form was filed in order to revise the title of the study from “Screening and evaluation of parent lines and hybrids” to “Phenotypic and genotypic characterization of parent lines and hybrids”.

Table 30. Reactions of the parent lines, released and elite hybrid lines (NCT) to different biotic stresses and results of the molecular marker genotyping conducted to confirm the presence of resistance genes.

Parent lines and hybrids	Biotic stress reaction				Genotype Data							
					Xa genes				*tsv1*		*Sub1*	
	Blast	**BPH**	**GLH**	**Tungro**	*Xa4*	*xa5*	*Xa7*	*Xa23*	RM336	RM5495	ART 5	SC3
PR40640H	R	R	*	MR	*	*	*	*	*	*	*	*
PR30A	S	R	R	S	+	–	–	–	H	+	–	–
PR30B	MR	R	R	*	*	*	*	*	*	*	*	*
PR39902-19R52	R	R	R	MR	+	–	–	–	–	–	–	+
PR40638H	S	R	R	MR	+	–	–	–	H	–	H	+
PR28A	S	R	R	S	+	–	–	–	–	–	–	+
PR28B	S	R	R	S	+	–	–	–	–	–	–	H
PR39902-19R56	S	R	R	MR	+	–	–	–	–	*	+	–
PR40639H	MR	R	*	S	+	–	–	–	–	–	–	–
PR29A	*	*	*	S	+	–	–	–	*	–	–	–
PR39902-19R76	R	R	*	MR	+	–	–	–	*	–	–	–
PR36474H (Mestiso 55)	R	R	R	*	+	–	–	–	–	–	–	–
IR79128A	R	R	R	MR	+	–	–	–	–	–	–	H
IR79128B	R	R	R	MR	+	–	–	–	–	*	–	–
PR31559-AR-32-4-3-2	S	R	R	MR	+	–	–	–	–	–	–	–
PR35664H (Mestiso 48)	R	R	R	MR	+	–	–	–	+	–	–	+
IR73328A	MR	R	R	MR	+	–	–	–	+	+	–	–
IR73328B	R	R	R	MR	+	–	–	–	+	+	–	–
MATATAG-2-25kr-263-4-23	S	R	R	S	+	–	–	–	+	–	–	–
PR36559H (Mestiso 49)	R	R	R	MR	+	–	–	–	+	–	–	–
IR80156A	R	R	R	MR	+	–	–	–	–	–	–	H
IR80156B	R	R	*	*	–	–	–	–	–	–	–	–
IR71866-3R-1-2-1B	R	R	R	MR	+	–	–	–	+	*	–	–
PR3511H	R	R	R	MR	+	–	–	–	–	–	–	–
IR80156A	R	R	R	S	*	–	–	–	–	*	–	–
IR80156B	R	*	*	S	+	–	–	–	–	–	–	–
PR36246HY-1-19-2-2R	MR	*	R	*	+	–	–	–	–	–	–	–
PR36420H	R	R	R	S	+	–	–	–	–	–	–	+
IR68897A	R	*	R	*	+	–	–	–	–	–	–	+
IR68897B	*	*	*	*	+	–	–	–	–	–	–	–
PJ23	MR	R	R	*	*	*	*	*	*	*	*	*
PR35711H	S	R	R	S	*	–	–	–	–	*	–	–
IR69702-52-3-3	S	R	R	S	+	–	–	–	–	–	–	H
PR36577H	MR	*	*	*	H	–	–	–	–	–	–	H
SN159 (08DS)	S	R	R	S	+		–	–	–	–	–	H
PR44123H	MR	R	R	S	*	–	–	–	–	–	–	–
PR39007H	MR	R	R	MR	*	–	–	–	–	–	–	
PR42598H	R	R	R	MR	*	–	–	–	–	–	–	
PR19A	MR	R	R	S	*	–	–	–	–	*	–	
PR19B	S	R	R	*	*	–	–	–	–	–	–	
PR20A	MR	*	*	*	+	–	–	–	–	–	–	
PR20B	MR	R	R	S	+	–	–	–	–	–	–	
PR2A	S	R	R	S	+	–	–	–	H	*	–	
PR2B	S	R	R	*	*	*	*	*	*	*	*	

* no data

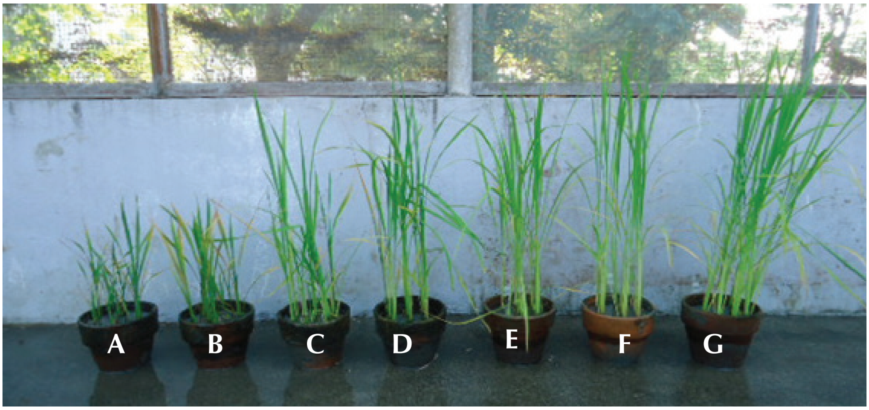


Figure 22. Response of selected entries to tungro. PR42279-HY-1-8-2-2-3 (A) demonstrates significant height reduction and yellow discoloration similar to the susceptible check IRGC105 (B) while PR42439HY-16-1-1-3-1 (C) and PR36645HY-8-1-2-2-2-2 (D) shows comparable resistance with the tolerant checks IRGC21473 (E), IRGC16680 (F) and IRGC16682 (G).

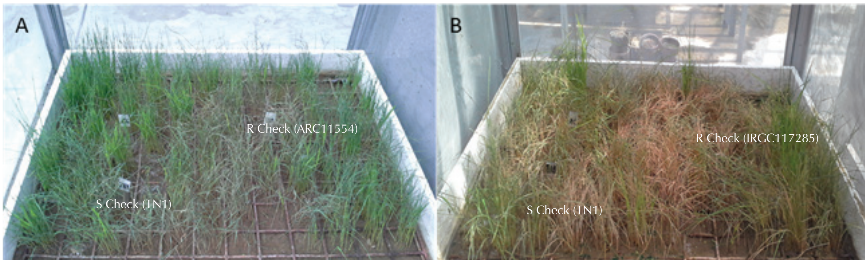


Figure 23. Screening set-up for GLH (A) and BPH (B) following the compartment box method inside the glasshouse.

Yield Prediction of single cross hybrids and combining ability analysis of parent lines

JD Caguiat, LV Gramaje, RA Millas and JE Carampatana

Demand for sustainable ways to increase the yield potential of rice cultivars is vital to address the plateau in rice production. Hybrid rice technology, among the various means to break yield barrier, offers an opportunity to enhance the yield of rice under fragile conditions as much as 15 to 20% yield advantage over the conventional high yielding varieties. At present, the implementation of hybrid rice technology is being hampered by the high cost of field evaluation. This is due to the strategy of breeding programs that includes performing all possible crosses in a group of inbred lines and then evaluating the single cross hybrids obtained, followed by the selection of the most promising ones. However, it is quite difficult and expensive to assess a very large number of developed parent lines and evaluation of all possible hybrids. Among the hybrid performance prediction methods, best linear unbiased prediction (BLUP), this combines field testing of related hybrids and obtaining pedigree information or genetic relatedness, holds great promise. Yield prediction of hybrid performance is a result of good combining ability. The combining ability of the different lines has a major importance in hybrid breeding since it provides information for parent selection and the nature and magnitude of gene action involved. The knowledge of genetic structure and mode of inheritance of different characters helps breeders to employ the suitable breeding methodology for their improvement

This study aimed to estimate kinship among parent lines using markers, to determine the yield performance of tested and untested single cross hybrids through best linear unbiased prediction, to measure the general and specific combining ability of hybrid parent lines for yield traits, and to identify the best performing hybrids and parents through BLUP and combining ability.

Highlights:

- In 2015 DS, 46 hybrid rice testcrosses were evaluated for combining ability of the hybrids` female and parent lines. The trial 30-hill plots were laid out in Randomized Complete Block Design with three replications (Figure 24). Genotype performance was evaluated against an inbred check (PSB Rc82) and a hybrid check (Mestiso 19) variety. Grain yield estimates (kg ha-1) ranged from 7,110.31±853.34 (PR47789H) to 11,269.31±853.34 (PR47775H) with a mean of 8,368.02±1,548.10 with a CV value of 14.09%. Calculated positive yield advantage (YA,%) ranged from 0.50 (PR47790H) to 53.42 (PR47775H) against PSB Rc82 and from 1.90 (PR47801H) to 43.10 (PR47775H) against Mestiso 19. Tiller number ranged from 11 (PR47792H, PR47776H, PR47790H) to 18 (PR47796H). Plant height (cm) ranged from 85.78 (PR47787H) to 115.45 (PR47802H). Based on initial analysis, low r2 values were obtained for correlations of grain yield to plant height (0.01) and tiller number (0.05) which suggest doing in-depth measurement with grain yield components (Table 31).

- Parent lines of the testcrosses were also evaluated simultaneously with that of the hybrids. Restorer lines as male parents and maintainer (B) lines to represent female parents were evaluated. Tiller number ranged from ten (PR36244-HY-1-10-3R) to 17 (PR35749-HY-R). The shortest parent line was Hanarambyeo (88.66) and the tallest was PR36248-HY-2-5-1R (121.44). Grain yield ranged from 4025.33 (PR2B) to 9094.67 (PR31559-AR32-4-3-2R). Against PSB Rc82, eight entries obtained YA of >5% with values ranging from 5.09 to 23.82. Three entries obtained a YA of >5% over Mestiso 19 with values ranging from 6.89 to 21.31.

- Frequency distribution of measurements of four parameters including maturity, plant height, maturity and grain yield suggest interesting behavior of the testing set. Majority of the maturity values occupy a common narrow bracket. Histogram for tiller number and plant height showed skewing to the left which tends to suggest short plant stature and average productive tiller count among the test set. Grain yield histogram is skewed to the right suggesting relatively higher measurements over the set mean.

- For combining ability analysis, four CMS lines were crossed with 15 restorer lines which generated 48 F1 hybrids. Yield performance of lines and testers and their GCA effect in 2015 DS is shown in Table 32. Among the restorer lines, PR36244-HY-1-10-3R showed the highest GCA of 0.74 and highest yields of 9.24t/ha. For the tester lines, IR73328A had the highest GCA value of 0.98 and with the highest yield of 9.49t/ha. The top 15 highest yielding lines among entries are shown in Table 33. The cross between IR68897A/Milyang23 gave the highest yield of 9.83t/ha, IR68897A/PR36248-HY-2-5-1R with 9.65t/ha and IR80559A/PR34142-5-1-3-2R with 9.44t/ha. For 2015 WS, three CMS lines were crossed with 15 restorer lines which generated 38 hybrids. Yield and morpho-agronomic characteristics of these entries will be evaluated on 2016WS. The combining ability data of complete set of crosses will be analyzed while yield prediction analysis will be done for incomplete crosses.

Table 31. Grain yield, yield advantage (YA), tiller number and height of rice hybrids with standard error values in the 2015DS Combining Ability Nursery evaluated against check varieties, PhilRice CES, 2015DS.

Genotype	Grain yield (kg ha-1)	Yield advantage (%)		Tiller number	Height (cm)
		PSB Rc82	Mestiso 19		
PR47775H	11269.31 ± 853.34	53.42	43.10	14 ± 1	100.09 ± 2.93
PR47803H	10606.00 ± 701.69	44.39	34.67	15 ± 1	101.05 ± 2.48
PR47794H	10552.00 ± 701.69	43.66	33.99	12 ± 1	107.16 ± 2.48
PR47800H	10524.33 ± 701.69	43.28	33.64	12 ± 1	104.00 ± 2.48
PR33875H	10518.81 ± 853.34	43.20	33.57	14 ± 1	99.34 ± 2.93
PR47777H	10232.67 ± 701.69	39.31	29.93	15 ± 1	105.39 ± 2.48
PR47804H	10135.71 ± 1197.98	37.99	28.70	16 ± 1	100.10 ± 2.48
PR47791H	9809.00 ± 701.69	33.54	24.55	14 ± 1	101.89 ± 2.48
PR47216H	9626.33 ± 701.69	31.05	22.23	14 ± 1	100.89 ± 2.48
IRRICA-003	9553.67 ± 701.69	10.05	10.06	13± 1	96.67 ± 2.48
IRRICA-004	9540.00 ± 701.69	9.90	9.90	15± 1	99.67 ± 2.48
PR35664H	9516.67 ± 701.69	29.56	20.84	12 ± 1	100.61 ± 2.48
PR47767H	9444.67 ± 701.69	28.58	19.93	12 ± 1	99.94 ± 2.48
PR47768H	9443.00 ± 701.69	28.56	19.91	15 ± 1	98.11 ± 2.48
PR47774H	9349.55 ± 853.31	27.29	18.72	13 ± 1	98.83 ± 2.48
PR47797H	9341.00 ± 701.69	27.17	18.61	15 ± 1	90.94 ± 2.48
PR47785H	9289.05 ± 853.31	26.46	17.95	15 ± 1	97.55 ± 2.48
PR47795H	9256.33 ± 701.69	26.02	17.54	14 ± 1	97.83 ± 2.48
PR47770H	9231.00 ± 701.69	25.67	17.21	13 ± 1	100.83 ± 2.48
PR47788H	9077.67 ± 701.69	23.58	15.27	15 ± 1	92.78 ± 2.48
PSB Rc 82	7345.33 ± 701.69			16 ± 1	93.65 ± 2.48
Mestiso 19	7875.33 ± 701.69			13 ± 1	101.94 ± 2.48

Table 32. Yield performance of lines and testers and their GCA effect in 2015DS.

Genotype Line	GCA effects	Yield (t/ha)
PR36244-HY-1-10-3R	0.74	9.24
PR36248-HY-2-5-1R	0.45	8.96
IR68019-34-2R	0.42	8.92
PR31559-AR-32-4-3-2R	0.40	8.90
C7324WH-13-1-1-3-2-1R	0.24	8.74
PR34142-5-1-3-2R	0.07	8.57
Namcheon	0.07	8.57
PJ23R	0.06	8.57
PR35749-HY-R	0.05	8.55
SRT-3R	0.04	8.55
PR36246-HY-1-19-2-2R	-0.06	8.45
Hanareumbyeo	-0.17	8.33
PR34302R	-0.47	8.04
Matatag 2-25kr-263-4-23R	-0.50	8.00
Milyang23	-0.96	7.54
Tester		
IR73328A	0.98	9.49
IR68897A	-0.11	8.39
IR80559A	-0.30	8.20
PR2A	-0.89	7.62

Table 33. Yield performance of hybrids and their SCA effect in 2015DS.

Hybrid	Tester	Line	SCA effects	Yield (t/ha)
PR47788H	IR68897A	Milyang23	1.32	9.83
PR47774H	IR68897A	PR36248-HY-2-5-1R	1.15	9.65
PR47216H	IR80559A	PR34142-5-1-3-2R	0.94	9.44
PR47775H	IR73328A	PR36248-HY-2-5-1R	0.86	9.36
IRRICA-001	IR68897A	SRT-3R	0.72	9.22
PR47786H	IR80559A	Hanareumbyeo	0.60	9.11
PR47767H	IR68897A	PR34142-5-1-3-2R	0.58	9.08
PR36020H	IR68897A	PR34302R	0.54	9.04
PR33875H	IR73328A	PJ23R	0.53	9.03
PR47796H	PR2A	IR68019-34-2R	0.52	9.02
PR47785H	IR73328A	Hanareumbyeo	0.51	9.01
IRRICA-004	IR80559A	IR68019-34-2R	0.50	9.00
PR47797H	IR68897A	Namcheon	0.47	8.98
PR47781H	PR2A	PJ23R	0.44	8.95
PR47800H	IR73328A	C7324WH-13-1-1-3-2-1R	0.39	8.89

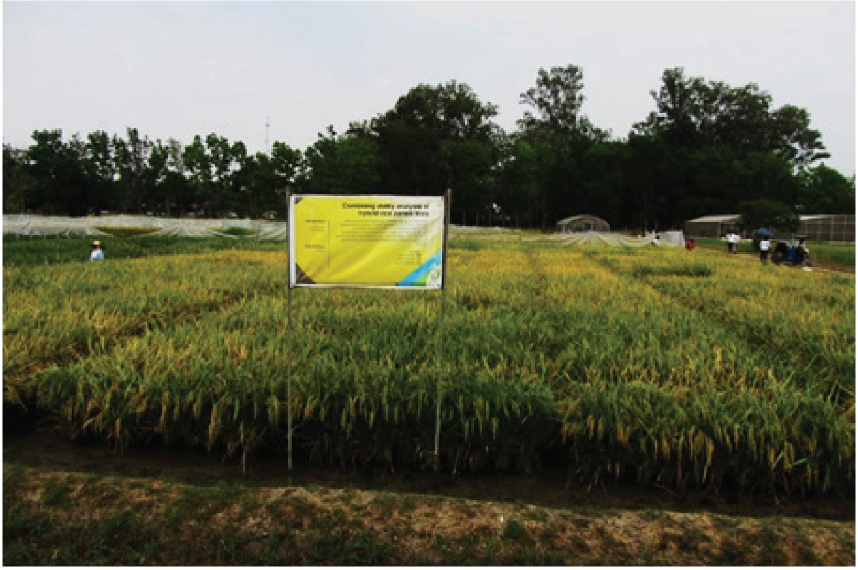


Figure 24. Combining ability nursery- yield trial, PhilRice CES, 2015DS.

Genetic improvement of hybrid parent lines for increased seed yield, BLB resistance, and salinity tolerance

IG Pacada, JC Santiago, GD Valida, CF Libayao, NV Desamero, LM Perez, EH Bandonill

To develop durable F1 hybrids for various stresses, continuous breeding and improvement of parent lines should be implemented. This study consists of three important component, these are screening of parent lines for saline environment, development of maintainer and CMS line with bacterial resistance gene, and enhancing outcrossing rate of CMS lines.

Highlights:

Salinity tolerance

- Ion determination results demonstrated two types of mechanism for salinity tolerance in the screened lines. One mechanism can be described by the observed higher accumulation of Na+ in shoots and roots (Figure 25). However, in terms of visual evaluation, some genotypes have shown less injury in the leaves despite the high Na+ concentration. The other mechanism involves tissue tolerance to salt stress wherein uptake of more Na+ is regulated through cellular compartmentation.

BLB resistance

- Gathered agronomic and morphological traits of homogenous lines for PVP application.

- Two lines were validated to have Xa4 gene only; 25 lines have Xa4+xa5 genes; and six lines with Xa4+xa5+Xa7 genes.

Enhancing outcrossing rate of CMS lines

- Four improved lines with BLB resistance converted into CMS lines using four cytosterility source. Advance progeny (BC3:4F1) showed complete sterility with natural outcrossing rate (NOR) that ranged from 10 to 20.8%.

- Five lines with exerted stigmas were selected from F4 generation.

- Identified new donor for exerted stigmas with indica and javanica grain type, and with plant height of 110cm.

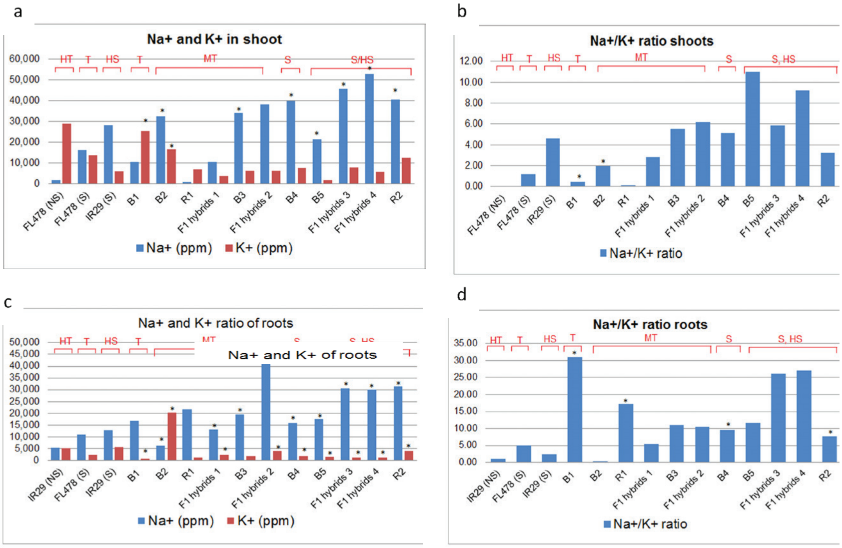


Figure 25. a) Na+ and K+ of shoots b) and its ratio; c) Na+ and K+ of roots d) and its ratio. * Indicate positively significant at α 0.05. Comparison of means of selected genotypes to the FL478.

Developing hybrid parent lines and hybrids at PhilRice Isabela

ATIO Rebong, DB Rebong II, JV Galapon, DKR Bumagat, and MAU Tabil

The study conducted two activities: 1) Yield trials of experimental hybrids and improved parent lines; and 2) Seed production of experimental hybrids and parent lines. Under activity 1, a total of 64 out of 111 chinese lines planted were thoroughly characterized and harvested in 2015 DS, while the rest were damaged by blast during the early vegetative and reproductive stages. Selected entries will be included in the source nursery for 2015 WS screening.

Important agro-morphological traits evaluated include: panicle length, number of filled and unfilled grains and maturity of entries. Panicle length ranged from 16.0 to 27.3cm, filled grains ranged from 43.8 to 170.8 grains while unfilled grains ranged from 13.8 to 97.5, 1000 grain weight ranged from 22.43 to 45.66 grams.

For 2015WS, a total of 161 elite lines selected from the 2015 DS source nursery and from other sources for irrigated and rainfed ecosystem were planted (24hills/entry at a spacing of 20 x 20cm). A total of 33 from the 161 entries tested were selected based on important agro-morphological traits including number of panicle length, filled and unfilled grains and maturity of entries. Panicle length ranged from 17.6 to 29.8cm, filled grains ranged from 114.8 to 140.6 grains while unfilled grains ranged from 16.1 to 33.7 and 1000 grain weight ranged from 20.3 to 43.5 grams.

In 2015 DS, the 10 selected elite restorer lines submitted for evaluation in the MET 0 (AYT) were monitored, yield of the entries ranged from 5.36 to 8.36t/ha. For the 2015 WS, the average yield of these entries in the MET 0 ranged from 4.25 to 7.39t/ha.

In DS, 45 out of 141 F5 lines, and 25 of 61 F6 lines were selected based on high yield and yield parameter data. While during the WS, 90 of 100 test entries (55 additional entries) in the F5, and only 5 from the 25 test entries in the F6 were selected. Selection was based on data gathered from agronomic parameters for the F5 and F6 populations which included panicle length ranging from 19.2 to 27.8 (F5) and 24.2 to 29.0cm (F6), filled grains ranged from 63.4 to 261.4 (F5) and 99.1to 161 grains (F6) while unfilled grains ranged from 16.0 to 67.3 (F5) and 21.8 to 56.1 grains (F6), 1000 grain weight ranged from 16 to 30 grams (F5) and 21.3 to 23.0 grams (F6). Average yield obtained from the F5 populations ranged from 3.0 to 9.4t/ha., while for the F6 population the ranged was from 3.7 to 7.1t/ha.

Evaluation trial for the test entries resumed only in the 2015 WS, materials were sown and transplanted in July 1, 2015 and July 26, 2015, respectively. A total of 38, 6, 20 and 5 entries were evaluated in the OYT, PYT (from 2014DS), PYT (from 2014 WS) and AYT, respectively.

From these materials, 23, 4, 14 and 3 test entries were selected to advance in preliminary and advanced yield trials for 2016DS. Two check varieties Mestiso 20 and NSIC Rc222 were used in the experiment. Due to Typhoon Lando which arrived during the mature stage of the plants, most of the trials were damaged causing lodging of the test entries; affecting the yield and yield component data.

	OYT	PYT (from 2014 DS)	PYT (from 2014 WS)	AYT
Total entries	38	6	20	5
Selected entries	23	4 SMI122001H SMI122068H SMI122087H SMI122135H	14	3 SMI9004H SMI102217H SMI102282H
Maturity (days)	100 – 118	114 – 119	110 – 119	107 – 115
Plant height (cm)	121.3 – 135.1	100.2 – 125.7	111.7 – 135.9	120 – 132
Productive tillers	8.7 – 13.7	13.1 – 14.6	11 – 14.6	11.5 – 13.7
Panicle length (cm)	25.35 – 29.25	25.35 – 28.35	24.7 – 27.95	28 – 30.4
Filled spikelets/ panicle	105.30 – 163.10	97.5 – 129.2	54.2 – 149	80.8 – 109.5
Unfilled spikelets/ panicle	17.60 – 73.30	27.3 – 65.5	15.3 – 65.8	60.6 – 92.5
Spikelets/ panicle (grains)	128.2 – 203.6	156.6 – 170	120 – 187.4	150.9 – 181.4
Spikelet fertility (%)	61.26 – 88.10	59.82 – 82.56	45.17 – 89.57	47.17 – 60.36
1000 grain weight (g)	23 – 32	27 – 29	22 – 38	27 – 32
Yield per ha (kg per ha)	471.94 – 5634.95	3148.33 – 4255.14	4441.06 – 8692.96	2809.73 – 4693.32

Selected entries will be simultaneously reproduced by 2016 DS

Seed production of experimental hybrids and parent lines

Seed production using the modified chimney isolation procedure/strict isolation method and pot crosses in the screenhouse

- In DS, genetically pure experimental hybrid seeds for the observational yield trial (OYT) ranging from 77 to 445g per cross combination, and for the preliminary and advance yield trials (PYT and AYT) from of 51 to 322g per cross combination were generated

- Three hundred to 700g each of the CMS parent lines of 25A, 97A, 28A and PR2A for use in generating testcrosses in the 2015WS were produced.

- Seed production included 26 hybrids from the OYT, 2 from the PYT and 3 from the AYT. These material will be evaluated in 2015WS.

Identification and use of wide compatibility genes (s5n) for enhancing heterosis in rice

IG Pacada, JC Santiago, LM Perez, TF Padolina, NL Manigbas

Wide compatibility varieties (WCVs) are special class of rice germplasm able to produce fertile hybrids when crossed to other rice subspecies like indica x japonica; indica x javanica; japonica x javanica. It contain wide compatibility gene (WCG) or neutral allele (S5n) that resolves the fertility barrier demonstrated in crossing two dissimilar subspecies or cultivar group. WCG is very important particularly in hybrid rice breeding as it can be used to further enhance the heterosis particularly for inter-subspecific hybrids.

Identification of WCV using conventional breeding alone is a very lengthy process and need several manpower to generate desirable number of crosses. The identification of molecular markers in conferring S5n gene simplifies the process of mining new rice germplasm with WCG and facilitates the marker aided breeding for WCG with technical precision.

Highlights:

- Evaluation of S5t-2 primer, a published S5n gene marker using the identified WCV in traditional test cross method is shown in Figure 26.

- Two genotypes exhibited possible S5n gene allele. The allele size detected is comparable to amplification products published by Yang et al (2009). However, further confirmation will be conducted to ensure the validity of result.

- Two more S5n gene published marker is still in the validation process.

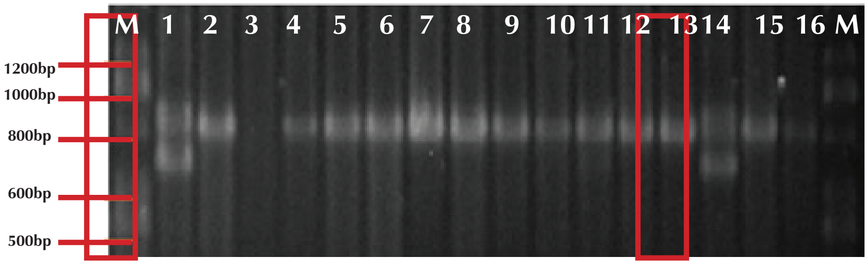


Figure 26. Amplification products using S5t-2 primer. M represent DNA ladder, Lane 1 to 15 identified WCV using traditional test cross method, and lane 16 is BPI 76, known WCV. Lane 1 and 14 showed comparable allele size to published S5n gene marker.

IV. Development of Thermo-Sensitive Genetic Male Sterile (TGMS) Lines and TGMS-Based Two-Line Hybrid Rice

Project Leader: SH Escamos

The discovery of thermo-sensitive genetic male sterility (TGMS) in rice provided new avenues to further exploit heterosis using the two-line system. TGMS are genic male sterile genotypes whose fertility/sterility behavior is conditioned by temperature regimes (Virmani, 1996). This system is useful in the Philippines where temperature differences exist due to elevation, latitude and time of year. The increased chances of finding high yielding hybrids and the more straightforward seed production of TGMS lines makes this system more economically viable.

With the release by the National Seed Industry Council (NSIC) of 2 TGMS-based hybrid rice varieties, the collaborative project between UPLB and PhilRice has demonstrated that breeding and use of TGMS lines to develop two-line hybrids can be successfully done in the Philippines. The project is aimed at developing stable and improved TGMS lines. Likewise, it aims to develop high yielding two-line hybrids that are pest resistant and with acceptable grain and eating qualities.

Highlights:

- Two line hybrids, M19 and M20, continued to be successfully commercialized by PhilRice.

- PRUP 10, a hybrid developed through this project, performed consistently well for 4 consecutive seasons in the National Cooperative Test (NCT). It was recommended to NSIC for release as commercial hybrid variety in Luzon and Mindanao as per deliberation during the RTWG meeting held last December 15, 2015.

- The project now has in the pipeline, stocks of breeding lines extracted by recurrent selection where potential TGMS and pollen parents can be derived. Identification of promising TGMS and pollen parents and utilizing them in testcrosses is on-going.

- Incorporating purple leaf sheath base coloration into male parents of two hybrids through backcrossing had been done. Promising purple-based M19 and M20 have been produced for possible entry to NCT as essentially derived hybrids in 2016 wet season.

- Incorporation of African and wild rice cytoplasm from different sources such as Oryza. glaberrima, O. rufipogon and O. barthiii is in progress in TGMS line development.

- One poster entitled "Phenotypic Marker in Testing TGMS-based Hybrids" was presented at the 23rd FCSSP Conference held at Clark Freeport Zone, Pampanga on May 11to16, 2015.

- One paper entitled "Effect of Selfed Female Parent on the Performance of Two TGMS-based Hybrids was presented during the 28th National Rice R & D Conference held at PhilRice CES on September 8 to10, 2016.

Development of new and diverse TGMS lines through hybridization and selection

SH Escamos, MAT Talavera and TM Masajo

To keep up with the challenge of developing better two-line hybrids, continuous development of new and more improved TGMS lines is an essential breeding component that needs to be pursued. The objective of the study is to develop new and diverse TGMS lines through hybridization and selection. Earliness and shorter stature, high outcrossing rate, resistance to pests and diseases and good grain quality are some of the criteria considered in selection. Development of TGMS lines with low critical sterility point (CSP) will help ensure safe and successful production of F1 seeds at male sterile environment (MSE).

Highlights:

- Research activities on the development of new improved and stable TGMS lines through hybridization and selection at both male sterile environment (MSE) and male fertile environment (MFE) were continued during the year.

- At MSE (Los Banos), TGMS lines and selected male parents and F1's were assembled and planted for making crosses. Seventy six crosses (76) crosses were produced during the year. Twenty-eight (28) F1 populations selected during the dry season (DS) were evaluated during the wet season (WS) while 31 F1 populations selected during the wet season will be evaluated as F2 in the coming 2016 DS. Sixty three (63) F2 populations and 1678 lines in the F3 to F7 were evaluated during the year from which 989 male sterile lines were selected.

- 853 male sterile selections from 2014 wet season and 237 male sterile selections from 2015 DS were evaluated at MFE site, Majayjay, Laguna and Tublay, Benguet, respectively.

- During the year, 37 advance male sterile lines were evaluated in the TGMS observation nursery at MSE and MFE. Thirteen (13) promising lines were identified and selected. Experimental hybrids using these TGMS lines were produced to evaluate their performance as female parent.

Development of new and diverse TGMS lines through recurrent selection

MLG Ortiguero and TM Masajo

To reinforce TGMS breeding work at PhilRice Los Baños, new initiative to develop TGMS lines through recurrent selection was added. Recurrent selection as a breeding method is generally used in cross-pollinated crops but could also be employed in self-pollinated crops like rice using genetic male sterility system to facilitate natural cross pollination. The main purpose of the method is to concentrate on fewer individuals in the population desirable traits through recurrent cycles of intercrossing and selection. Compared to the generally used hybridization and pedigree selection in extraction of inbred lines, intercrossing among individuals in recurrent selection keeps plants in heterozygous conditions allowing for more chances of genetic recombination.

Highlights:

- The study has produced many inbred lines from recurrent selection where potential TGMS parents can be derived and identified. Development of TGMS lines involves shuttling of breeding materials between MSE and MFE.

- In 2015 dry season (DS), 440 F3, 99 F4 and 141 F5 lines were planted at MSE site (Los Baños). From these lines, 222 male sterile plants in the F3, 36 in the F4 and 78 in the F5 were selected. Selections were ratooned and brought to MFE site (Tublay, Benguet) for evaluation and multiplication of seeds in 2015 wet season. Selections will compose the F4, F5 and F6 pedigree nurseries at MSE site (Los Baños) this 2016 DS.

- At MFE site, 634 F3 and 465 F4 plant selections were grown for evaluation and seed multiplication in Majayjay, Laguna. Selected and harvested were 497 F3 and 311 F4 plants. These selections were planted and evaluated at MSE site (Los Baños)during the 2015 WS. Selected were 297 male sterile plants from F4 and 159 from F5. Selections were ratooned and brought to MFE site (Majayjay, Laguna) for evaluation and multiplication of seeds in 2016 DS.

- The two TGMS composite populations, TPP1 and TPP2, planted during the 2015 DS were in the seventh cycle of intercrossing and selection. From each population, 300 sterile and 150 fertile plants were selected during the season. Ratoons from the sterile plant selections were lifted and replanted at MFE site (Tublay, Benguet) for further selection and fertility evaluation. Seeds from selected sterile and fertile plants were collected and processed separately from each population and to be used for another cycle of recombination.

- Promising F4 lines were used in test crosses to produce experimental hybrids for early generation testing of yielding ability of F1. Lines involved will continue to be kept as entries in the pedigree nurseries.

- In 2015 wet season (WS), thirteen lines (7 in F4 and 6 in F5) were used as parents in the generation of experimental hybrids.

- Six advance TGMS lines which were completely male sterile in MSE and with good panicle exsertion were identified as potential parents during the season.

Identification and development of pollen parents for two-line hybrids

MAT Talavera and TM Masajo

Essential to hybrid development programs for both two-line and three-line system is the availability and identification of potentially good-performing pollen parents. Characters such as yield, plant height, lodging resistance, maturity, resistance to pest and diseases, grain acceptability, tolerance to abiotic stresses, and pollen-shedding ability are among the considerations in the selection of pollen parents. Drawing pollen parents from existing inbred variety development programs has been the common practice in hybrid breeding. But lately, with growing interest on hybrids and increased demand for pollen parents, finding suitable and diverse inbreds as male parents of hybrids has become increasingly difficult. Furthermore, access and use of improved germplasm developed and introduced from elsewhere are covered by PVP and MTA and provisions therein could be rather restrictive. While the TGMS project at Los Banos will continue to identify and source pollen parents from available materials, it is doing breeding purposely to develop better pollen parents for TGMS hybrids.

Highlights:

- The study is producing breeding materials from composite populations by recurrent selection where inbred lines with potential of becoming successful pollen parents can be identified and extracted.

- 363 plant selections from composite populations were established in pedigree nurseries (F4 to F7) during the dry season. Twenty-one plants each in the F4 and F5 and 13 plants in the F6 were selected. Some promising uniform lines in the advanced generation (11 in the F5 and 4 in the F6) were used as parents in making experimental hybrids during the 2015 DS. The experimental hybrids were evaluated in 2015 WS Hybrid Observation Nursery (HON). Processing of harvests is in progress.

- Purification of 25 pollen parents selected from F5 to F7 generations was done in 2015 WS. These breeding lines will be used as new parents in developing experimental hybrids in 2016 DS.

- Three pollen parent composite populations were raised during the wet season. Selection of potential pollen parent is on-going.

- Converting (morphological tagging) green-base pollen parents into purple-base genotypes to facilitate identification of true F1 hybrids from selfed individuals, if any, as early as the seedling stage was undertaken. This will eliminate the need for the costly and lengthy "grow-out tests". Two highly selected TGMS hybrid pollen parents were morphologically tagged with purple coloration at the leaf sheath through backcrossing.

- 8 and 10 purple-based lines of M19 and M20 pollen parents, respectively, derived from BC5 were evaluated. From these lines, 3 derived from M19 and 3 from M20 pollen parents were selected.

- Selected pure lines of purple-based TG101M and TG102M from BC5 were used as pollen parents to produce purple version of Mestiso19 and Mestiso 20. Three and 5 purple-based version of Mestiso 19 and Mestiso 20 hybrids, respectively, were made and evaluated in the advance yield trial during the dry season. Results indicate that the yields of hybrids are comparable with Mestiso 19 and Mestiso 20. The best hybrid combination were seed increased and will be entered in the 2016 wet season trial of the NCT as an "essentially derived" hybrid.

- Nine purple-based lines extracted from BC3 were identified as promising pollen parents. These lines will be evaluated further for their suitability as pollen parents.

Development of two-line experimental hybrids

SH Escamos, MAT Talavera, MLG Ortiguero and TM Masajo

In order to increase the chances of finding good performing hybrids, test crossing the TGMS lines with many and diverse pollen parents is essential. Not all hybrids exhibit positive heterosis for economic traits, hence there is a need to produce sufficiently large number of experimental hybrids for testing and evaluation. The objective of the study is to generate as many experimental hybrids as possible to increase the probability of finding hybrids with superior heterosis for economic traits.

Highlights:

- Two-line experimental hybrids were generated through handcrossing using 19 TGMS lines (5 are new) and 100 pollen parents during the dry season. Promising lines from the NCT, the UPLB breeding nurseries, NSIC released varieties, wide hybridization-derived lines, advance lines derived from recurrent selection were used as male parents. Advance lines from backcrosses (BC3 and BC4) in the development of purple-based genotypes were also used as male parents in making new crosses. During the wet season, 13 TGMS lines and 175 pollen parents were planted and used in making experimental hybrids.

- 496 new experimental hybrids were produced during the year. Performance of these new hybrids was evaluated in the Hybrid Observation Nursery (HON).

Evaluation and field performance testing of promising hybrids

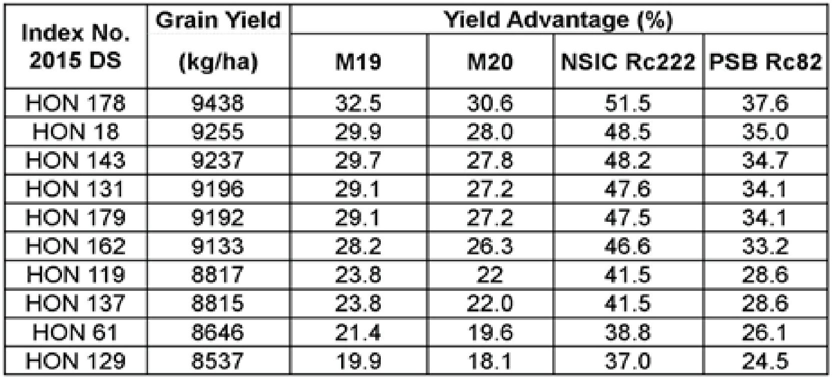
MAT Talavera, DJ Lalican, SH Escamos and TM Masajo

Before a hybrid can be nominated to the NCT, it has to pass a series of evaluation and testing to determine its overall performance. The experimental hybrids have to undergo testing in the (HON) to eliminate obviously inferior performing entries. Selected hybrids are elevated to the Preliminary Yield Trial (PYT) and Advance Yield Trial (AYT) for a more thorough evaluation of yield, field reaction to insects and diseases and of the grain and milling qualities. Promising hybrids are channeled to multi-location and yield potential trials. The objective is to evaluate the performance of experimental hybrids and identify and select the best performing hybrid combinations for the National Cooperative Tests (NCT).

Highlights:

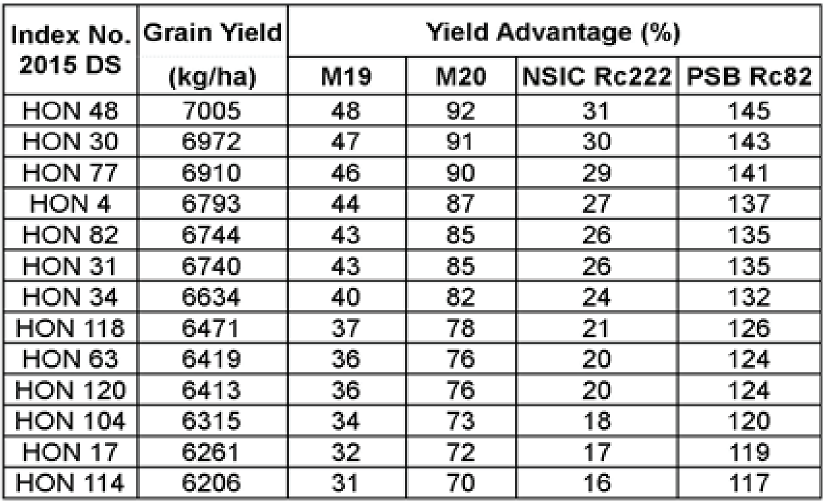
- 200 experimental hybrids were evaluated in the Hybrid Observational Nursery (HON) during the dry season using Mestiso 19 and Mestiso 20 as hybrid checks, and PSB Rc 82 and NSIC Rc 222 as inbred check varieties (Table 34). 28 hybrid entries surpassed the yield of the hybrid check Mestiso 19. HON 178 gave the highest yield (9,438 kg/ ha) followed by HON 18 (9255 kg/ha). F1 seeds were produced in 2015 WS for testing in PYT in the coming 2016 DS. Meanwhile, 100 hybrids were planted in the HON during the 2015 wet season. Grain yield of hybrids ranged from 1708 kg/ha to 7005 kg/ha. 34 hybrids gave significantly better yield performance than the higher yielding hybrid check, Mestiso 19 (Table 35). HON 48 yielded the highest (7,005 kg/ha) followed by HON 30 (6972 kg/ha) and HON 77 (6910kg/ha). F1 seeds of these promising hybrids will be produced in 2016 DS for further testing in the Hybrid Preliminary Yield Trial (HPYT) in 2016 WS.

Table 34. Grain yield (kg/ha) of good performing hybrids in the HON, 2015 DS.



Index No. 2015 DS	Grain Yield (kg/ha)	Yield Advantage (%)			
		M19	M20	NSIC Rc222	PSB Rc82
HON 178	9438	32.5	30.6	51.5	37.6
HON 18	9255	29.9	28.0	48.5	35.0
HON 143	9237	29.7	27.8	48.2	34.7
HON 131	9196	29.1	27.2	47.6	34.1
HON 179	9192	29.1	27.2	47.5	34.1
HON 162	9133	28.2	26.3	46.6	33.2
HON 119	8817	23.8	22	41.5	28.6
HON 137	8815	23.8	22.0	41.5	28.6
HON 61	8646	21.4	19.6	38.8	26.1
HON 129	8537	19.9	18.1	37.0	24.5

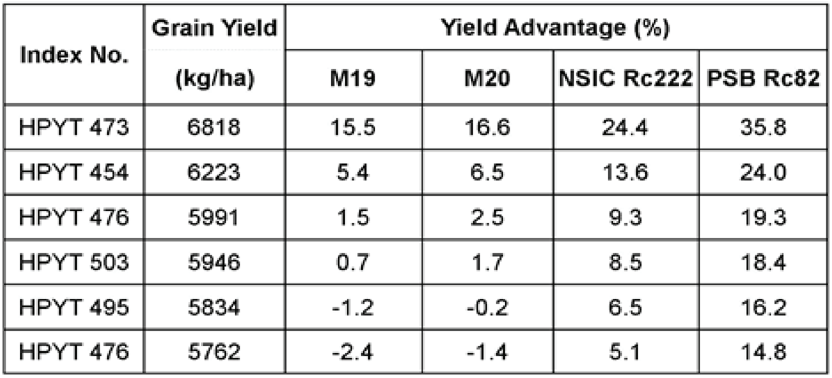
Table 35. Grain yield (kg/ha) of good performing hybrids in the HON, 2015 WS.



Index No. 2015 DS	Grain Yield (kg/ha)	Yield Advantage (%)			
		M19	M20	NSIC Rc222	PSB Rc82
HON 48	7005	48	92	31	145
HON 30	6972	47	91	30	143
HON 77	6910	46	90	29	141
HON 4	6793	44	87	27	137
HON 82	6744	43	85	26	135
HON 31	6740	43	85	26	135
HON 34	6634	40	82	24	132
HON 118	6471	37	78	21	126
HON 63	6419	36	76	20	124
HON 120	6413	36	76	20	124
HON 104	6315	34	73	18	120
HON 17	6261	32	72	17	119
HON 114	6206	31	70	16	117

- In the Hybrid Preliminary Yield Trial (HPYT), 48 experimental hybrids were evaluated during the dry season. In the first set, one hybrid (HPYT 473) gave an outstanding performance (Table 36). It significantly outyielded all the checks. This hybrid gave a 15.5% and 16.6% yield advantage over the hybrid checks M19 and M20, respectively while yield advantage over the inbred checks, PSB Rc 82 and NSIC Rc 222 were 35.8% and 24.4%, respectively. Three hybrids also gave positive yield advantage over the hybrid checks but the differences were not significant. The yield of hybrids ranged from 4851 to 6818kg/ha. In the second set of HPYT, six hybrids gave positive yield advantage over the hybrid checks but differences were not significant (Table 37). The yield of hybrid entries range from 5994 to 7012 kg/ha. Based on overall evaluation, 13 hybrids were selected to undergo another season of evaluation in the preliminary yield trial while 6 hybrids will be included in the advance yield trial.

Table 36. Grain yield (kg/ha) of good performing hybrids in the preliminary yield trial, 2015 DS (set1).



Index No.	Grain Yield (kg/ha)	Yield Advantage (%)			
		M19	M20	NSIC Rc222	PSB Rc82
HPYT 473	6818	15.5	16.6	24.4	35.8
HPYT 454	6223	5.4	6.5	13.6	24.0
HPYT 476	5991	1.5	2.5	9.3	19.3
HPYT 503	5946	0.7	1.7	8.5	18.4
HPYT 495	5834	-1.2	-0.2	6.5	16.2
HPYT 476	5762	-2.4	-1.4	5.1	14.8

- Meanwhile, 28 experimental hybrids were evaluated in the HPYT during the wet season (Table 37). Two hybrids (HPYT 515 and HPYT 511) showed superiority over M20 with yield advantage of 11.2 and 9.7%, respectively. Also, 8 hybrids outyielded the best inbred check NSIC Rc222 with a yield advantage ranging from 15.2 to 21.7%. The yield of hybrids ranged from 4176 to 5411kg/ha.

- Eighteen (18) promising hybrids comprised the Advance Yield Trial (AYT) conducted during the dry season (Table 38). No hybrid entry significantly outyielded the hybrid checks, M19 and M20, however, 9 hybrids gave more than 5% yield advantage over M19. Only one hybrid (HAYT 133) significantly outyielded the higher yielding check NSIC Rc 222 while 8 hybrids showed superiority over PSB Rc 82. Yield of hybrid entries range from 5693 to 7813kg/ha.

Table 37. Grain yield (kg/ha) of good performing hybrids in the preliminary yield trial, 2015 DS (set 2).

Index No	Grain Yield (kg/ha)	Yield Advantage (%)			
		M19	M20	NSIC Rc222	PSB Rc82
HPYT 507	7012	6.5	14.3	13.6	9.7
HPYT 517	6853	4.2	11.8	11.1	7.3
HPYT 509	6808	3.4	11.0	10.3	6.5
HPYT 527	6777	2.9	10.5	9.8	6.0
HPYT 522	6703	1.8	9.3	8.6	4.86
HPYT 523	6673	1.4	8.8	8.1	4.4

Table 38. Grain yield (kg/ha) of good performing hybrids in the preliminary yield trial, 2015 WS.

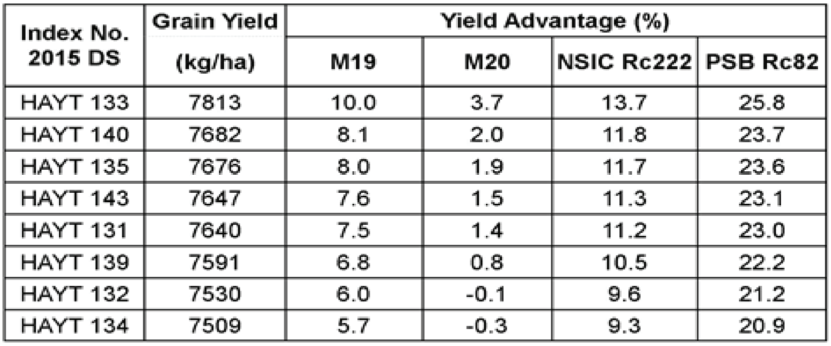
Index No.	Grain Yield (kg/ha)	Yield Advantage (%)			
		M19	M20	NSIC Rc222	PSB Rc82
HPYT 515	5411	8.6^{ns}	11.2^{*}	21.7^{*}	27.9^{*}
HPYT 511	5323	7.1^{ns}	9.7^{*}	20.4^{*}	26.8^{*}
HPYT 538	5215	5.2^{ns}	7.9^{ns}	18.7^{*}	25.2^{*}
HPYT 537	5157	4.1^{ns}	6.8^{ns}	17.8^{*}	24.4^{*}
HPYT 532	5069	2.4^{ns}	5.2^{ns}	16.4^{*}	23.1^{*}

- Included in the Advance Yield Trial were 3 and 5 hybrids which are purple-based version of Mestiso 19 and Mestiso 20, respectively. Results indicate that the yields of purple-based hybrids and the original green-based Mestiso 19 and Mestiso 20 are comparable.

- The 2015 WS Advance Yield Trial (AYT) was composed of 14 experimental hybrids, 2 inbred checks (PSB Rc82, NSIC Rc222) and 2 hybrid checks (M19 and M20). Hybrid entry AYT 127 gave a yield significantly higher than M20 with yield advantage of 10.5 percent (Table 40). However, none of the hybrids under evaluation had yield significantly higher than M19. Ten (10) hybrids showed superiority over NSIC

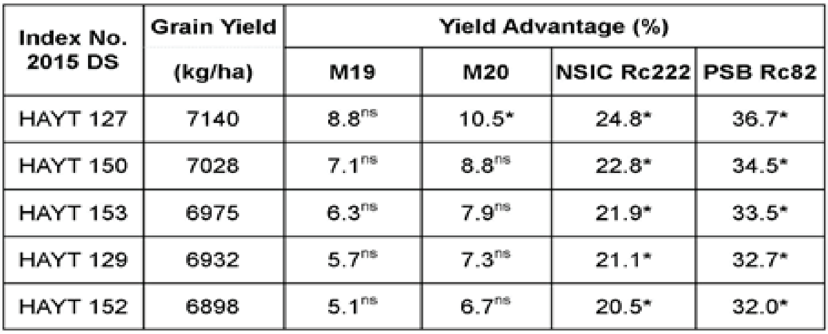
Rc222 with yield advantage ranging from 15.1 to 24.8%. However during the season, strong wind brought by typhoon Lando caused lodging in 3 hybrid entries. In terms of disease incidence, none of the hybrids tested showed RTV symptoms except for inbred check PSB Rc82. Yield of hybrids ranged from 5395 kg/ha to 7140 kg/ha.

Table 39. Grain yield (kg/ha) of good performing entries in the hybrid advance yield trial, 2015 DS.



Index No. 2015 DS	Grain Yield (kg/ha)	Yield Advantage (%)			
		M19	M20	NSIC Rc222	PSB Rc82
HAYT 133	7813	10.0	3.7	13.7	25.8
HAYT 140	7682	8.1	2.0	11.8	23.7
HAYT 135	7676	8.0	1.9	11.7	23.6
HAYT 143	7647	7.6	1.5	11.3	23.1
HAYT 131	7640	7.5	1.4	11.2	23.0
HAYT 139	7591	6.8	0.8	10.5	22.2
HAYT 132	7530	6.0	-0.1	9.6	21.2
HAYT 134	7509	5.7	-0.3	9.3	20.9

Table 40. Grain yield (kg/ha) of good performing entries in the hybrid advance yield trial, 2015 WS.



Index No. 2015 DS	Grain Yield (kg/ha)	Yield Advantage (%)			
		M19	M20	NSIC Rc222	PSB Rc82
HAYT 127	7140	8.8^{ns}	10.5*	24.8*	36.7*
HAYT 150	7028	7.1^{ns}	8.8^{ns}	22.8*	34.5*
HAYT 153	6975	6.3^{ns}	7.9^{ns}	21.9*	33.5*
HAYT 129	6932	5.7^{ns}	7.3^{ns}	21.1*	32.7*
HAYT 152	6898	5.1^{ns}	6.7^{ns}	20.5*	32.0*

F1 seed production of two-line hybrids for testing and evauation

SH Escamos, MAT Talavera and TMMasajo

Producing sufficient amounts of F1 seeds for testing is essential in the development of hybrids. This activity will help ensure that performance testing will not be constrained by limitations in the ability to produce/ reconstruct adequate amount of seeds of experimental hybrids particularly those destined for PYT, AYT, and the NCT.

Highlights:

- Sufficient quantities (40-300 grams) of F1 seeds of 85 promising experimental hybrids for PYT and AYT were successfully produced during the dry season. During the WS, more than 60 grams were produced from 21 hybrids but less than 60 grams from 66 hybrids.

- Eight small S x P plots for promising hybrids were established during the dry season but only 5 were successful. F1 yield of 5 hybrids range from 5 to 18 kg with two purple versions of M20 yielding more than 15 kgs. No yield was obtained from three S X P plots of purple-based Mestiso 19 due to severe shortage of irrigation water, resulting to no yield.

- S x P of purple-based M19 and M20 were established during the wet season. F1 seed yields for M19 and M20 were 11.23 kg and 23.12kg, respectively.

- F1 seed production of PRUP 10, a promising entry in the NCT was undertaken during the dry season. The plot suffered drought during the early stage which affected the synchronization of flowering. Twenty-two (22) kgs F1 seeds were produced. A larger S X P plot (.3 ha) of PRUP 10 was established during the wet season. Typhoon Lando came right at time of flowering of the SX P plot. However, despite the setback, 150kg F1 seed was produced.

V. Breeding of Specialty Rice

Project Leader: EC Arocena

Aromatic, glutinous, and pigmented rice are some of the specialty types that commands higher price in the market. Their yield, however are much lower than the regular rice. Recently, the demand is increasing; hence, there is a need to improve the yield potential and resistance of the existing varieties. Moreover, consumers are now becoming conscious on their wellness and the nutritional content of their rice intake. Thus, development and improvement of this kinds of rice are continuing efforts.

Development of aromatic, glutinous, pigmented, and iron/zinc-dense rice varieties

EC Arocena, KB Geneston, HT Ticman, GMOsoteo, and RCBraceros

Rice varietal development largely depends on the breeders and their ability to understand a range of breeding-related disciplines. It involves different steps depending upon the objectives, breeding methodologies and rice production systems. Blending the efforts of an interdisciplinary team undoubtedly achieve maximum results. However, the first and foremost is how well the breeders identify genetic donors based on the target traits and objectives set. Use of parental with diverse genetic make-up will simultaneously expand the genetic base for selection and opportunity to select promising lines with the target novel and/or superior characteristics of agronomic importance.

Highlights:

Line Development

- Results of the breeding efforts during the season are presented in Table 41. More crosses for glutinous and pigmented rice should be generated this WS.

- Majority of the selected plants in the hybrid populations (HP) and pedigree nursery (PN) were aromatic as shown in Figure 27. Each group was further segregated into excellent, good and fair kernel qualities (Figure 28). Only those plants with excellent to fair kernel qualities were advanced for further selection. Plants with poor kernel quality were discarded.

Table 41. Results of breeding efforts, 2015.

Nursery	Number of entries evaluated	Number of entries selected	Remarks
Parentals	160 varieties/lines	160 varieties/lines	Most of these entries have the desired quality characteristics, yield enhancing traits and resistance specifically for blast, BLB and tungro
New crosses	–	99 Aromatic (A), 53 Glutinous(G), 44 Pigmented(P) and 66 Zn/Fe	Seed setting of the crosses made was affected by inclement weather condition in WS
F_1 (crosses)	156A, 63G, 62P and 121 Zn/Fe	91 A, 29 G, 17 P and 89 Zn/|Fe for HPS 7A, 15G, 2 P for generation advance	Other crosses were discarded owing to poor plant type and susceptibility to BLB and blast 11A, 17P and 4Zn/Fe were stored in the cold room to be planted in 2016DS
MBN (Hybrid populations for generation advance)	77A, 20G, 24P, 80Zn/Fe	33A, 6G, 10P and 26Zn/Fe for plant selection 16A, 5G, 4P, 25Zn/Fe retained for generation advance	In the DS,13A, 6P and 5Zn/Fe were discarded owing to poor plant type, severe lodging and susceptibility to BLB, sheath blight and blast. Selection during the WS was also limited due to severe lodging and germination of the plants brought by two typhoons that visited the area when the plants were at soft dough (Kabayan) and hard dough/maturity (Lando).
HPS (Hybrid populations intended for single plant selection)	58A, 29G, 30P, 15Zn/Fe	Field selection= 12982 individual plants Laboratory = 3661 plants 1673A, 1480G, 1140P, 296 Zn/Fe	Selection during the WS was also limited due to severe lodging and germination of the plants brought by two typhoons that visited the area.
Pedigree Nursery (PNG)	3110 pedigree lines (1603A, 635G, 295P 577 Zn/Fe)	Final selection= 795 A, 319 G, 153 P, 260 Zn/Fe. Of these, 55A, 19G, 3P and 21 Zn/Fe uniform lines were elevated to AON for 2015 WS planting	Selection during the WS was also limited due to severe lodging and germination of the plants brought by two typhoons that visited the area.

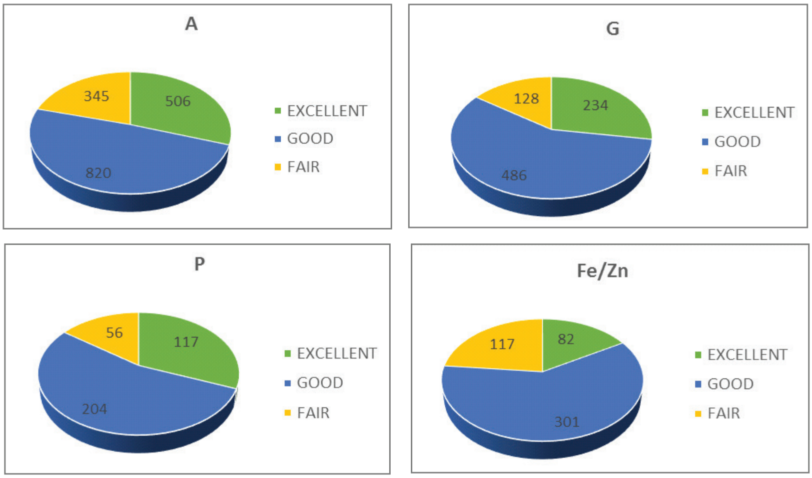


Figure 27. Kernel quality of the selected plants per specialty types from the HPS and PN, 2015DS.

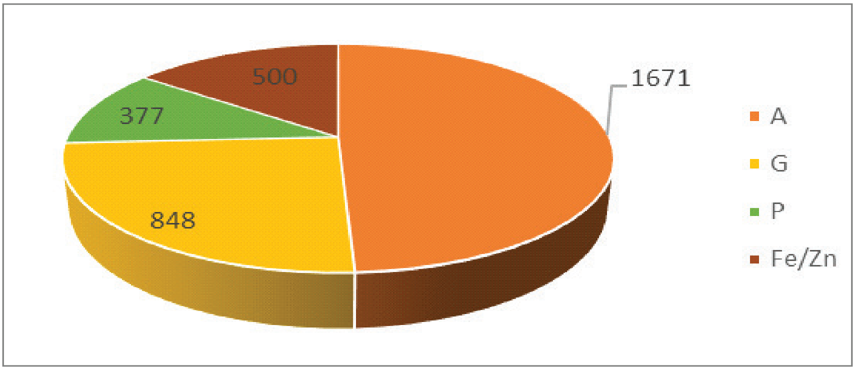


Figure 28. Selected plants in the hybrid populations (HP) and pedigree nursery (PN).

Promising lines in the performance trials

- In the Advanced Observation Nursery (AON), out of the 247 entries evaluated, 36 (A-21, Zn/Fe-5, P-10) were retained for further evaluation and 67 (A-24, Zn/Fe-19, G-10, P-14) were elevated to Preliminary Yield Trial (PYT). There were 31 non-aromatic entries but with high yields ranging from 6292kg/ha to 9589kg/ha and with good to excellent kernel qualities were transferred to AON-IL (18) and PYT-IL (13). Figure 29 shows the yield performance of the ten top yielding entries per specialty types elevated to (PYT). Yield range involving these entries were 7496kg/ha-8674kg/ha for A, 7219kg/ha-

9738kg/ha for Zn/Fe, 6962kg/ha-9635kg/ha for P and 5638kg/ha-9294kg/ha for G. These entries showed better yield performance than the corresponding group check variety.

- Promising entries were also identified among 130 PYT entries. Of these, 59 were retained for further evaluation. There were 2 A, 3 Zn/Fe, 1 P elevated to the multi-location yield trial (MYT) 2015WS evaluation in CES awaiting slots in the MET. Seed samples of these test entries were submitted to the Rice Chemistry and Food Science Division for grain quality evaluation. Figure 30 shows the other promising test entries with comparable to or better yield performance than the corresponding specialty type check variety.

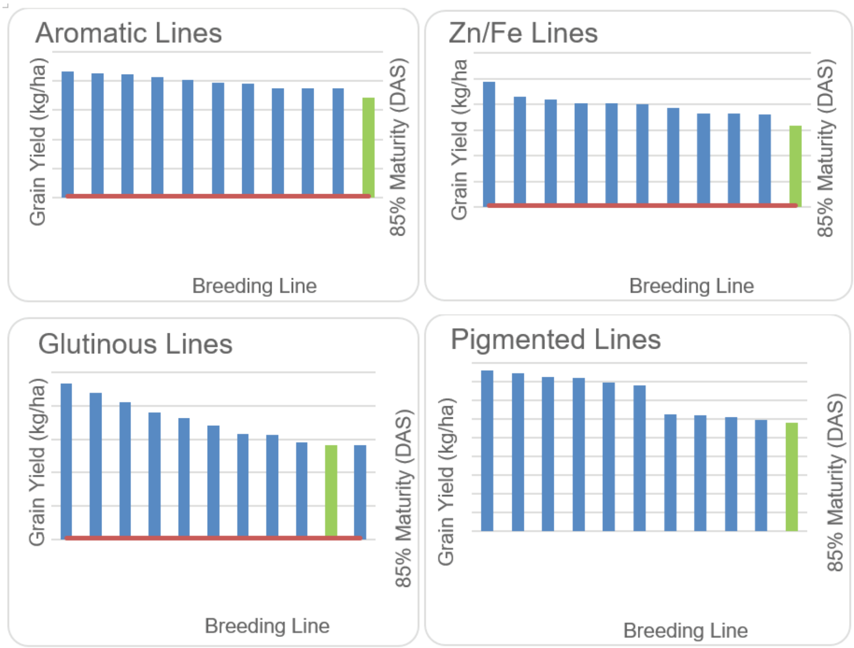


Figure 29. Yield performance and maturity of the top yielding entries per specialty types in the AON, 2015DS.

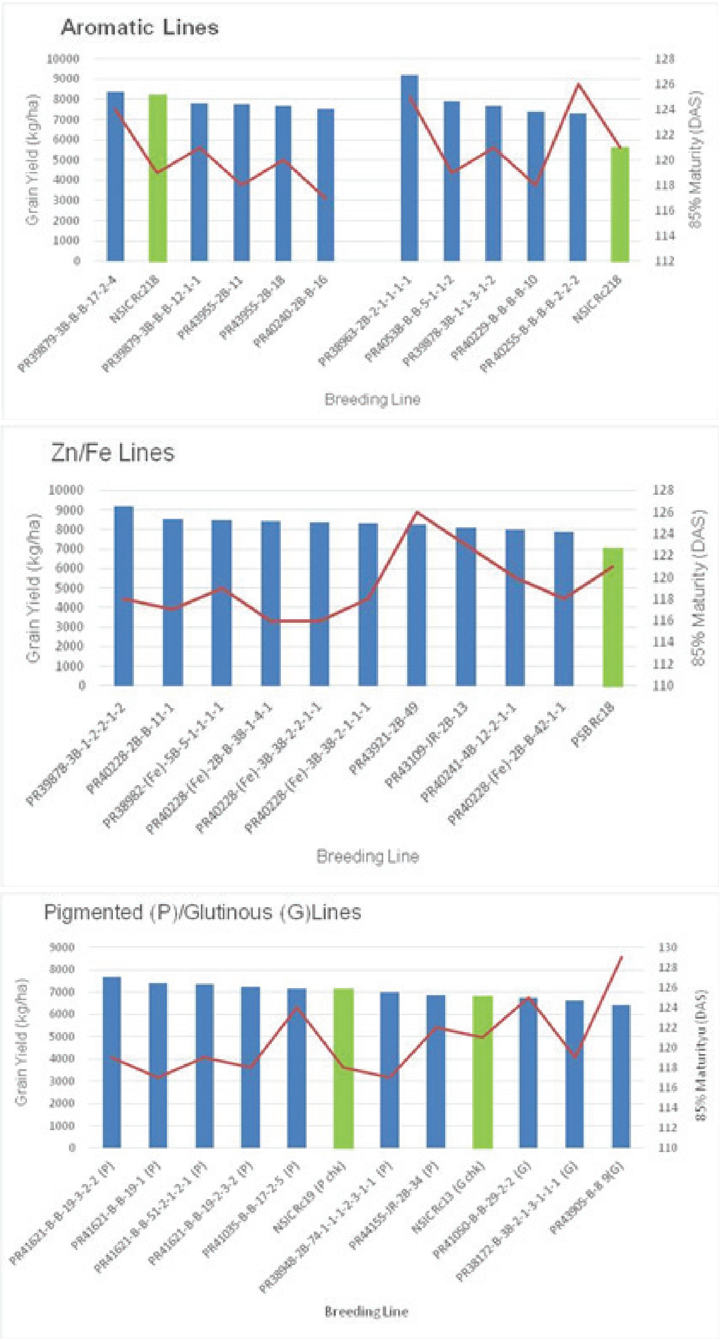


Figure 30. Yield performance and maturity of the top yielding entries per specialty types in the PYT, 2015DS.

Promising lines in the multi-location trials

- In the most advance stage of Multi-Environment Yield Trial (MET, Stage 2 module 2), there were 22 entries evaluated during the season. PR38168-2B-3-1-3-1-1-1-2, an aromatic line, ranked 7th across 7 test locations with an average yield of 5.43t/ha. This entry ranked 2nd in PhilRice San Mateo and 3rd in PhilRice Agusan with yields of 7.64t/ha and 5.79t/ha., respectively. Its AMMI Stability Values (ASV) across sites was 0.57 and ranked 12th majority of the test entries yielded comparably with the while its Yield Stability Index (YSI) was 19 and ranked 5th among 22 test entries. PR38963-(Fe)-B-5-4-2-1-1, another entry in the same group, ranked 10th with an average yield of 5.40t/ha. It registered the highest yield (7.71t/ha) in PhilRice San Mateo and 2nd in PhilRice CES with 9.06t/ha yield.

- PR38012-3B-1-3, a promising aromatic line which completed the required trials in MET was elevated to NCT for Special Purpose (NCT-SP), 2015W.

- In the NCT-SP, out of the 8 A, 8 G and 8 Zn/Fe test entries, there were 4 A, 7 G and 2 Zn/Fe PhilRice developed lines under evaluation. Under Maligaya condition, three A entries showed numerically higher yield performance than the aromatic check, NSIC Rc128 (9.9t/ha). These were PR38949-B-29-2 (10.7/ha), PR36905-B-1-11-2-1-1-1(10.7t/ha) and PR36914-B-9-4-1-6-4-1(10.3t/ha). These entries ranked 2nd, 3rd and 4th, respectively. Among the glutinous entries, PR34859-B-4-1-1-2-1 was the top yielder (10.8t/ha) with 9.0% yield advantage over NSIC Rc13 (9.9t/ha), the highest yielding check. PR41035-B-B-17-2-3-1 (9.4t/ha), another G entry, outyielded NSIC Rc15 (8.6t/ha) by 9.3%. Among the micronutrient-dense test entries, PR38963 (Fe)-B-7-1 (10.2t/ha) ranked 2nd with 20% yield advantage over PSB Rc82 (8.5t/ha), the yield check and 50% over MS13 (6.8t/ha), the micronutrient check variety.

Evaluation and utilization of fragrance markers for high-yielding aromatic breeding materials

TE Mananghaya, MV Embate, KC Geneston, HT Ticman , EC Arocena and LM Perez

Fragrance (aroma) is considered one of the most important grain quality traits in rice because aromatic rice cultivars command premium prices in the market today. However, the trait is recessive and thus breeding of aromatic rices needs extensive labor and has to involve large numbers of breeding materials to develop and identify a progeny with the target aromatic trait. Thus, molecular markers associated with fragrance trait will assist rice breeders to develop a high yielding variety with excellent grain quality in simple and inexpensive method. This study aims to evaluate a marker system to be used in marker assisted selection for fragrance trait in rice, and thus in aromatic breeding program.

Highlights:

- Assembled and evaluated new functional markers, the FMbadh2-E2A, FMbadh2-E2B and ous and 143 plants were negative to fragrance gene. The F2 plants detected positive to fragrance gene and found aromatic trait using KOH method were selected for forward breeding.

- Polymorphism survey using multiplex fragrance markers were conducted in 102 germplasm materials composed of 96 Philippine landraces and 6 improved varieties. Black Rice labelled in North Cotabato for its export quality was detected negative to fragrant allele, as well as Malagkit Sungsong and Improved Malagkit Sungsong (IMS-2). NSIC Rc128, NSIC Rc342 and NSIC Rc344, released rice varieties claimed aromatic also showed homozygous non fragrant allele using the diagnostic markers. While, NSIC Rc148, NSIC Rc218, Asucena and Binarit showed diagnostic allele for homozygous fragrant allele (Figure 31). Out of 96 traditional varieties evaluated, 74 F2 plants were identified positive to fragrant allele. These potential parents can be used as pollen donor for aromatic rice breeding in PhilRice.

- Segregating population of PR40476-3B-1-1/HHZ12-DT10-SAL1-DT1, PR37994-B-20-2-2-1/PR34627-B-44-2-1-2-1-1, HHZ3-SAL13-Y1-SAL1/PR37343-B-6-3-2-2-2 were established for evaluation of fragrance trait. For each cross combination, 200 F2 plants were individually tagged and leaf samples were collected prior to DNA genotyping using fragrance markers. A total of 600 F2 plants were evaluated and 284 plants showed fragrant allele, 112 detected heterozygous and 143 plants were negative to fragrance gene. The F2 plants detected positive to fragrance gene and found aromatic trait using KOH method were selected for forward breeding.

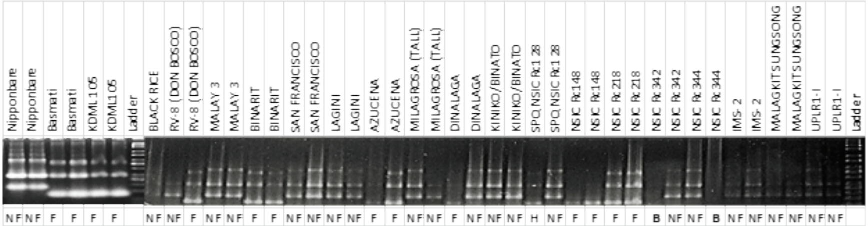


Figure 31. Result of DNA analysis of selected parents and traditional rice cultivars using fragrance markers (Bradbury 2005).

Table 42. Summary of DNA genotyping of F2 segregating plants for detection of fragrant trait using multiplex PCR fragrance markers.

Field Code				Fragrance Genotyping		
2015 DS	Parentage	Pedigree Name	Generation	Fragrant	Non-Fragrant	Heterozygous
HPS-SP-1-1	PR40476-3B-1-1/HHZ12-DT10-SAL1-DT1	PR46405-B-1	F2:3	157	21	24
HPS-SP-5-1	PR37994-B-20-2-2-1/PR34627-B-44-2-1-2-1-1	PR46409-B-5-1	F2:3	64	71	46
HPS-SP-6-1	HHZ3-SAL13-Y1-SAL1/PR37343-B-6-3-2-2-2	PR46416-B-6-1	F2:3	63	51	42

Production of golden rice introgression lines in the background of selected popular varieties with resistance to tungro and bacterial leaf blight

CC Adeva, RT Miranda, CFS Te, NR Sevilla and AA Alfonso

Golden Rice (GR), which contains elevated levels of the pro-vitamin A beta-carotene in the grains, was developed about a decade ago through biochemical engineering of the carotenoid biosynthetic pathway. It is eyed as an additional food-based strategy to combat the pervasive and persistent problem of vitamin A deficiency (VAD) especially in most rice-eating countries. VAD can damage the immune system and decrease the body's ability to resist or fight infections; thereby, increasing the risk of mortality from common diseases, especially among women and young children. It may also result in impaired vision, including night blindness and permanent blindness. In the Philippines, about four out of ten children aged six months to five years and three out of every ten school-aged children have VAD. In addition, one out of every five pregnant and one out of every five lactating mothers have VAD. VAD continues to adversely affect many people despite nutrition interventions such as vitamin A fortification and supplementation programs that seek to provide adequate vitamin A to those at risk. Further research has elevated the amount of vitamin A to a meaningful level (up to 36 μg/g) and preliminary results indicate high conversion rate (4:1) of beta-carotene from GR into retinol. The Golden Rice donor is a US commercial variety that grows poorly under Philippine condition. This projects aims to develop Golden Rice adapted under Philippine condition.

Highlights:

- Phenotypic and genotypic evaluations were done to characterize the identified 2-in-1 line donor, PR37171-1-1-1-2-2-1-1 (also designated as LINE 27) and NSIC Rc120, also known as Matatag 6 (tungro resistant donor).

- LINE 27 and NSIC Rc120 were both phenotypically screened for Rice Tungro Virus (RTV) and Bacterial Leaf Blight (BLB) resistance. Table 43 shows that Line 27 has intermediate reaction while NSIC Rc120 has resistance reaction against RTV. For BLB screening, LINE 27 was confirmed to have high resistance reaction against Race 3 (Maligaya Race) and Race 6, the most virulent Xanthomonas oryzae pv. oryzae (Xoo) strain; while NSIC Rc120 shows resistance reaction only to Race 3.

- Line 27 and NSIC Rc120 along with ARC11554 (positive check) and Taichung Native 1 (TN1) (negative check) were genotypically evaluated using Simple Sequence Repeat (SSR) markers RM5495 and RM8213 linked to rice tungro spherical virus 1 (tsv1) loci for tungro resistance and Green leafhopper resistance-14 (Glh14) loci for green leafhopper (GLH) resistance. Figure 32 shows that LINE 27 has similar expected band size to TN1 which is susceptible to tungro spherical virus but resistant to green leafhopper which is similar to the expected band size of ARC11554. On the other hand, NSIC Rc120 has similar expected band size to ARC11554 possessing both resistance to tungro spherical virus and green leafhopper.

- Two F2 populations of reciprocal crosses between LINE 27 and NSIC Rc120 were generated and advanced. In addition, four new F1s were generated with one backcross and three double crosses between F1 and LINE 27.

Table 43. Phenotypic reactions of different lines to Races 3 and 6 of Xoo at 14-days after inoculation and to tungro resistance at three to four weeks after inoculation.

ENTRY CODE	Race 3		Race 6		RTV Rating
	Lesion length (cm)	BLB Rating	Lesion Length (cm)	BLB Rating	
Line 27	0.2	R	0.1	R	I
NSIC Rc120	2.57	R	31.9	S	R
ARC11554	–	–	6.2	I	R
UTRIMERAH	–	–	16.7	S	R
IR64	–	–	–	–	MS
TN1	33.8	S	30.9	S	S
IR24	10.4	MS	29.03	S	–
IRBB4	11.8	MS	11.7	MS	–
IRBB5	12.3	MS	11.9	MS	–
IRBB7	18.4	S	19.6	S	–
IRBB21	9.49	I	11.9	MS	–
IRBB61	3.37	R	8.2	I	–

Legend: RTV Rating: R – resistant; MS – moderately resistant; I – Intermediate; S –Susceptible
Lesion length/BLB Rating: 0-5 cm (R-Resistant); >5-10 cm (I-Intermediate); >10-15 cm (MS Moderately susceptible); >15 cm (S-Susceptible)

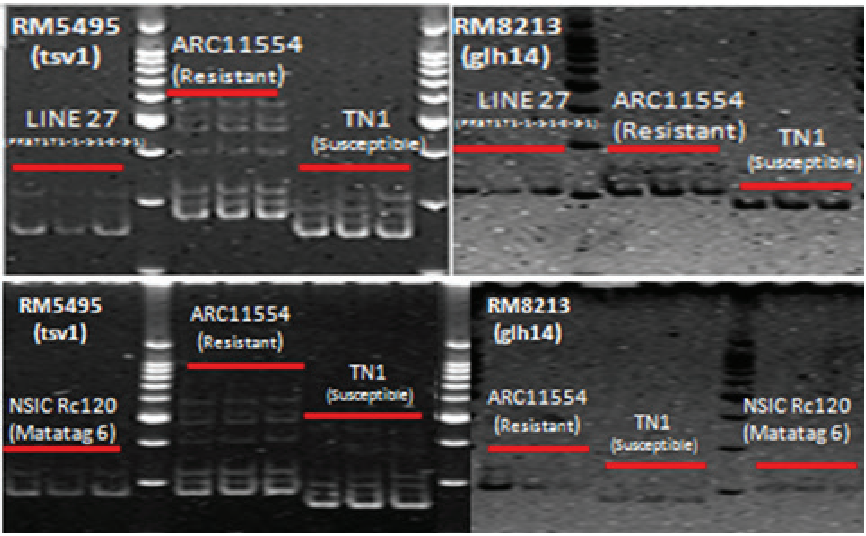


Figure 32. PCR amplification of LINE 27 (PR37171-1-1-1-2-2-1-1) and NSIC Rc120 (Matatag 6) together with resistant (ARC11554) and susceptible (TN1) checks for rice tungro virus using functional SSR markers: RM5495 (tsv1 for tungro resistance) and RM8213 (Glh14 for GLH resistance). L = DNA marker (100 bp).

VI. Development of Rice Barieties Adapted to Rainfed and Stress Environments

Project Leader: NL Manigbas

There are many restricting factors affecting rice growth and development under different environmental conditions. These factors greatly affect yield which in turn affects the ability to cater the continual increase in rice demand of the increasing population. Under these complex and variable environments, breeding objectives must shift to developing varieties which are adapted to specific target environment. To address this constraints and challenges, different breeding strategies, which include integrated management technologies, Marker-Assisted Selection, classical hybridization and selection, in vitro culture, in vitro mutagenesis, anther culture, root plasticity development, and incorporation of tungro and bacterial blight disease resistance genes are employed to generate and develop improved breeding lines for the target ecosystem.

Breeding drought-tolerant rice varieties

NV Desamero, CC Cabusora, MV Chico, JC Bagarra, GD Valida, JC Bagarra

Drought is a major restricting factor in rice production under rainfed ecosystem. Developing drought tolerant varieties with high yield potential is one of the challenges in breeding for rainfed lowland rice environment. To cope with this challenge, different breeding strategies, which include classical hybridization and selection, in vitro culture, in vitro mutagenesis and anther culture are employed to generate and develop improved breeding lines for the target ecosystem. This study prioritizes drought tolerance improvement, along with other associated traits. Other traits crucial to adaptation and adoption in the target environments, which include high yield, good grain and eating quality and resistance to prevailing major diseases, are likewise considered in variety development.

Highlights:

1. Trait Discovery
    - Evaluation of 19 traditional rice varieties (TRV's) for drought tolerance at seedling stage identified 3 (15.8%) tolerant cultivars, viz. Payakan, Pinyas and C-1, and 16 (84.2%) susceptible on the basis of drought recovery rate (DRR). Seed increased 102 tolerant plants from 17 TRV's will be evaluated for uniformity, agronomic traits and drought tolerance at reproductive stage in 2016 DS. Re-screening for validation of the identified TRV's for drought tolerance at seedling stage is in progress.

    - Evaluation for blast resistance of the 17 TRV's with drought tolerance identified 7 (41.2%) resistant, 7 (41.2%) with intermediate resistance and 3 (17.6%) susceptible. TRV Pinyas is resistant to blast, and Payakan has intermediate resistance. The TRV's will be re-screen for validation in 2016 DS.

- Evaluation of 153 in vitro-derived mutant lines identified 32 (54.2%) of the 59 lines from Jepun and 80 (85.1%) of the 94 lines from Ydamdo as tolerant to moderately tolerant to drought at seedling stage, with DRR ranging from 40.4% to 97.9%. A total of 287 plant selections were made and were seed increased for further evaluation and line development in 2016 DS.

- Due to non-functioning of the air condition unit of the dark incubation room for callus induction, anthers from four pigmented TRV's, viz., Ballatinaw-luna, Ballatinaw-Dati, Lastog and Ominio cultufred in 2015 DS did not respond. Optimum temperature is crucial in callus induction of anthers. Acquisition of new units is in progress.

2. Breeding line development

A. Conventional Breeding Approach (Classical Hybridization and Selection)

i. Generation of F1 progeny and early generation line development

- In 2015 60 single crosses were made (Table 39), 28 in dry season and 32 in wet season. The crosses combined drought tolerance with submergence, saline tolerance and other desirable agronomic traits, selecting new released varieties and high yielding elite inbred lines as female parents and drought, submergence, saline, combined saline-submergence tolerant elite lines as males. Some TRVs were used as donor for abiotic stress tolerance and disease resistance. A total of 2,960 F1 seeds (1,534 in DS and 1,426 in WS) were generated and for evaluation and F2 seed production in 2016 DS.

- In DS, 3 F2 populations from the cross Zhonghua 1/ NSIC Rc194, NSIC Rc212/BPI 76, NSIC Rc222/ BPI 76, were established resulting in the selections of 128 plants with well exserted panicles and 90 to100cm plant height. Further evaluation of the selected lines for uniformity and other agronomic traits will be done in 2016 DS.

- In WS, due to lodging caused by the typhoon Lando, random bulk selection was done for the 5 F2 populations (SHZ-2/ HHZ5-SAL8-DT3-SUB1, HHZ5-SAL8-DT3-SUB1/SHZ-2, PSB Rc50/ NSIC Rc300, NSIC Rc194/ NSIC Rc182 and NSIC Rc298/ NSIC Rc194). In 2016 DS these crosses will be subjected to appropriate conditions (abiotic and biotic stress) for plant selection using the subsets that were made during random bulk selection.

ii. Advanced and fixed line generation

- In 2015 DS, 6,238 breeding lines from 132 crosses at F3 to F7 generation, were evaluated in the pedigree nursery for line selection and advance. A total of 1,577 (19%) lines from 91 crosses were selected based on phenotypic acceptability. In 2015 WS, 3,143 breeding lines from 97 crosses at F3 to F7 generations were planted for evaluation and selection for generation advance. From the 202 F3 families, 93 (46%) were selected and 109 (54%) were discarded. From F4 generation, 616 (32%) and 1,309 (68%) lines were dropped. From F5, F6 and F7, 616 (32%), 186 (44%) and 153 (63%) lines were selected, respectively. Higher selection efficiency was obtained from wet season (40%) than in dry season (25%).

- In 2015, evaluation of 1,833 breeding lines (1,354 from DS and 479 from WS) from 34 crosses (24 from DS and 10 from WS) at F8 generation, resulted in the selection of 267(14.5%) lines (148 from DS and 208 from WS) based on good phenotypic acceptability, uniformity and kernel quality. Selections will be evaluated for reproductive drought stress tolerance in 2016 DS.

- Based on uniformity and phenotypic acceptability, a total of 282 from 34 crosses from F6 to F8 were selected and will be screened for reproductive drought stress tolerance in 2016 DS. Lines that will be selected in mass screen will be forwarded to observational nursery for yield trial evaluation.

iii. Blast screening

- Two batches of screening was done in 2015. Batch 1 was consisted of 163 stable lines, from which 98 (60%) lines were identified resistant, 37 (23%) intermediate and 28 (17%) lines susceptible. Selected lines will be subjected for grain quality evaluation in 2016 DS. F2 segregating populations from 13 crosses were scored based on its overall infection. Healthy plants from the segregating populations were harvested and seed increased for further evaluation in 2016 DS.

- Batch 2 was consisted of 31 F4 populations and 32 F5 populations. From the F4 populations, 21 (68%) were resistant, 2 (6%) were intermediate and 8 (26%) were susceptible, whereas in F5 populations, 24 (75%) were resistant, 1 (3%) was intermediate and 7 (22%) were susceptible. A total of 40 healthy plants from each resistant lines were transplanted for seed increase in 2015 WS, for 2016 DS evaluation.

Table 44. Generated F1 seeds (naked) from single crosses made in 2015, PhilRice CES.

No.	Parentage	No. of F_1 seeds	Target Trait
Dry Season Crosses			
1	NSIC Rc288/FL478	36	Drought and Salinity tolerance
2	PR38560-1-Azucena-Coll.No. 1528-M5R-1 DrS 111/FL478	75	Drought and Salinity tolerance
3	NSIC Rc238/PR40858-310-NSIC Rc9-M4R-310 DrS1067	59	Drought tolerance, High Yielding
4	NSIC Rc238/ PR41395-NSIC RC9-IVM2009DS 1-11-4 DrS1085	180	Drought tolerance, High Yielding
5	NSIC Rc288/ PR34358-5-Pokkali-AC-37-M5R-15 DrS93	91	Drought tolerance, High Yielding
6	NSIC Rc308/ PR40858-310-NSIC Rc9-M4R-310 DrS1067	73	Drought tolerance, High Yielding
7	NSIC Rc240/ PR34358-5-Pokkali-AC-37-M5R-15 DrS93	22	Drought tolerance, High Yielding
8	NSIC Rc300/ PR34358-5-Pokkali-AC-37-M5R-15 DrS93	50	Drought tolerance, High Yielding
9	PR34358-5-Pokkali-AC-37-M5R-15 DrS93/ DESO	34	Drought tolerance, High Yielding
10	Kinandang Patong/ DESO	30	Drought tolerance, High Yielding
11	PSB Rc18 sub1/ DESO	26	Drought tolerance, High Yielding
12	NSIC Rc120/ PR34358-5-Pokkali-AC-37-M5R-15 DrS93	78	Drought Tolerance, Tungro Resistance
13	NSIC Rc182/PR38560-1-Azucena-Coll.No. 1528-M5R-1 DrS 111	133	Drought Tolerance, Tungro Resistance
14	NSIC Rc182/PR34358-5-Pokkali-AC-37-M5R-15 DrS93	43	Drought Tolerance, Tungro Resistance
15	NSIC Rc188/PR34358-5-Pokkali-AC-37-M5R-15 DrS93	31	Drought Tolerance, Tungro Resistance
16	PSB Rc68/ PR34358-5-Pokkali-AC-37-M5R-15 DrS93	20	Drought and Submergence tolerance
17	PR34358-5-Pokkali-AC-37-M5R-15 DrS93/ Kinandang Patong	69	Drought Tolerance, Deep Rooting
18	NSIC Rc288/Kinandang Patong	55	Drought Tolerance, Deep Rooting
19	PR38560-1-Azucena-Coll.No. 1528-M5R-1 DrS 111/NSIC Rc188	59	Drought Tolerance, Saline Tolerance
20	NSIC Rc300/ PSB Rc68	56	Drought Tolerance, Submergence Tolerance, Saline, High Yielding
21	PSB Rc68/ NSIC Rc120	70	Drought Tolerance, Submergence Tolerance, Saline, High Yielding
22	PR385260-1-Azucena-Coll.No. 1528-M5R-1 DrS 111/PSB Rc18	72	Drought Tolerance

Table 44. Generated F1 seeds (naked) from single crosses made in 2015, PhilRice CES. Con't.

23	PR38560-1-Azucena-Coll.No. 1528-M5R-1 DrS 111/ PR34358-5-Pokkali-AC-37-M5R-15 DrS93	37	Drought Tolerance
24	PR40858-310-NSIC Rc9-M4R-310 DrS1067/ PR34358-5-Pokkali-AC-37-M5R-15 DrS93	19	Drought Tolerance
25	PR41395-NSIC Rc9-IVM2009DS 1-11-4 DrS1085/ PR34358-5-Pokkali-AC-37-M5R-15 DrS93	25	Drought Tolerance
26	NSIC Rc120/ Kinandang Patong	37	Drought Tolerance, Tungro Resistance, Deep Rooting
27	NSIC Rc188/ Kinandand Patong	31	Drought Tolerance, Tungro Resistance, Deep Rooting
28	NSIC Rc308/Kinandang Patong	23	Drought Tolerance, High Yield, Deep Rooting
Wet Season Crosses			
29	IVC-21 (DrS 40)/FL378	45	Submergence Tolerance, Drought Tolerance, Grain Quality, Saline Tolerance
30	IVC-21 (DrS 40)/FL478	29	Submergence Tolerance, Drought Tolerance, Grain Quality, Saline Tolerance
31	IVC-21 (DrS 40)/IR86385-38-1-1-B	39	Submergence Tolerance, Drought Tolerance, Grain Quality, Saline-Submergence Tolerance
32	IVC-21 (DrS 40)/IR86385-58-2-1-B	36	Submergence Tolerance, Drought Tolerance, Grain Quality, Saline-Submergence Tolerance
33	IVC-21 (DrS 40)/IR86385-194-2-1-B	57	Submergence Tolerance, Drought Tolerance, Grain Quality, Saline-Submergence Tolerance
34	NSIC Rc240 (TUBIGAN 22)/Ciherang-Sub1	21	High Yielding, Submergence Tolerance
35	NSIC Rc240 (TUBIGAN 22)/IR86385-58-2-1-B	58	High Yielding, Saline-Submergence Tolerance
36	NSIC Rc298 (TUBIGAN 23)/FL378	24	High Yielding, Saline Tolerance
37	NSIC Rc298 (TUBIGAN 23)/FL478	20	High Yielding, Saline Tolerance
38	NSIC Rc298 (TUBIGAN 23)/NSIC Rc194 (SUBMARINO 1)	33	High Yielding, Submergence Tolerance
39	NSIC Rc298 (TUBIGAN 23)/PSB Rc18 Sub1	36	High Yielding, Submergence Tolerance
40	NSIC Rc298 (TUBIGAN 23)/IR86385-38-1-1-B	28	High Yielding, Saline-Submergence Tolerance
41	NSIC Rc298 (TUBIGAN 23)/IR86385-58-2-1-B	44	High Yielding, Saline-Submergence Tolerance

Table 44. Generated F1 seeds (naked) from single crosses made in 2015, PhilRice CES. Con't.

51	NSIC Rc308 (TUBIGAN 26)/FL378	40	High Yielding, Saline Tolerance
52	NSIC Rc308 (TUBIGAN 26)/FL478	45	High Yielding, Saline Tolerance
53	NSIC Rc308 (TUBIGAN 26)/PSB Rc18 Sub1	90	High Yielding, Submergence Tolerance
54	NSIC Rc308 (TUBIGAN 26)/IR86385-38-1-1-B	29	High Yielding, Saline Tolerance
55	NSIC Rc308 (TUBIGAN 26)/IR86385-58-2-1-B	29	High Yielding, Saline Tolerance
56	NSIC Rc308 (TUBIGAN 26)/IR86385-194-2-1-B	97	High Yielding, Saline Tolerance
57	DEZO 300/FL378	26	High Yielding, Saline Tolerance
58	DEZO 300/IR86385-38-1-1-B	38	High Yielding, Saline-Submergence Tolerance
59	DEZO 300/IR86385-58-2-1-B	20	High Yielding, Saline-Submergence Tolerance
60	NSIC Rc218/FL478	19	High Yielding, Saline Tolerance
Total		2,960	

Table 45. Breeding line evaluation and selection made in 2015 dry and wet season for generation advance.

Generation	Dry Season					Wet Season				
	Evaluation		Selection			Evaluation		Selection		
	no. of cross	no. of lines	no. of cross	no. of lines	Efficiency (%)	no. of cross	no. of lines	no. of cross	no. of lines	Efficiency (%)
F_3	2	162	1	82	51	3	202	3	93	46
F_4	28	1,458	22	422	29	13	1,925	13	616	32
F_5	37	1,063	27	244	23	22	422	21	186	44
F_6	41	1,880	32	350	19	27	244	27	153	63
F_7	24	1,675	9	479	29	32	350	32	209	60
Total	**132**	**6,238**	**91**	**1,577**	**25**	**97**	**3143**	**96**	**1,257**	**40**

Table 46. Lines selected at F8 generation, 2015 WS, PhilRice CES.

No.	Parentage	No. of lines
Dry season		
Drought tolerance		
1	PR38560-1-Azucena-Coll. No. 1528-M5R-1 DrS 111/PSB Rc82	11
2	PR38583-IR64-AC97WP-135 8-4-1/PSB Rc82	18
3	PR37443-13/PR38560-1-Azucena-Coll. No. 1528-M5R-1 DrS 111	5
4	BP 227 B-MR-1-5/NSIC Rc218//PR38793-2B-24-2	15
5	NSIC Rc192/NSIC Rc148//WAB 891 SG 9	3
Submergence tolerance		
6	PR25769-B-9-1/1*PSB Rc18-Sub1	13
7	AZUCENA-IRGC 328/PR39397-7-153-240//IR64-Sub1	16
8	NERICA 2/PR39397-7-153-240//IR64-Sub1	6
Saline-Submergence tolerance		
10	FL378/PSB Rc18-Sub1	86
11	PR25769-B-9-1/1*PSB Rc18-Sub1	35
Wet season		
Drought tolerance		
1	NERICA 4/PR30245-AC-128	1
2	Salumpikit/IR64	4
3	BP 227 B-MR-1-5/NSIC Rc218//PR38793-2B-24-2	1
4	PR38583-IR64-AC97WP-135 8-4-1/SHZ-2	3
5	PR25769-B-9-1/1*NSIC Rc222	6
6	PR30025-99AC-WSAL-1087/SHZ-2	4
7	NSIC Rc192/NSIC Rc148//NSIC Rc120	6
8	PR30245-AC-128/SHZ-2	7
Drought tolerance, submergence tolerance		
9	PR34350-4-Pokkali-AC-24-M_5R-10 DrS 88/PSB Rc18-Sub1	5
10	PR25769-B-9-1/1*PSB Rc18-Sub1	3
11	PR34363-4-Pokkali-AC-45-M_5R-19 DrS 97/PSB Rc18-Sub1	17
12	AZUCENA-IRGC 328/PR39397-7-153-240//NSIC Rc194	2
Total		**267**

B. Doubled-haploid Breeding

- Since the aircon unit of the culture room for plant regeneration bagged down, callus pieces from the anther cultured crosses, NSIC Rc212/BPI 76 and NSIC Rc222/BPI 76 in 2015 DS were not regenerated. Optimum condition (light, temperature and humidity) is important in obtaining plant regeneration response of the tissues. Request for new units are in progress.

- The 77 advanced doubled haploid lines generated from six genotypes were evaluated for agronomic traits and yield under irrigated (well-watered) and managed drought condition in the 2015 DS observational nursery (ON) trials, and under irrigated and rainfed condition in the WS. The results were reported in Activity 3 (Field performance evaluation).

C. Mutation Breeding

i. NSIC Rc222 seed-mutant lines

- Genotyping of 42 NSIC Rc222-derived mutant lines for Glh14 (gene for GLH resistance) and tsv1 (gene for RTD resistance) using SSR markers RM8213 (GLH) and RM 5495 (RTD), identified 12 (28.6%) lines positive to both genes, with alleles the same as ARC11554 (Figure 33). Evaluation of these lines for amylose content identified 9 (23.7%) lines with lower AC of 21.2% to 22.0% than the wild type, which has 24.1%.

- Evaluation of these lines (SM5 generation) for agronomic traits in 2015 WS, showed that there were segregation in plant height, thus a single plant variability evaluation was implemented. Encoding of data is still in progress. A total of 616 SM6 sub-lines were generated and will be evaluated for uniformity in agronomic traits, grain quality and RTD resistance in 2016.

ii. Y Dam Do and Jepun IVC lines

- A total of 102 IVM3 lines from Y Dam Do were evaluated for uniformity, agronomic traits and yield, from which 100 (98%) lines were uniform and 2 (2%) lines were segregating. Based on phenotypic acceptability, 10 (10%) lines were selected with grain yield of 2.055t/ha to 5.615t/ha, and based on yield, 38 (38%) lines (6.185t/ha to 9.603t/ha) were selected with yield comparable or better than NSIC Rc222 (6.228 t/ha). Yield component evaluation of the lines is still in progress. Selections will be further evaluated, validated, and will be screened for reproductive drought tolerance in 2016 DS.

- A total of 70 IVM3 lines from Jepun were also evaluated for uniformity, agronomic traits and yield, from which 64 (91%) lines were uniform and 6 (9%) lines segregating in plant height. A selection of 8 (11%) lines was made based on yield (comparable or better than NSIC Rc222). Yield of the selections ranged from 5.609 to 8.388t/ha. Yield component evaluation of the lines is still in progress. Selections will be further evaluated, validated, and will be screened for reproductive drought tolerance in 2016 DS.

iii. Advanced mutant lines

- Evaluation of 34 stable in vitro mutant lines from six genotypes, viz., FR13A, Tanggiling, Negros, Namsagui 19, Kawilan and Mestizo 29, for drought tolerance at seedling stage identified 2 (5.6%) tolerant and 12 (33.3%) moderately tolerant lines, 12 (33.3%) susceptible and 10 (27.8%) highly susceptible lines (Table 42). Evaluation for grain quality of these lines is in progress.

- The performance of 178 stable mutant lines from 10 genotypes under ON-irrigated and managed drought in 2015 DS and under irrigated and rainfed condition in WS was evaluated and the results were reported in Activity 3 (Field Performance).

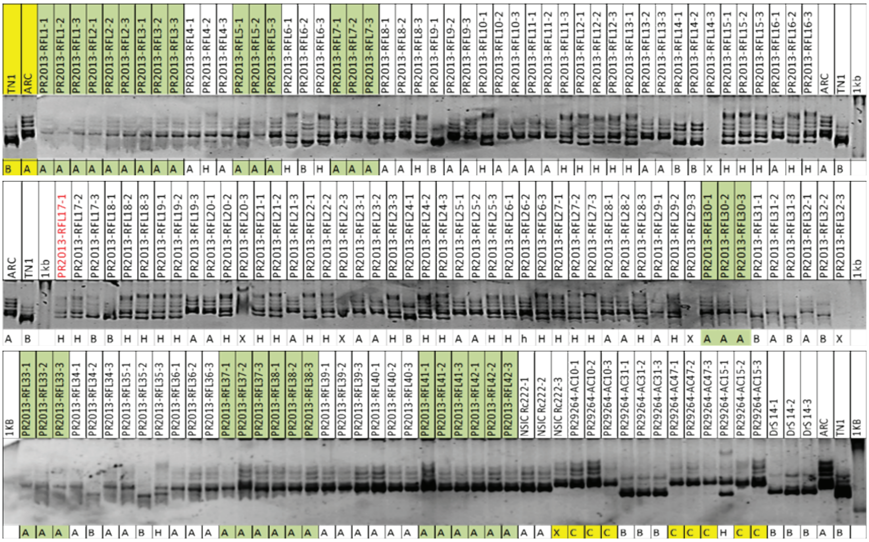


Figure 33. Polymorphism survey of tsv gene RM5495 in 42 NSIC Rc222-seed mutant derived lines. (Note: Entries in green are genotypes carrying tsv allele).

Table 47. Evaluation of IVC lines derived from Y Dam Do and Jepun for agronomic traits and yield in 2015 DS, PhilRice CES.

Agronomic Trait	A. Y Dam Do IVC Lines						B. Jepun IVC Lines					
	Minimum	Maximum	Range	Mean	StDev	CV	Minimum	Maximum	Range	Mean	StDev	CV
Days to Heading	76	101	25	93	5.7	6.1	79	101	22	91	5.6	6.1
No. of productive tillers	9	32	23	17	2.9	17.1	7	28	20	16	3.3	20.3
Plant Height at maturity (cm)	86	159	73	101	10.2	10.1	83	138	55	98	11.4	11.7
Panicle length (cm)	18	27	9	23	1.7	7.2	20	26	6	23	24.7	107.5
Grain yield (tha^{-1})	1.186	9.603	8.417	4.917	1.896	38.6	0.325	8.388	8.063	3.877	1.826	47.095

3. Field Performance Evaluation

In 2015, 210 breeding lines together with check varieties (IR64, PSB Rc14, NSIC Rc192 and NSIC Rc222) were evaluated for growth and yield performances under irrigated and managed drought in DS and irrigated and rainfed condition in WS. The trials were arranged in Randomized Complete Block Design with 3 replications. The seeds were sown in raised seedbed method and transplanted after 21 DAS. For irrigated condition, seedlings were transplanted in 8.8 m2 plots while in rainfed set up 6.4 m2 (8 rows each 4 meter long) with 20 cm interplant distance.

- In DS, under irrigated condition, 31 (14.9%) lines out yielded the highest yielding check, NSIC Rc222 by 0.11% (0.007t/ha) to 23.6% (1.467t/ha). Under managed drought 44 (21%) breeding lines out yielded PSB Rc14 (2.239t/ha) by 2.7% (0.062 t/ha) to 129% (2.902t/ha).

- In WS, under favorable condition, 87 (41%) lines yielded 3.9% (3.570t/ha) to 72% (5.905t/ha) higher than the population mean (3.436t/ha), and 12 (6%) lines yielded 3.6% (0.177t/ha) to 19.3% (0.957t/ha) higher than PSB Rc14 (4.881 t/ha). Under rainfed condition, 103 (49%) breeding lines had 5% yield advantage over the population mean (3.057t/ha), and 15 (7%) lines out yielded NSIC Rc222 (4.202t/ha) by 7.5% (0.315t/ha) to 40.5% (1.701t/ha).

- Combining the yield performance of the 4 trials (irrigated & managed-drought in DS, and irrigated & rainfed in WS) identified 105 (50%) lines as potential selection for multi-environment trial (MET). These lines were identified in comparison with the checks or mean population grain yield performance. The final selection of the lines was done on the basis of the performance across the four trials under different conditions.

- Grain yield during the WS was affected by typhoons "KABAYAN" and "LANDO", resulting to a lower yield range compared to the DS.

Mass screening for salinity, submergence and seedling stage drought tolerance

NV Desamero, JC Bagarra, GD Valida

An efficient and effective screening facility and protocol for abiotic stress tolerance is a key component and a must requirement for a successful rice breeding program for addressing developing and improving varieties with tolerance to abiotic stress. The mass screen protocol must be cost effective and must produce reliable and repeatable results. Pre-selection of breeding materials under controlled or managed condition increases selection efficiency in the target environment where the breeding lines are bred for.

Highlights:

1. Drought tolerance screen at seedling stage

    - The mass screen of the 288 entries (unreplicated), which were composed of in vitro-derived mutants identified 182 (63%) genotypes exhibiting some degree of tolerance to drought stress at seedling to early vegetative stage (Table 48). Of these genotypes, 28 were highly tolerant (HT), 78 tolerant (T) and 76 moderately tolerant (MT). Four in vitro-derived mutant populations were identified to be highly diverse with a Shannon-Weaver index (SWI) value ranging from 3.03 to 4.03.

    - For the 155 entries composed of stable mutant lines, TRVs and promising lines under observational nursery (replicated), 40 (26%) genotypes exhibited some degree of tolerance to drought stress at seedling to early vegetative stage (Table 49). Of these genotypes, 1 HT, 6 T and 33 MT.

    - Four F2:3 segregating populations composed of 4,117 plants were evaluated (Table 50). Of these plants, 1,827 (44.4%) were recovered and selected as putatively drought tolerant. A range of 43% to 46% with an average of 44% plant recovery from drought stress was obtained. The recovered plants were grown to maturity and the F4 seeds harvested will be established in the pedigree nursery for line development.

Table 48. Drought recovery response of early generation putative mutant lines (unreplicated), PhilRice CES, 2015

No.	Entries	Tissue Culture Technique	No. of Lines	Tolerance of Parent	HT		T		MT		S		HS		SWI
					n	%	n	%	n	%	n	%	n	%	
1	Y Dam Do	IVC	95	–	16	16.8	39	41.1	25	26.3	10	10.5	4	4.2	4.03
2	Jepun	IVC	58	HS	1	1.7	8	13.8	22	37.9	21	36.2	6	10.3	3.03
3	PR30025-99AC-WSAL-1087/ SHZ-2/CHINOIS 6	AC-DHL	24	T/T/HT	3	12.5	16	66.7	5	20.8	0	0	0	0	2.36
4	PSB Rc90/ PSB Rc18-Sub1	AC-DHL	5	T/HT	3	60	2	40	0	0	0	0	0	0	1.96
5	FL378/ PSB Rc18-Sub1	AC-DHL	25	– /HT	4	16	11	44	8	32	2	8	0	0	3.39
6	FL478/PSB Rc18-Sub1	AC-DHL	15	HT/HT	1	6.7	2	13.3	8	53.3	3	20	1	6.7	3.62
7	Salumpikit	IVM	66	–	0	0	0	0	8	12.1	22	33.3	36	54.5	2.59
		Total	**288**		**28**	**9.7**	**78**	**27.1**	**76**	**26.4**	**58**	**20.1**	**47**	**16.3**	

1) HT, highly tolerant (score 1) = 90-100% plants recovered; T, tolerant (3) = 70-89%; MT, moderately tolerant (5) = 40-69%; S, susceptible (7) = 20-39%; HS, highly susceptible (9) = 0-19%.

2) SWI - Shannon-Weaver diversity index

Table 49. Drought recovery response of stable mutant lines and traditional varieties (replicated), PhilRice CES, 2015.

No.	ENTRIES	Tissue Culture Technique	No. of Lines	Tolerance of Parent	HT		T		MT		S		HS	
					n	%	n	%	n	%	n	%	n	%
1	Traditional varieties	–	31	–	1	3.2	2	6.5	5	16	9	29	14	45
2	Mestizo 29	IVC	5	MT	0	0	0	0	2	40	3	60	0	0
3	Tanggiling	IVC	10	MT	0	0	1	10	4	40	4	40	1	10
4	Kawilan	IVC	4	MT	0	0	0	0	2	50	1	25	1	25
5	FR13A	IVC	8	MT	0	0	0	0	0	0	4	50	4	50
6	Namsagui	AC	2	MT	0	0	0	0	1	50	0	0	1	50
7	Negros	IVM	7	MT	0	0	1	14	3	43	0	0	3	43
8	Released varieties	–	6	–	0	0	0	0	0	0	3	50	3	50
9	Materials under ON	–	82	–	0	0	2	2.4	16	20	61	74	3	3.6
Total			**155**		**1**	**1**	**6**	**4**	**33**	**21**	**85**	**55**	**30**	**19**

HT, highly tolerant (score 1) = 90-100% plants recovered; T, tolerant (3) = 70-89%; MT, moderately tolerant (5) = 40-69%; S, susceptible (7) = 20-39%; HS, highly susceptible (9) = 0-19%.

Table 50. Plant recovery of F2:3 populations from seedling to early vegetative drought stress, PhilRice CES, 2015.

No.	Cross	Initial seedlings that emerged	Plant recovered from drought stress		No. of plants with seeds harvested	
			n	%	n	%
1	HHZ5SAL8-DT3-Sub1/SHZ-2	1001	450	45.0	126	13
2	SHZ-2/HHZ5SAL8-DT3-Sub1	766	327	42.7	50	6
3	NSIC Rc222/BPI 76	1296	594	45.8	37	3
4	NSIC Rc240/HHZ5SAL8-DT3-Sub1	1054	456	43.3	105	10
Total		**4117**	**1827**	**44.4**	**318**	**7.7**
Minimum		**766**	**327**	**42.7**	**37**	**4.8**
Maximum		**1296**	**594**	**45.8**	**126**	**9.7**
Average		**1029**	**457**	**44.4**	**80**	**7.7**

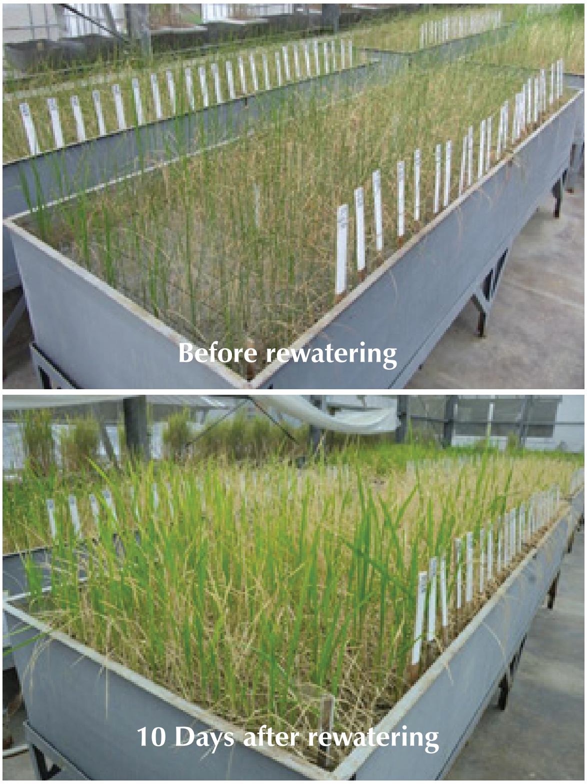


Figure 34. Drought tolerance mass screen set-up before and after re-watering, 2015 DS, PhilRice-CES.

2. Salt tolerance screen at seedling stage

- Single factor experiment using seawater as source of NaCl from 2 sites namely Brgy. Lawis, Labrador, Pangasinan and Ibona, Dingalan, Aurora was done to test for possible use in screening and to produce evaluation score for roots. Visual salt injury on shoots showed that table salt gives earlier response than the treatments using seawater. Also, scanned root samples were analyzed using WinRHIZO program to quantify the roots. Evaluation score for roots will be determined.

- A total of 316 breeding materials composed of 30 TRVs, 16 SADRI lines, 30 parentals, 176 NSIC Rc222 IVM-derived and 2 seed mutation derived lines, 62 AC-DHL from three crosses: PSB Rc90/PSB Rc18-Sub1, FL378/PSB Rc18-Sub-1 and FL478/PSB Rc18-Sub-1 and a total of 3,515 plants from the cross PSB Rc50/ NSIC Rc300 (F2) were evaluated in saline hydroponic solution for salt stress tolerance at seedling stage. Of these materials, 227 (72%) exhibited tolerance to salt stress distributed as follows: 1 HT, 87 T, 139 MT (Table 51) and 165 (5%) plants survived in the F2 population.

Table 51. Salinity tolerance mass screen at seedling stage, 2015DS, PhilRice-CES.

No.	Entries	Total No. of Entries	HT		T		MT		S		HS	
			n	%	n	%	n	%	n	%	n	%
1	TRV	30	0	0	11	37	16	53	2	6.7	1	3
2	SADRI	16	0	0	8	50	4	25	4	25	0	0
3	Parentals	30	1	3	25	83	4	13	0	0	0	0
4	AC-DHL-derived	62	0	0	30	48	27	44	5	8	0	0
5	Mutants	178	0	0	13	7	88	49	67	38	10	6
Total		**316**	**1**	**0.3**	**87**	**27.5**	**139**	**44.0**	**78**	**24.7**	**11**	**3.5**

HT, highly tolerant (score 1) = normal growth, no leaf symptoms; T, tolerant, (3) = nearly normal growth, but leaf tips or few leaves whitish and rolled; MT, moderately tolerant (5) = growth severely retarded, most leaves rolled, only a few are elongating; S, susceptible (7) = complete cessation of growth, most leaves dry, some plants dying; HS, highly susceptible (9) = almost all plants dead or dying.

3. Submergence tolerance screen at seedling stage

- Of the 128 breeding materials composed of 8 IVC-derived FR13A lines, 27 parentals, 36 hybrid parentals, 12 maintainer lines, 23 promising lines under MET and 22 AC-DHL from three crosses, viz., PSB Rc90/PSB Rc18-Sub1, FL378/PSB Rc18-Sub-1 and FL478/PSB Rc18-Sub-1, 25 (20%) genotypes were identified to exhibit some degree of tolerance (4 HT, 3 T, 18 MT) to submergence stress.

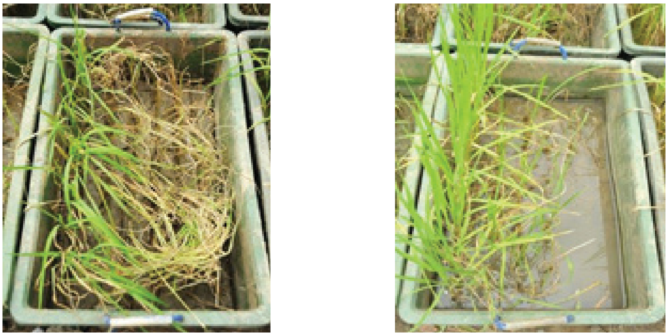
- A total of 7,470 plants from 11 segregating F2 populations were evaluated in concrete tank for submergence tolerance, with FR13A as tolerant check and IR42 as susceptible check (Table 52). Of these plants 2,545 (34.1%) were recovered and selected as putatively submergence tolerant. A range of 25% to 74% with an average of 34% plant recovery from submergence stress was obtained. Leaf sampling was done for genotyping to confirm the presence of sub1 gene. The recovered plants were grown to maturity and the F3 seeds harvested will be established in the pedigree nursery for line development.

Table 52. Summary of submergence tolerance mass screening of 11 segregating F2 populations, 2015 DS & WS, PhilRice.

No.	PR Number	Cross	Initial seedlings that emerged	Plants recovered from submergence stress		No. of plants with seeds harvested	
				n	%	n	%
1	PR45822	BPI 76/Ciherang-Sub1	83	14	16.9	31	37.3
2	PR45826	PSB Rc18-Sub1/NSIC Rc240//PSB Rc18/PSB Rc68	189	52	27.5	104	55.0
3	PR45814	NSIC Rc9/NSIC Rc194	56	20	35.7	22	39.3
4	PR47477	NSIC Rc240/ HHZ5SAL8-DT3-SUB-1	1241	39	3.1	6	0.48
5	PR47480	NSIC Rc194/ HHZ8-SAL6-SAL3Y2	1233	37	3.0	10	0.81
6	PR47490	SHZ-2/HHZ 5-SAL8-DT3-Sub1	1534	59	3.8	14	0.91
7	PR47462-4	NSIC Rc300/IR64-Sub1	549	390	71	252	45.9
8	PR47463-5	NSIC Rc298/IR64-Sub1	1628	1202	73.8	908	55.8
9	PR47461-7	NSIC Rc226/IR64-Sub1	579	456	78.8	403	69.6
10	PR47465-9	NSIC Rc224/IR64-Sub1	184	132	71.7	101	54.9
11	PR47465-10	NSIC Rc224/IR64-Sub1	194	144	74.2	134	69.1
12	PR47490	SHZ-2/ HHZ5-SAL8-DT3-SUB1	1690	433	25.6	*In progress*	*In progress*
13	PR47474	NSIC Rc298/ NSIC Rc194	3832	844	22.0	*In progress*	*In progress*
		Total	**12,992**	**3,822**	**29.4**	**1,985**	**15.3**
		Minimum	**56**	**14**	**25.0**	**6**	**10.7**
		Maximum	**3832**	**1202**	**31.4**	**908**	**23.7**
		Average	**999**	**294**	**29.4**	**180**	**18.1**

(A) 21-day old seedlings before submergence

(B) After desubmergence (DADesub)



(C) 4 DADesub

(D) 18 DADesub

Figure 35. Submergence tolerance mass screen setup wherein the tolerant check FR13A and susceptible check, IR29 were planted leftmost and rightmost side of each tray, respectively, 2015DS, PhilRice-CES.

Mass screening for reproductive stage drought tolerance

JM Niones, VAC Marcelo, MAR Orbase and NV Desamero

Drought stress during reproductive stage coincides with pollen meiosis and fertilization and hence causes drastic yield reduction in rice. Selection for yield is the main concern of any breeding programs but the efficiency of screening methodologies not only depends on selection for yield, but the combination of high yield and putative secondary traits adapted to drought stress in the rainfed lowlands. Visual scoring methods have been proven most suitable (De Datta et al., 1988) while other methods are not sufficiently convenient or are insufficiently correlated to yield (Garrity and O'Toole, 1995). Traits of correlated value combined with the selection of yield per se, can improve the plant breeding process either in parental selection or in the screening of segregating populations (Fischer et al., 2002).

Highlights:

- A total of 2188 advanced breeding lines, traditional varieties along with 5 checks (IR64, PSB Rc14, PSB Rc68, NSIC Rc192 and NSIC Rc222) were evaluated under managed drought stress at reproductive stage using the augmented RCB design in the 2015 dry (1276 test entries) and wet season (912 test entries).

- Three cycles of drought stress were imposed during the dry season (DS) lasting for 17, 14 and 24 days with soil water potential reaching -21kPa at the 1st cycle and -31kPa for the 2nd and 3rd cycles prior to re-watering (Figure 36.1). During the wet season (WS), soil water potential reached a maximum of -13kPa and a total rainfall of 796.7mm (Figure 36.2). During the DS, standing water depth at 2-3cm standing water level with a water table depth of 6 to 13.5cm below soil surface dropped with the ranged of 59 to 92cm during drought cycles. The soil moisture content (%, SMC) was reduced from 40 to 57.1% to 28.6 to 8.2% before re-watering (Figure 36.1). At the WS, WTD dropped to a maximum of 50cm below soil surface and %SMC at 33.5 to 48.1 (Figure 36.2).

- During the drought stress, days of heading ranged from 71 to 116 days after sowing (DAS), plant height ranged from 48cm to 161cm, productive tiller numbers ranged from 0 to 28 per plant, and unproductive tiller number ranged from 0 to19 per plant. The grain yield of entries ranged from 0 to 47.16 g/plant with an average of 11.91 g/plant whereas the mean yield of check varieties ranged from 8.49 g/plant (IR64) to 16.52g/plant (PSB Rc68). During the WS, heading ranged from 65 to 109 DAS, plant height from 81 to 167cm, number of productive tillers from 4 to 23 and number of unproductive tillers from 0 to 6. The yield of entries ranged from 4.04 to 50.7 g/plant with a mean yield of 19.77g/plant. The mean yield of check varieties ranged from 17.63g/plant (PSB Rc68) to 22.12g/plant (NSIC Rc222) (Table 53).

- Leaf rolling scores at the 1st and 2nd cycle of drought ranged from 0-5, whereas scores of 0 to 9 were observed under the last cycle of drought. Furthermore, 46% of the entries obtained of final recovery scores greater than 90%. Canopy temperature (CT) of the test entries at the three cycles of drought ranged from 23.3 to 37.9°C. (Figure 37). At the rainfed condition, no leaf rolling was exhibited and CT ranged from 10.6 to 26.1°C.

- Yield showed a positive and significant correlation with % drought recovery, plant height, no. of productive tillers, filled and unfilled grains, % spikelet fertility, 1000 grain weight, shoot biomass and no. of productive tillers. While days to heading, plant canopy temperature, LRS, phenotypic acceptability (PA) showed negative significant correlation (Figure 38).

- A total of 186 (22.46 %) of the entries were selected based on yield and its significant correlated traits such as phenotypic acceptability, canopy temperature and productive tillers under managed drought condition at reproductive stage.

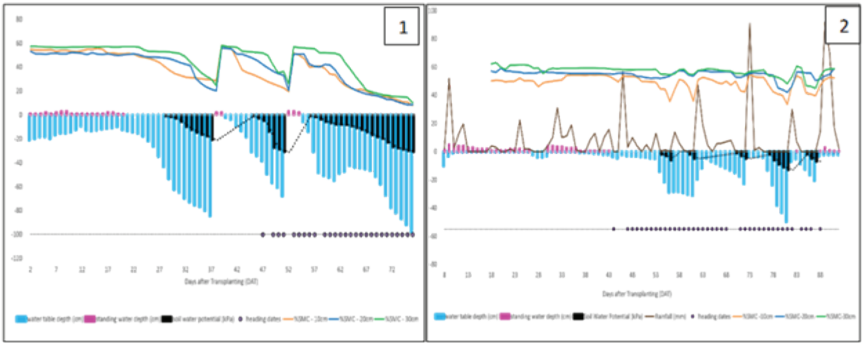
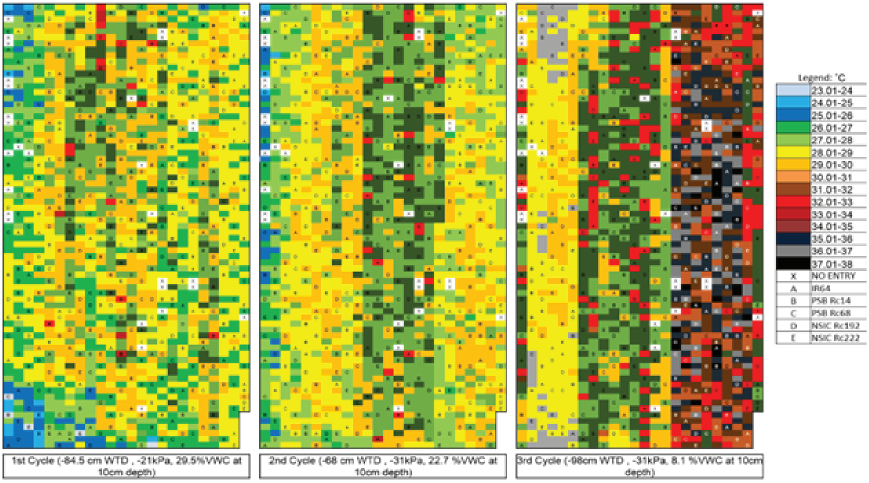


Figure 36. Soil hydrology in the 2015DS (1) and 2015WS (2) under managed drought stress at reproductive stage.



1st Cycle (-84.5 cm WTD , -21kPa, 29.5%VWC at 10cm depth)

2nd Cycle (-68 cm WTD , -31kPa, 22.7 %VWC at 10cm depth)

3rd Cycle (-98cm WTD , -31kPa, 8.1 %VWC at 10cm depth)

Figure 37. Leaf canopy temperatures under managed drought at reproductive stage in 2015DS

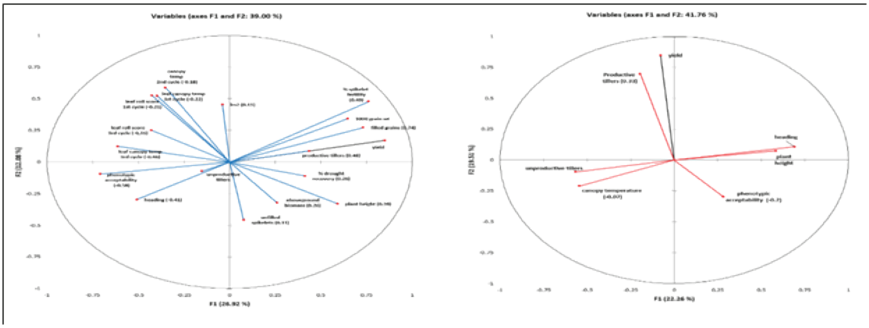


Figure 38. Biplot of yield, agro-morphological traits, drought scores and yield components with significant Pearson correlation, r values under 2015 reproductive drought and rainfed condition.

Figure 39. Test entries and check varieties under managed drought stress at reproductive in the 2015 dry seasons.

Table 53. Summary of descriptive statistics of checks and entries under 2015 dry and wet seasons.

Yield and Agro-Morphological Traits		Yield (g/plant)		Heading (DAS)		Plant Height (cm)		Productive Tillers		Unproductive Tillers		CT1	CT2	CT3	CT	PA	
		DS	WS	DS	WS	DS	WS	DS	WS	DS	WS		DS		WS	DS	WS
Checks	IR64	8.49	21.33	100	79	63	103	11	12	4	3	28.4	28.1	31.5	18.2	7	5
	PSB Rc14	9.85	19.52	87	81	69	102	14	12	5	3	28.9	29.4	32.0	18.5	6	5
	PSB Rc68	16.52	17.63	99	95	85	122	13	10	5	3	28.3	28.9	31.1	17.8	4	6
	NSIC Rc192	11.45	20.66	89	78	88	114	10	10	5	2	28.8	29.2	31.8	18.1	7	5
	NSIC Rc222	11.51	22.12	96	83	76	110	14	12	6	3	28.7	29.1	31.7	18.1	6	5
Entries	mean	11.91	19.77	95	82	76	106	13	11	6	3	28.9	29.2	31.8	18.0	6	1
	min	0.00	4.04	71	65	48	81	0	4	0	0	23.4	24.7	27.2	10.6	1	1
	max	47.16	50.70	116	109	161	167	28	23	19	6	34.5	32.7	38.0	26.1	9	5

Multi-environment and adaptability tests of breeding lines in drought-prone rainfed lowland

JM Niones, MAR Orbase, VAC Marcelo, TA Sigari, NV Desamero and NL Manigbas

Genotype and environment interaction (G x E interactions) complicates the selection of superior genotypes within a range of environments. Hence, early multi-environment trials (MET's) of advanced breeding lines is economical and one of the best strategy in the development of location-specific adapted varieties than the centralized evaluation of these entries. MET strategy have been incorporated and routinely practiced in PhilRice in developing rice cultivars under target environment of RFL ecosystem. Since 2011, a total of 656 breeding lines from different breeding sources have been assembled and evaluated for multi-environment trials in target areas. A total of 86 elite lines have been selected from 2011 to 2015 ready for NCT nomination. In 2015DS, 154 breeding lines together with 6 check varieties (IR64, PSB Rc14, PSB Rc68, NSIC Rc222, NSIC Rc288 and NSIC Rc240) were evaluated under managed drought stress. Meanwhile in 2015WS, 50 new breeding lines, 15 released varieties and 5 varieties were evaluated in 7 different sites in Nueva Ecija, Nueva Vizcaya, Batac, Isabela, Los Baños, Negros, Agusan and Midsayap under rainfed environments (Table 54).

Highlights:

- In 2015DS, genotypes showed significant difference for plant height, heading days, tiller production and yield under managed-drought condition (Table 55).

- Three cycles of drought and re-watering was implemented during the trial. The first cycle was imposed 15 days after transplanting (DAT) with initial water table depth of 27 cm from soil surface and soil moisture content (SMC) of 33% at 15 and 26% at 30 cm. Water was withheld for 26 days after drought imposition (DADI) or until the leaf of IR64 (susceptible check) started to roll, and with soil water potential of -48 kPa, prior to re-watering (Figure 40). Furthermore, 2nd and 3rd cycle lasted for 13 and 19 days, respectively. Water table depth (WTD) reached 77 and 81cm below soil surface and soil water tension of -60 and -69 until re-watering.

- Yield of entries ranges from 18 to 2789 kg/ha, days to flowering ranges from 83 to 119 DAS, plant height from 50 to 71cm and number of tiller ranges from 11 to 24 as compared to check varieties where yield ranges from 81to 560kg/ha, days to flowering from 88 to 108 DAS, plant height from 56 to 73cm and number of tillers from 13 to 20.

- Out of 154, 16% (25 test entries) of the entries shown higher yield or 5% yield advantage than PSB Rc68 (560 kgha-1), the highest yielding check. Yield of these entries ranges from 595 to 2879 kgha-1. And 13 of these entries showed yields more than 1000 kgha-1 (1134 to 2879kg/ha) while under full irrigation yields of these entries range from 5460 to 8237 kgha-1.

- The top 10 test entries selected showed a greater 5% yield advantage over the best performing check variety, good phenotypic acceptability, good drought response and high % recovery. These entries will be nominated to NCT (Table 55).

- 2015 WS can be described with frequent heavy rains and typhoon during rice crop growth. In Philrice CES, high frequency of rainfall was observed during vegetative stage until reproductive stage however Negros experienced less rainfall during vegetative stage but high frequency of heavy rains during reproductive stage (Figure 41).

- High amount of rainfall was recorded in Negros with 1260.3 mm while Philrice CES recorded only 911.8mm of rain despite the occurrence of two typhoons. WTD in Philrice CES ranges from 2 to 31 whereas WTD in Negros ranges from 0-81 cm below soil surface. Lowest WTD in Negros was recorded during the vegetative stage (Figure 42).

- ANOVA showed that yields were significantly affected by E and G which explained 43.6 and 26% of the total variation.

- In CES, yield of entries ranges from 1406 to 4295 kgha-1, 2386 to 4651 kgha-1 in Batac and 857 to 4055 kgha-1 in Negros. On the other hand, yield of checks in CES ranges 1991 to 4145kg/ha, 3092 to 4271 in Batac and 1202 and 3703 kgha-1. Mean yield of test entries for all sites showed a larger magnitude over mean yield of checks indicating their better performance over the checks (Figure 43)

- Differential yield rankings were observed across sites (CES, Negros and Batac) indicating the presence of GEI. PSB Rc82 were the highest yielder in CES, PR45719-KDML105-SM2012DS-400-5 in Batac (4651 kgha-1) and NSIC Rc354 in Negros (4055 kgha-1) (Figure 44).

- Fifteen (21%) breeding lines out-yielded the mean yield of checks (3499 kgha-1) in CES, 24 (34%) in Batac (3569 kgha-1) and 16 (23%) in Negros (2351 kgha-1).

- Out of the 65 test entries, 3 lines consistently showed higher yield advantage over the mean yield of checks across environments and these are PR39955-B-5-1-2-3-1 (PR41398-ICRL2008WS-PSB Rc68 29-2-1 and Raeline 7.

- Top ten performing entries were selected based on the mean yield across sites. Yield of these entries ranges from 3247 to 3967 kgha-1 (Table 56).

- Stability analysis and final selection of breeding lines will be performed upon availability of data from other sites.

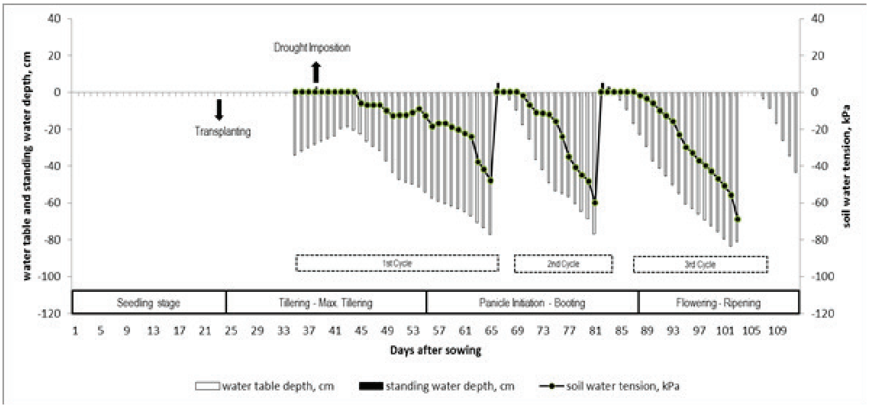


Figure 40. Water table depth, height of surface water and soil surface tension of MET experimental set-up in PhilRice CES, 2015DS.

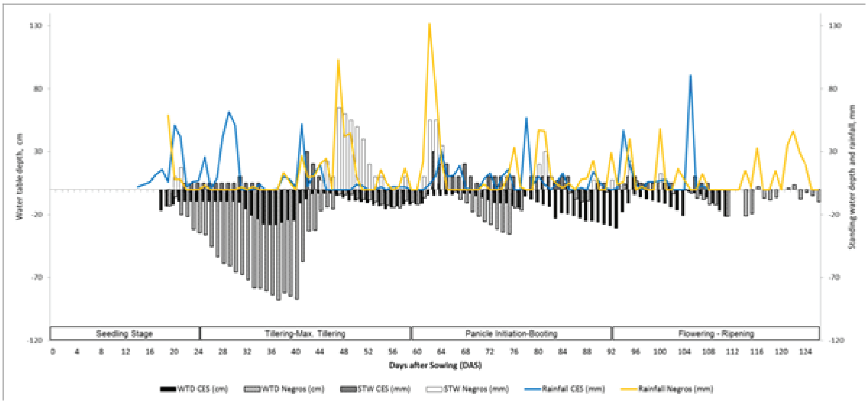


Figure 41. Water table depth, height of surface water and rainfall of MET experimental set-up in PhilRice CES and PhilRice Negros, 2015WS.

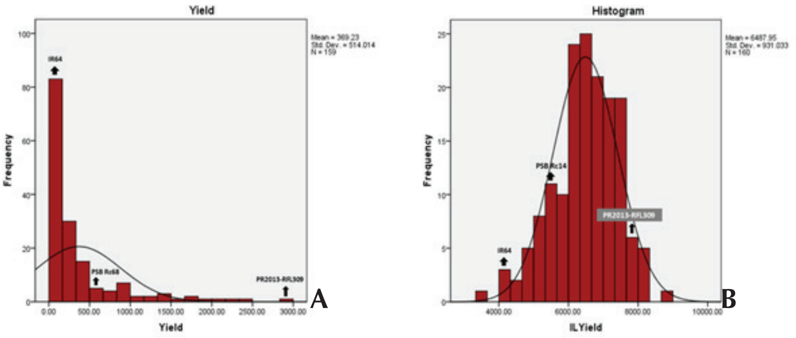


Figure 42. Frequency distribution of 154 breeding lines for yield under managed drought stress (a) and fully irrigated condition (b).

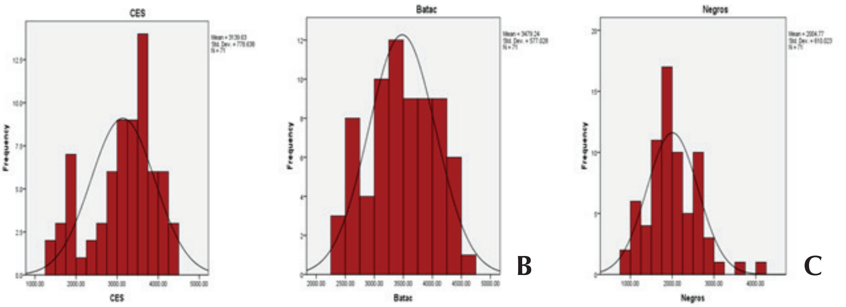


Figure 43. Frequency distribution of 70 breeding lines and varieties for yield in (a) PhilRice CES (b) Batac and (c) Negros, MET 2015WS.

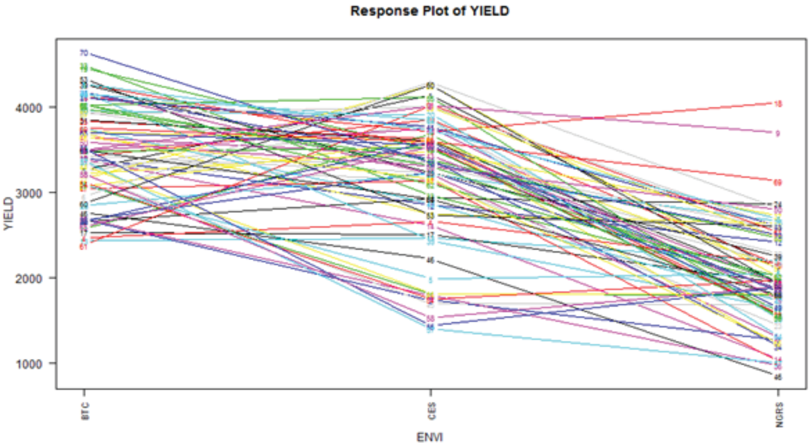


Figure 44. Response plot of yield of the 70 breeding lines across 3 environments, MET 2015WS.

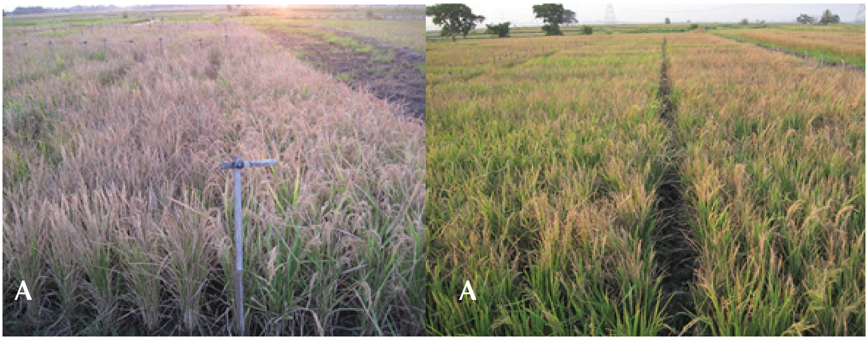
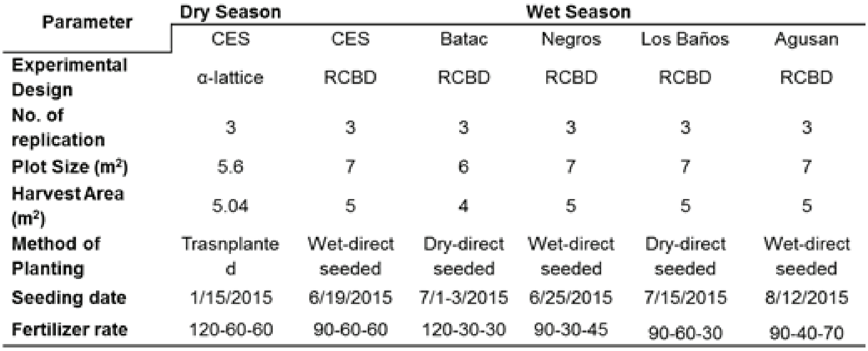


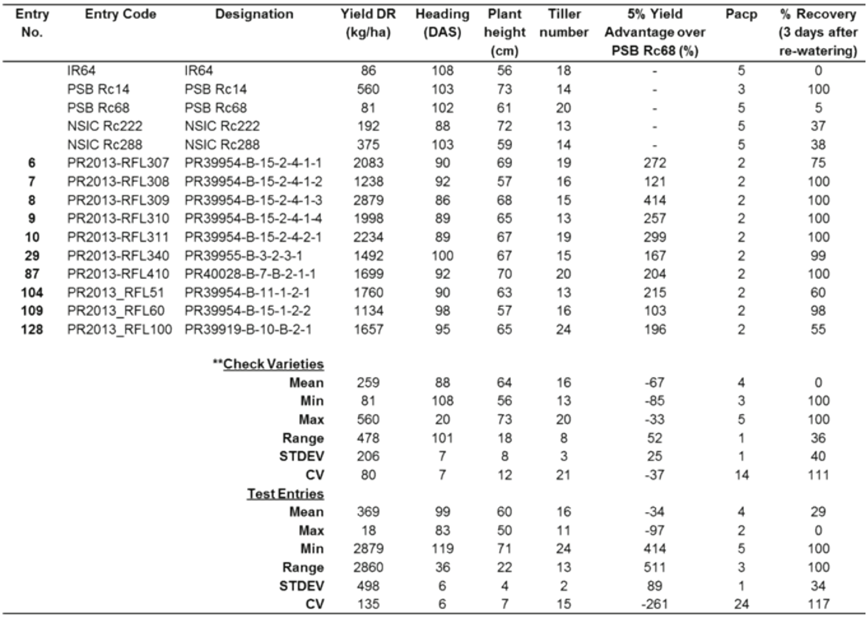
Figure 45. Susceptible (a) and tolerant (b) breeding line evaluated in MET experimental field (c), 2015DS, PhilRice CES.

Table 54. Details of the experiment, MET 2015WS.



Parameter	Dry Season	Wet Season				
	CES	CES	Batac	Negros	Los Baños	Agusan
Experimental Design	α-lattice	RCBD	RCBD	RCBD	RCBD	RCBD
No. of replication	3	3	3	3	3	3
Plot Size (m^2)	5.6	7	6	7	7	7
Harvest Area (m^2)	5.04	5	4	5	5	5
Method of Planting	Trasnplanted	Wet-direct seeded	Dry-direct seeded	Wet-direct seeded	Dry-direct seeded	Wet-direct seeded
Seeding date	1/15/2015	6/19/2015	7/1-3/2015	6/25/2015	7/15/2015	8/12/2015
Fertilizer rate	120-60-60	90-60-60	120-30-30	90-30-45	90-60-30	90-40-70

Table 55. Variability statistics of agro-morphological traits of 154 breeding lines and 6 check varieties.

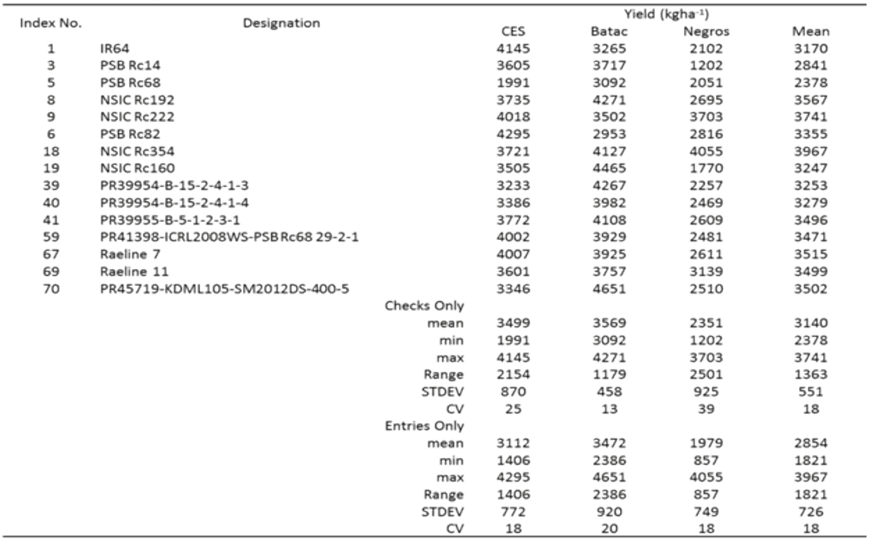


Entry No.	Entry Code	Designation	Yield DR (kg/ha)	Heading (DAS)	Plant height (cm)	Tiller number	5% Yield Advantage over PSB Rc68 (%)	Pacp	% Recovery (3 days after re-watering)
	IR64	IR64	86	108	56	18	-	5	0
	PSB Rc14	PSB Rc14	560	103	73	14	-	3	100
	PSB Rc68	PSB Rc68	81	102	61	20	-	5	5
	NSIC Rc222	NSIC Rc222	192	88	72	13	-	5	37
	NSIC Rc288	NSIC Rc288	375	103	59	14	-	5	38
6	PR2013-RFL307	PR39954-B-15-2-4-1-1	2083	90	69	19	272	2	75
7	PR2013-RFL308	PR39954-B-15-2-4-1-2	1238	92	57	16	121	2	100
8	PR2013-RFL309	PR39954-B-15-2-4-1-3	2879	86	68	15	414	2	100
9	PR2013-RFL310	PR39954-B-15-2-4-1-4	1998	89	65	13	257	2	100
10	PR2013-RFL311	PR39954-B-15-2-4-2-1	2234	89	67	19	299	2	100
29	PR2013-RFL340	PR39955-B-3-2-3-1	1492	100	67	15	167	2	99
87	PR2013-RFL410	PR40028-B-7-B-2-1-1	1699	92	70	20	204	2	100
104	PR2013_RFL51	PR39954-B-11-1-2-1	1760	90	63	13	215	2	60
109	PR2013_RFL60	PR39954-B-15-1-2-2	1134	98	57	16	103	2	98
128	PR2013_RFL100	PR39919-B-10-B-2-1	1657	95	65	24	196	2	55
		****Check Varieties**							
		Mean	259	88	64	16	-67	4	0
		Min	81	108	56	13	-85	3	100
		Max	560	20	73	20	-33	5	100
		Range	478	101	18	8	52	1	36
		STDEV	206	7	8	3	25	1	40
		CV	80	7	12	21	-37	14	111
		Test Entries							
		Mean	369	99	60	16	-34	4	29
		Max	18	83	50	11	-97	2	0
		Min	2879	119	71	24	414	5	100
		Range	2860	36	22	13	511	3	100
		STDEV	498	6	4	2	89	1	34
		CV	135	6	7	15	-261	24	117

under managed drought condition, MET 2015DS.

Note: *from 2014 MET fully irrigated data **Descriptive statistics of check varieties and test entries; IL, irrigated; DR, drought

Table 56. Variability statistics of agro-morphological traits of the top ten performing breeding lines and varieties and 5 check varieties across 3 environments, MET 2015WS.



Index No.	Designation	Yield (kgha^{-1})			
		CES	Batac	Negros	Mean
1	IR64	4145	3265	2102	3170
3	PSB Rc14	3605	3717	1202	2841
5	PSB Rc68	1991	3092	2051	2378
8	NSIC Rc192	3735	4271	2695	3567
9	NSIC Rc222	4018	3502	3703	3741
6	PSB Rc82	4295	2953	2816	3355
18	NSIC Rc354	3721	4127	4055	3967
19	NSIC Rc160	3505	4465	1770	3247
39	PR39954-B-15-2-4-1-3	3233	4267	2257	3253
40	PR39954-B-15-2-4-1-4	3386	3982	2469	3279
41	PR39955-B-5-1-2-3-1	3772	4108	2609	3496
59	PR41398-ICRL2008WS-PSB Rc68 29-2-1	4002	3929	2481	3471
67	Raeline 7	4007	3925	2611	3515
69	Raeline 11	3601	3757	3139	3499
70	PR45719-KDML105-SM2012DS-400-5	3346	4651	2510	3502
	Checks Only				
	mean	3499	3569	2351	3140
	min	1991	3092	1202	2378
	max	4145	4271	3703	3741
	Range	2154	1179	2501	1363
	STDEV	870	458	925	551
	CV	25	13	39	18
	Entries Only				
	mean	3112	3472	1979	2854
	min	1406	2386	857	1821
	max	4295	4651	4055	3967
	Range	1406	2386	857	1821
	STDEV	772	920	749	726
	CV	18	20	18	18

**Descriptive statistics of check varieties and test entries

Pyramiding salinity and submergence tolerance in high yielding rice varieties

NV Desamero, LM Perez, TE Mananghaya, JC Bagarra, AAS Chin, JS Concepcion

Enhancing selection efficiency using molecular markers were employed and integrated with classical breeding approach to pyramid salinity and submergence tolerance into high yielding cultivars, subsequently resulting in the development of improved variety with multi-abiotic stress tolerance. Three activities were done to achieve the objective of the study; (1) Introgressing Sub1 QTL into high yielding genotypes through marker-aided backcrossing (MAB) and marker-aided selection (MAS) (2) Introgressing saltol QTL into high yielding variety or breeding line and (3) Pyramiding salinity and submergence (sal-sub) tolerance.

Highlights:

1. Introgressing sub1 QTL into high yielding genotypes through marker-aided backcrossing (MAB) & selection (MAS)

- Evaluation of 25 test entries (Table 57) under managed submergence stress for 9 days in the field tank and non-stress condition was conducted in 2015 DS. The non-stress grain yield ranged from 2.795t/ha to 6.192t/ha, while the yield under stress ranged from 0.662 t/ha to 2.736t/ha. Plant survival higher than IR64-Sub1 or Submarino 1 (92%) was obtained from eight test genotypes, viz., PR41543-B-14-2-1-2 (99%), PR42294-2-2-1-31 (97%), PR42151-B-38-1-1-2 (97%), PR42271-1-1-6-40 (96%), Ciherang-Sub1 (96), PR42289-3-7-6-30 (95%), PR42151-B-40-1-1-2 (93%) and PR42300-4-2 (93%). Under non-stress, 8 test entries out yielded Ciherang-Sub1 (4.052t/ha), 1 entry with yield better than PSB Rc68 (5.129 t/ha) and 11 outyielding IR64-Sub1 (3.942 t/ha). Under stress condition, the yield was reduced by 0.738 t/ha to 3.714t/ha or 26 to 84%, with 7 test entries yielding higher than Ciherang-Sub1 (2.004t/ha), 10 entries with yield better than PSB Rc68 (1.899 t/ha) and 17 outyielding IR64-Sub1 (1.114t/ha). PR42156-B-2-3-1-2 performed best both in non-stress (6.192t/ha) and stress condition (2.736t/ha).

- A total of 5,310 plants from 177 fixed lines at F7 generation of 7 crosses introgressing sub1 gene (Table 58) were subjected to 9 days submergence at vegetative stage in the field tank, resulting in the survival of 1,068 (20%) plants from 158 lines. Leaf samples were collected from all surviving plants for DNA extraction. Initial genotyping with sub1 markers of 3 prioritized plants per line, selected on the basis of phenotypic acceptability, was performed, identifying 103 (58%) of the 177 plants positive for both Art5 and SC3 markers. The sub1 positive plants will be established, panicle to a row in 2016 DS, for uniformity observation and seed increase for use in the subsequent comparative performance evaluation.

- Three segregating F2:3 breeding populations, i.e., BPI 76/ Ciherang-Sub1 (PR45822), NSIC Rc9/NSIC Rc194 (PR45826) and PSB Rc18-Sub1/NSIC Rc240//PSB Rc18/PSB Rc68 (PR45814) with potentially introgressed sub1 gene were established in 2015 DS in cemented tank for submergence tolerance screen. The surviving 328 (13%) plants were genotyped with Art5 and SC3 markers for sub1 gene , resulting in DNA amplification in 166 (51%) plants, and no amplification in 162 (49%) plants (Table 59). Of the 166 plants with amplifications, 110 (68%) were homozygous or heterozygous in either marker, or combination of the two markers. The genotyped F4 submergence tolerant plants were established in the screenhouse to produce seeds for use in generation advance, further evaluation and selection. The selected F4 plants (family) will be planted in pedigree nursery in 2016 DS for generation advance (F5) and line development.

- In 2015 WS, 101 F3 plants from ZHONGHUA1/ NSIC Rc194 (PR47492) were planted in pedigree nursery for phenotypic acceptability. Leaf samples were collected for genotyping with sub1 gene markers. Only one plant was identified positive with the indel marker Art5, while 35 (35%) were positive for the SC3 marker. Twenty six (26%) were heterozygous. Considering the two markers, 61 F3 plants with DNA amplifications were selected to comprise the breeding families. These families will be phenotyped for submergence stress tolerance and evaluated for field performance (Table 60).

2. Introgressing saltol QTL into high yielding variety or breeding line

- The 4,580 plants from 3 F4 bulk and 3 F5 populations were screened for salt stress tolerance at seedling stage, resulting in the survival of 1,544 (34%) plants (Table 61). The 1,201 surviving families and segregating F5 populations were planted in the pedigree nursery. Of these plants 150 were selected based on phenotypic acceptability. The selected plants will be planted for evaluation, plant selection and generation advance in 2016 DS.

- The 8 in-vitro mutagenesis (IVM)-derived lines from FR13A were submerged and the leaves of surviving plants were collected for genotyping. The inconsistent phenotyping and genotyping results will be revalidated. The same surviving plants were genotyped for the four QTL SSR markers associated with saline tolerant (saltol) genes. Three of the eight (38%) IVM lines were positive to the markers (Table 62). The plants are being seed increased and will undergo saline screening at seedling stage in 2016 DS.

- Three single crosses (NSIC Rc288/FL478, PR38560-1-Azucena-Coll.No. 1528-M5R-1 DrS 111/FL478, and PR38560-1-Azucena-Coll.No. 1528-M5R-1 DrS 111/NSIC Rc188), introgressing the saltol gene into drought tolerant recipient genotypes were made yielding 36, 75 and 59 F1 seeds respectively, totaling to 170.

- In 2015 WS 11 crosses were made to introgress saltol gene from FL478, FL378, IR86385-38-1-1-B, IR86385-58-2-1-B and IR86385-194-2-1-B into high yielding varieties, viz., NSIC Rc298, NSIC Rc300, NSIC Rc308, Dezo 300 and NSIC Rc218, yielding 521 F1 naked seeds (Table 63). The harvested F1 seeds will be planted in 2016 DS to generate F2 populations. The F2 populations will be subjected to saline tolerance screen where the surviving plants will be genotyped with robust saltol markers followed by generation advance of the phenotypically and genotypically selected plants..

3. Pyramiding salinity and submergence (sal-sub) tolerance

- A selection of 20 from 83 F7 lines (generated from BYB program) from sal-sub crosses (Table 64) established in the pedigree nursery (PN) will be advanced to uniformity and seed increase nursery and will be subjected to multi-trait evaluation in 2016 DS.

- The 18 F7 lines of the cross PR41561 (FL378/PSB Rc18-Sub1) were subjected to submergence stress in the field tank. The144 F8 surviving plants were genotyped resulting in the identification and selection of 86 F9 lines, which will be evaluated for uniformity selection, and seed increase in 2016 DS.

- Two new crosses, i.e., NSIC Rc300/PSB Rc68 and PSB Rc68/NSIC Rc120) were made in 2015 DS to pyramid salinity, submergence and drought tolerance in high yielding varieties, yielding 56 and 70 F1 seeds, respectively, with a total of

126 F1 seeds. The F1 seeds will be established in 2016 DS to generate the F2 populations. The F2 populations will be subjected to stresses and genotyping with SC3 and ART5 markers. The genotyped surviving plants will be subjected to generation advance. As necessary the selected positively genotyped F2 plants will be used for backcrossing, the progenies of which will be advanced to PN for evaluation, selection and generation advance.

- A total of 628 F1 naked seeds were generated from 14 cross combinations using high yielding varieties/lines and IRRI developed saline-submergence tolerant lines (Table 65). The harvested seeds will be established in 2016 DS to produce the F2 populations. The F2 populations will be divided for selection under stress and non-stress for agronomic trait selection and advancement to F3 generation. The F2:3 bulk populations may also be generated from the F2 plants for subsequent generation of F2:3 families.

Table 57. Plant survival (%) and grain yield (t/ha) of 25 genotypes subjected to nine days of submergence stress at vegetative stage, laid-out in RCBD, with two replications, PhilRice-CES, 2015 DS.

No.	Field Code	Entry Name	Designation	Plant Survival (%)	Adjusted grain yield (tha^{-1} at 14%MC)			
					NON-STRESS	STRESS	YIELD DIFF	MEAN
1	PR15DS-FAV-2	IR42	IR42	24^{d-***}	2.795^{e}	0.662^{b}	2.133	1.729^{d}
2	PR15DS-FAV-3	Ciherang-Sub1	Ciherang-Sub1	96^{a}	4.052^{b-e}	**2.004^{ab}**	2.048	3.028^{a-d}
3	PR15DS-FAV-4	IR64	IR64	80^{abc}	4.162^{b-e}	1.481^{ab}	2.68	2.822^{a-d}
4	PR15DS-FAV-5	IR64-Sub1	IR64-Sub1	92^{ab}	3.942^{b-e}	1.114^{ab}	2.828	2.528^{bcd}
5	PR15DS-FAV-6	IVC-109	PR38584-IR64-AC97WP-128 ID 18-1-4	83^{abc}	4.876^{abc}	1.162^{ab}	3.714	3.019^{a-d}
6	PR15DS-FAV-7	ICRL-2008WS-84	PR41398-ICRL2008WS-PSB Rc68 18-2-1	$40^{bcd-***}$	4.085^{b-e}	0.846^{ab}	3.239	2.466^{a-d}
7	PR15DS-FAV-8	ICRL-2008WS-155	PR41398-ICRL2008WS-PSB Rc68 30-1-2	37^{cd-***}	4.371^{bcd}	0.706^{ab}	3.665	2.539^{a-d}
8	PR15DS-FAV-9	PR14DS_SUB-OST-95	PR42151-B-40-1-1-2	93^{ab}	4.117^{b-e}	2.444^{ab}	1.673	3.281^{abc}
9	PR15DS-FAV-10	PR14DS_SUB-OST-101	PR42151-B-38-1-1-2	97^{a}	3.349^{cde}	1.811^{ab}	1.538	2.58^{a-d}
10	PR15DS-FAV-11	PR14DS_SUB-OST-239	PR41543-B-14-2-1-2	99^{a}	3.696^{b-e}	2.132^{ab}	1.564	2.914^{a-d}
11	**PR15DS-FAV-12**	**PR14DS_SUB-OST-284**	**PR42156-B-2-3-1-2**	90^{abc}	**6.192^{a***}**	**2.736^{a***}**	3.456	4.464^{a***}
12	PR15DS-FAV-13	PSB Rc68	PSB Rc68	76^{a-d}	5.129^{ab}	1.899^{ab}	3.229	3.514^{abc}
13	PR15DS-FAV-14	IVC SM 748-1	PR41905-Samba Mahsuri-Sub1-IVC2010DS 27-2-1	84^{abc}	3.899^{b-e}	1.599^{ab}	2.3	2.749^{a-d}
14	PR15DS-FAV-15	IVC SM 800	PR41905-Samba Mahsuri-Sub1-IVC2010DS 47-1*	82^{abc}				
15	PR15DS-FAV-16	NSIC Rc128 Sub-1-1-6-40	PR42271-1-1-6-40	79^{abc}	3.952^{b-e}	1.084^{ab}	2.868	2.518^{bcd}
16	PR15DS-FAV-17	NSIC Rc128 Sub-1-1-5-25	PR42271-1-1-6-40	96^{a}	4.867^{abc}	**2.68^{ab***}**	2.187	3.774^{ab***}
17	PR15DS-FAV-18	NSIC Rc152 Sub-3-7-6-30	PR42289-3-7-6-30	95^{a}	3.436^{cde}	1.927^{ab}	1.509	2.682^{a-d}
18	PR15DS-FAV-19	NSIC Rc152 Sub-3-7-6-54	PR42289-3-7-6-54	78^{abc}	3.808^{b-e}	1.449^{ab}	2.358	2.629^{a-d}

Table 57. Plant survival (%) and grain yield (t/ha) of 25 genotypes subjected to nine days of submergence stress at vegetative stage, laid-out in RCBD, with two replications, PhilRice-CES, 2015 DS. (Con't)

19	PR15DS-FAV-20	NSIC Rc154 Sub-2-2-1-4	PR42294-2-2-1-4	91^{ab}	4.005^{b-e}	2.079^{ab}	1.925	3.042^{a-d}
20	PR15DS-FAV-21	NSIC Rc154 Sub-2-2-1-31	PR42294-2-2-1-31	97^{a}	3.803^{b-e}	2.476^{ab}	1.327	3.14^{a-d}
21	PR15DS-FAV-22	NSIC Rc160 Sub-4-2	PR42300-4-2	93^{ab}	2.896de	2.158^{ab}	0.738	2.527^{a-d}
22	PR15DS-FAV-23	NSIC Rc160 Sub-8-29	PR42300-8-29	72^{a-d}	3.588^{b-e}	1.529^{ab}	2.059	2.559^{a-d}
23	PR15DS-FAV-24	NSIC Rc160 Sub-12-2	PR42300-12-2	52^{a-d}	3.759^{b-e}	0.905^{ab}	2.853	2.332^{cd}
24	PR15DS-FAV-25	PR41561-B-2-Sal1-1-1-Sub1	PR41561-B-2-Sal1-1-1-Sub1	79^{abc}	3.865^{b-e}	1.932^{ab}	1.933	2.899^{a-d}
25	PR15DS-FAV-26	PR39924-B-4-B-2	PR39924-B-4-B-2	63^{a-d}	3.787^{b-e}	0.742^{ab}	3.045	2.265^{cd}
Minimum				24	2.795	0.662	0.738	1.729
Maximum				99	6.192	2.736	3.714	4.464
Range				75	3.397	2.074	2.976	2.735
Average				79	4.018	1.648	2.37	2.833
Standard deviation				20.53	0.712	0.64	0.791	0.549
Variance				421.29	0.507	0.41	0.626	0.302
Coefficient of variance				26.07	17.726	38.833	33.396	19.39
Critical value of studentized range (Tukey's)				5.802	5.821	5.854		5.891
Critical Value of Dunnett's t Test (vs. IR64-Sub1)				3.217	3.235	3.097		3.206
Pr>F								
REPLICATION				0.7905	0.1232	0.5742		0.8887
GENOTYPE				0.0001	<.0001	0.0039		0.0017
ENVIRONMENT								<.0001
GENOTYPE*REPLICATION								0.7155
REPLICATION*ENVIRONMENT								0.3368
GENOTYPE*ENVIRONMENT								0.0118

Note: *PR41905-Samba Mahsuri-Sub1-IVC2010DS 47-1 grain yield was not included due to >50% off types FR13A seeds do not germinate

Table 58. Phenotyping and genotyping at F7 generation subjected to submergence stress for 7 days at vegetative stage, field tank, 2015 DS and WS, PhilRice CES.

Cross Combination	No. of Lines*	No. of Plants Before Submergence	Survival			No. of Plants Positive for Sub1 gene (homozygous in both ART5 and SC3 markers)**
			No. of Lines	No. of Plants	%	
PSB RC 10/NSIC Rc194	42	1260	42	380	30	37
PR33374-28-1-5-B-B-MES/NSIC Rc194	31	930	18	69	7	13
PR37443-13/NSIC Rc194	18	540	16	71	13	10
PR34350-4-Pokkali-AC-24-M5R-10 DrS 88/PSB Rc18-Sub1	51	1530	48	334	22	41
PR25769-B-9-1/1*PSB Rc18-Sub1	3	90	3	28	31	0
AZUCENA-IRGC 328/PR39397-7-153-240//PSB Rc82	27	810	26	128	16	0
AZUCENA-IRGC 328/PR39397-7-153-240//NSIC Rc194	5	150	5	58	39	2
Total	**177**	**5310**	**158**	**1068**		**103**

Note:
* each line planted 30 hills
**Three plants per line based on PACP after de-submergence were prioritized for DNA extraction

Table 59. Summary table of phenotyping and genotyping of F2:3 breeding populations submerged at seedling stage, cemented tank, 2015 DS, PhilRice CES

Designation	Cross Combination	No. of plants screened ($F_{2:3}$)	No. of plants survived (F_4)	ART5				SC3				Number of plants							
				A	B	H	TOTAL	A	B	H	TOTAL	ART5 B + SC3B	ART5 B + SC3A	ART5 A + SC3B	ART5H + SC3H	ART5H + SC3A	ART5 A + SC3H	ART5 B + SC3H	ART5H + SC3B
PR45822	BPI 76/ Ciherang-Sub1	1440	83	1	16	16	33	16	15	–	31	9	7	1	–	9	–	–	5
PR45814	NSIC Rc9/ NSIC Rc194	600	56	25	–	–	25	16	5	–	21	–	–	5	–	–	–	–	–
PR45826	PSB Rc18-Sub1/ NSIC Rc240/ PSB Rc18/ PSB Rc68	480	189	33	24	42	99	33	31	36	100	12	9	3	21	4	6	5	14
TOTAL		2520	328	59	40	58	157	65	51	36	152	21	16	9	21	13	6	5	19

Legend: A-IR42 allele; B-FR13A allele; H-heterozygous band

Note: The F_4 plants (PRxxxxxx-B-B-SubM#) survived were planted in the screenhouse for generation advance, 2015 WS. The plants positive for the sub1 allele of different combination will be observed for comparative performance (2015 WS)

Table 60. Genotyping score of PR47492 F3 families, 2015 WS, PhilRice CES.

Designation	Cross Combination	No. of plants planted (F_3)	ART5				SC3				Number of plants							
			A	B	H	TOTAL	A	B	H	TOTAL	ART5 B + SC3B	ART5 B + SC3A	ART5A + SC3B	ART5H + SC3H	ART5H + SC3A	ART5 A + SC3H	ART5B + SC3H	ART5H + SC3B
PR47492	ZHONGHUA 1/ NSIC Rc194	101	100	1	–	101	40	35	26	101	1	–	34	–	–	26	–	–

Table 61. Plants selected under seedling saline stress from F4 population (F2:3-derived from Bicol, pooled seeds) and F5 families from Cagayan, 2015 WS, PhilRice CES.

Glasshouse Code	Designation	Parentage	Number of seeds sown	Number of plants (family) with seeds harvested	Number of plants planted in pedigree nursery	Number of plants selected
PR14WS-SALBi1_Baybay	PR41563-B-B-B_{Bay}	FL478/NSIC Rc160	480	181	164	41
PR14WS-SALBi1_Bagacay	PR41563-B-B-B_{Bag}	FL478/NSIC Rc160	480	136	79	5
PR14WS-SALBi1_Bacacay	PR41563-B-B-B_{Bac}	FL478/NSIC Rc160	480	271	205	12
PR14WS-SALBi2_Baybay	PR41560-B-B-B_{Bay}	FL478/PR33382-25-1-1-MES	480	101	92	3
PR14WS-SALBi2_Bagacay	PR41560-B-B-B_{Bag}	FL478/PR33382-25-1-1-MES	480	166	116	3
PR14WS-SALBi2_Bacacay	PR41560-B-B-B_{Bac}	FL478/PR33382-25-1-1-MES	480	33	25	2
PR14WS-SALBi3_Baybay	PR42847-B-B-B_{Bay}	NSIC Rc160/FL478	480	219	176	8
PR14WS-SALBi3_Bagacay	PR42847-B-B-B_{Bag}	NSIC Rc160/FL478	480	185	135	30
PR14WS-SALBi3_Bacacay	PR42847-B-B-B_{Bac}	NSIC Rc160/FL478	320	134	116	16
PR14WS_SALCAG01	PR41561-B-4-1-B_{Cg}	FL378/PSBRc18-Sub1	60	15	12	4
PR14WS_SALCAG06	PR41570-B-22-2-B_{Cg}	FL478/1*PSBRc82	60	8	5	2
PR14WS_SALCAG10	PR42193-B-24-1-B_{Cg}	FL478/GSR 205	60	21	14	10
PR14WS_SALCAG11	PR42193-B-28-1-B_{Cg}	FL478/GSR 205	60	24	23	4
PR14WS_SALCAG12	PR42193-B-36-1-B_{Cg}	FL478/GSR 205	60	11	9	2
PR14WS_SALCAG13	PR42193-B-51-1-B_{Cg}	FL478/GSR 205	60	7	5	3
PR14WS_SALCAG14	PR42193-B-54-1-B_{Cg}	FL478/GSR 205	60	32	25	5
l			**4580**	**1544**	**1201**	**150**

Table 62. Genotyping of FR13A IVM derived lines with saltol markers (AP3206, RM10711, RM10793, RM10701, 2015 DS, PhilRice CES.

No.	CODE	ENTRY	GENOTYPING			
			AP3206	RM10711	RM10793	RM10701
		FL478	B	B	B	B
		IR29	A	A	A	A
1	**FR13A 1**	FR13A-IVM2012DS 98-6	C	A	A	A
2	**FR13A 2**	FR13A-IVM2012DS 99-3	B	B	B	B
3	**FR13A 3**	FR13A-IVM2012DS 99-5	B	B	B	B
4	**FR13A 4**	FR13A-IVM2012DS 100-3	B	B	B	B
5	**FR13A 5**	FR13A-IVM2012DS 100-4	A	A	B	A
6	**FR13A 6**	FR13A-IVM2012DS 100-8	C	A	A	A
7	**FR13A 7**	FR13A-IVM2012DS 101-1	B	A	B	A
8	**FR13A 8**	FR13A-IVM2012DS 101-10	B	A	B	A

Legend: *A-IR29 B-FL478 C-bond other than A and B*

Table 63. F1 progenies generated to introgress saltol into high yielding varieties, PhilRice CES, 2015 WS.

Cross Combination		No. of F_1 naked seeds
Female Parent	**Male Parent**	
NSIC Rc298 (TUBIGAN 23)	FL378	21
NSIC Rc298 (TUBIGAN 23)	FL478	24
NSIC Rc300 (TUBIGAN 24	FL378	20
NSIC Rc300 (TUBIGAN 24)	FL478	141
NSIC Rc308 (TUBIGAN 26)	FL378	49
NSIC Rc308 (TUBIGAN 26)	FL478	40
NSIC Rc308 (TUBIGAN 26)	IR86385-38-1-1-B	45
NSIC Rc308 (TUBIGAN 26)	IR86385-58-2-1-B	29
NSIC Rc308 (TUBIGAN 26)	IR86385-194-2-1-B	29
DEZO 300	FL378	97
NSIC Rc218	FL478	26
TOTAL		**521**

Table 64. Line selections from crosses aimed at combining sub1 and saltol genes, 2015 DS, PhilRice CES.

No	Cross Combination	PR Number	Trait	Selection						Undergone Screening
				F_4	F_5	F_6	F_7	F_8	F_9	
1	FL478/PSB Rc18-Sub1	PR41566	Saline and Submergence Tolerance	65*	8	6	5	5		Sub, Sal
				39**	24	4	4			Sal
2	FL478/NSIC Rc160	PR41563	Saline Tolerance, High Yield	20	39	29	15			on-farm Sal
3	FL478/PR39397-7-153-283	PR41562	Saline and Submergence Tolerance	10	15	-				dropped
4	FL478/PR33382-25-1-1-MES	PR41560	Saline and Drought Tolerance, RTD Resistance	77	75	70	21	14		Sal
5	FL378/PSB Rc18-Sub1	PR41561	Saline and Submergence Tolerance	64	41	21	18	144	86	Sub, Sal
6	FL478/PR25769-B-9-1	PR41565	Saline and Drought Tolerance	149	12	9	8	-		dropped
7	FL478/PSB Rc82//NSIC Rc160	PR41569	Saline Tolerance, Blast Resistance, High Yield	28	6	8	1	1		on-farm Sal
	Backcrosses									
1	FL478/1*PSB Rc82	PR41570	Saline Tolerance, Blast Resistance, High Yield	134	27	77	78	-		dropped
2	Fl478/1*PR39397-7-153-283	PR45172	Saline and Submergence Tolerance	27	25	9	6			-
3	FL478/1*NSIC Rc160	PR45173	Saline Tolerance, High Yield	6	3	1	1			-
4	FL478/1*Raeline 10	PR45174	Saline and Stagnant Tolerance, RTD Resistance	17	13	10	9			-
5	FL478/1*PR33382-25-1-1-MES	PR45175	Saline and DroughtTolerance, RTD Resistance	16	15	10	3			-
TOTAL				652	303	254	83	164	86	

Table 65. F1 progenies generated to combine high yielding and saline-submergence traits, PhilRice CES, 2015WS.

Cross Combination		No. of F_1 naked seeds
Female Parent	Male Parent	
IVC-21 (DrS 40)	IR86385-38-1-1-B	39
IVC-21 (DrS 40)	IR86385-58-2-1-B	36
IVC-21 (DrS 40)	IR86385-194-2-1-B	57
NSIC Rc240 (TUBIGAN 22)	IR86385-58-2-1-B	58
NSIC Rc298 (TUBIGAN 23)	IR86385-38-1-1-B	28
NSIC Rc298 (TUBIGAN 23)	IR86385-58-2-1-B	44
NSIC Rc298 (TUBIGAN 23)	IR86385-87-1-1-B	24
NSIC Rc298 (TUBIGAN 23)	IR86385-194-2-1-B	105
NSIC Rc300 (TUBIGAN 24)	IR86385-38-1-1-B	36
NSIC Rc300 (TUBIGAN 24)	IR86385-58-2-1-B	41
NSIC Rc300 (TUBIGAN 24)	IR86385-87-1-1-B	58
NSIC Rc300 (TUBIGAN 24)	IR86385-194-2-1-B	44
DEZO 300	IR86385-38-1-1-B	38
DEZO 300	IR86385-58-2-1-B	20
TOTAL		**628**

Breeding heat-tolerant rice in the Philippines

NL Manigbas, LB Madrid

Rice grows optimally between 20 to 35°C and becomes increasingly sensitive to increasing temperatures especially during flowering which can eventually reduce yields (Redona, et al 2007). Matthews et al. (1994 a, b) reported that the severe losses in South, Southeast and East Asia for rice was due to a threshold temperature effect that caused spikelet sterility but that genetic variation with regard to the threshold can provide significant opportunity to switch varieties as temperature rose. They found yield changes (i.e., increase or decrease) for India to range from -3 to +28%, for Malaysia from +2 to +27%, for the Philippines from -14 to +14%, and for mainland China from -18 to -4%. Rice yields could be affected as climate change may give a significant addition to future stresses and maybe beyond the capability of the existing rice cultivars to adapt to the conditions (Manigbas and Sebastian 2007). Therefore the development of rice varieties for high temperature tolerance is very important in addressing climate change scenarios in rice growing areas where 90 to 95% of the population depends on rice. There is a need to breed rice varieties that can tolerate higher temperatures or can avoid exposure to high temperatures by having shorter growing seasons or flowering that occurs during cooler periods of the day (Redona et al 2007).

Highlights:

- High temperature condition occurred in Philrice-CES on April 27-May 11, 2015 (Figure 46) . Data showed that temperature went as high as 39.2°C, a condition suitable for screening and selecting heat-tolerant rice lines. Most rice breeding materials were exposed to this condition during 2015 dry season.

- Dry season of 2015 Preliminary Yield Trial revealed 22 tolerant and 143 intermediate lines. PR42130-M-1-B-3-2-B-9-B had the highest yield obtained which was 6.99t/ha-1.

- All entries under observational nursery were already uniform. Sterility data revealed 59 tolerant, 139 intermediate and only 14 intolerant. All entries were further evaluated on 2015 wet season.

- Two hundred ninety-nine entries were selected in the pedigree nursery. Two hundred forty eight had sterility data. Based on data gathered, 96 lines were tolerant and only 14 were intolerant. Most lines were intermediate.

- Two elite heat-tolerant lines submitted for further evaluation ranked 2nd and 3rd based on yield in Preliminary Multi-Environment Trial.

- There were nine QTLs identified for HT tolerance. Six major QTLs: 3 for fertility (qHTfert1, qHTfert3, qHTfert4), 1 for time of flowering (qHTtof10), 1 for dehiscent temperature and 1 for heading day (qHThd3). Three minor QTLs identified were qHTdt4, qHTdt5 and qHTdt10 for dehiscent high-temperature (Figure 48).

- Four elite lines were submitted to Multi-environmental Trial and six lines for NCT (Table 66).

- Forty lines were sent to Iguig, Cagayan for yield test.

- There were 62 elite lines screened for drought

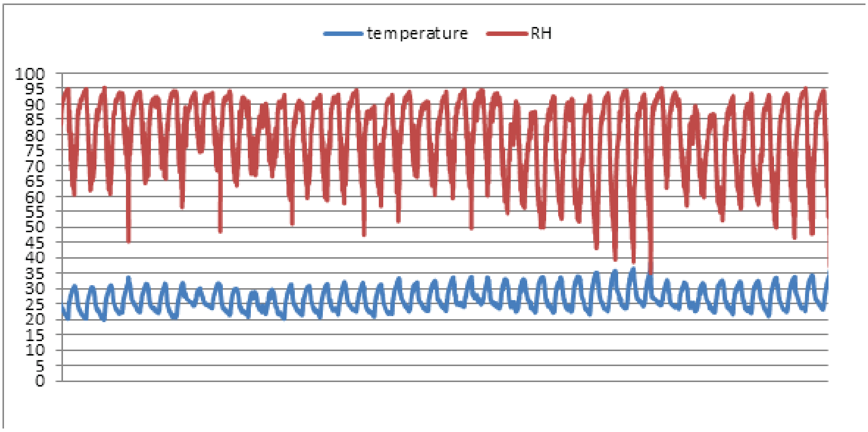


Figure 46. Temperature and percent relative humidity from March 25-May 11, 2015.

Table 66. Elite lines submitted to National Cooperative Testing and Advance Yield Testing.

NCT	AYT
PR42026-34-1-3-B-2	PR42130-M-1-B-3-2-B-9
PR42130-M-1-B-6-2-B-7	PR42073-7-3-1-2-3
PR44500-A3-3-2-2	PR42086-5-3-3-1-1
HTVN-13-9-2-1-1-B	PR44440-6-4-3-2
PR 40330-4-2-7-1-2-1	
PR42132-M(I)-1-B-8-B-B-6	

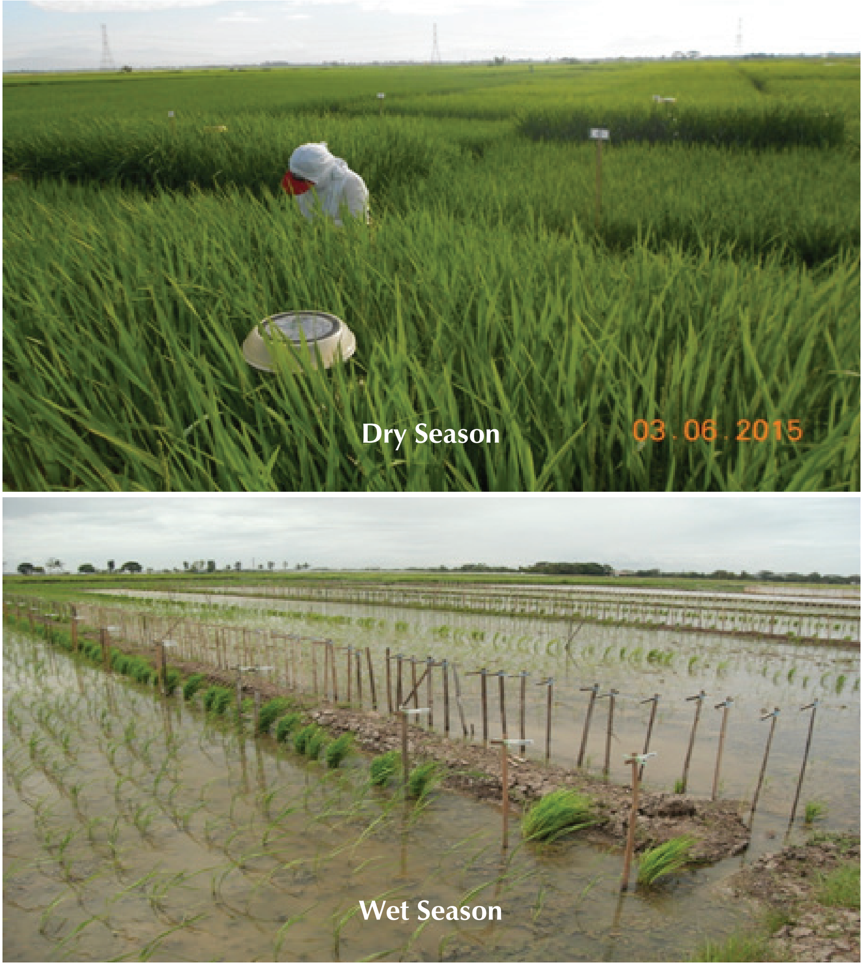


Figure 47. Heat-tolerant field establishment 2015.

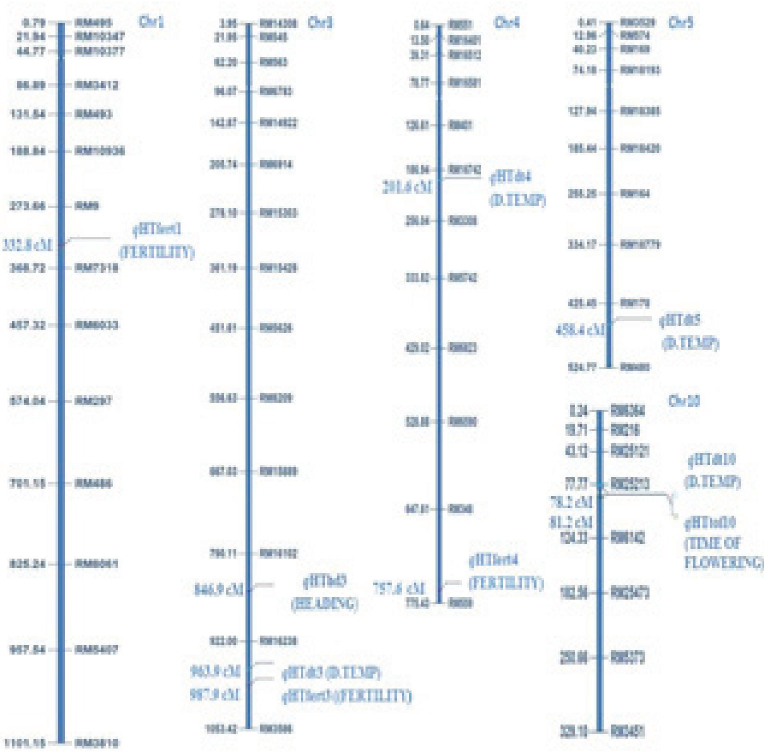


Figure 48. QTL linkage map for HT tolerance showing the putative location of genes.

Genetic improvement of locally-adapted rice cultivars and elite lines for upland and drought-prone rainfed lowland environments

VC Lapitan and MJTMercado

Rice is cultivated under diverse ecosystems ranging from irrigated to rainfed upland to rainfed lowland. In the Philippines, rainfed lowland and upland areas are considered important system of growing rice. They have great potential in increasing rice productivity and hence, in helping attain the country's goal of self-sufficiency (Francisco, 2010). However, these areas which occupy about 38% of the total cropped rice area, contribute only 21% to total rice production (Khush, 1997). Primarily, the lower productivity in these areas is caused by the frequent occurrence of drought due to a failure of rain or a long spell between two rains. It was predicted that due to climate change water shortage will be further experienced in years to come (Wassmann et al., 2009) and therefore the effects of drought in agriculture particularly in rice farming are predicted to become worse (Bates et al., 2008). Drought is a major production constraint of upland and rainfed lowland rice areas. Damage from drought may occur at the seedling and tillering stages, and on some occasions the damage is also severe at the reproductive stage. Yield losses caused by drought at the combined anthesis and seedling stages were about double those caused by weeds, which was the second-ranked constraint (Widawsky and O'Toole 1990).

The need to address the constraints affecting yield is very important in order to cater the continual increases in demand by the country's population that is growing 2.3% per annum in general and to provide the need of many rural poor who rely on rice farming under rainfed conditions, in particular. Several approaches such as integrated management technologies and irrigation enhancements can be employed to mitigate drought stress due to climate change; however, drought tolerant varieties developed through plant breeding are more accessible to farmers than these interventions that might require large investments by farmers. The continued application of conventional breeding and the recent developments in non-conventional approaches offer significant potential for improving yield growth and adaptation to drought in upland and drought-prone rainfed lowland environments.

Highlights:

- Table 67 shows the total number of entries evaluated and selected during 2015 DS both under rainfed lowland (favorable) and upland (managed drought) conditions. The selected entries will be advanced to next generations in 2015 WS

- Heavy infestation of tungro virus under rainfed lowland condition was observed in 2015 DS.

- Evaluation of breeding materials under managed drought stress condition, targeting reproductive stage, started at F4 generation. The seeds of selected F3 entries from rainfed lowland were divided and evaluated both under rainfed and upland conditions. Figure 49 shows the plants being evaluated under upland condition.

- For drought stress screening targeting reproductive stage, withholding of irrigation started around panicle initiation. The field was irrigated when the soil water tension was around -50 to -70 kPA at a 30cm depth. Piezometer and tensiometer apparatus were installed in the field to monitor the timing of irrigation. Ability of the plants to recover from stress after irrigation was also being considered in the selection process (Figure 50).

- Utilization of marker-assisted selection (MAS) is being employed in this study to select for breeding materials with Pup1 gene. So far, a total of 1355 BC2F2 materials were selected with Pup1 gene through MAS and will be advanced to BC2F3 this 2015 WS.

- For Preliminary Yield Trial (PYT), evaluation of the selected 111 entries under rainfed lowland condition (favorable) will be on its second season while it will be the first trial under upland condition this 2015 WS.

Table 67. Number of entries selected during 2015 DS and for evaluation in 2015 WS. Numbers in parenthesis are entries evaluated in 2015 WS.

Generation	No. of entries selected in 2015 DS	No. of entries for evaluation in 2015 WS	Remarks
Rainfed Lowland (Favorable)			
F1	–	23	
F2	360 (1802)		
F3	–	360	
F5	69 (429)		
F6	–	69	
F7	56 (60)		
F8	117 (123)		
ON	–	173	56 from F7 & 117 from F8
PYT	111	111	PYT 2
BC2F2	1355 (6916)		with Pup1 gene based on MAS
BC2F3	–	1355	with Pup1 gene based on MAS
Upland (Managed drought stress condition)			
F4	127 (1122)		
F5	37 (429)	70	
F6	7 (35)	98	In the 98 entries, 29 came from upland and 69 from F5- rainfed lowland)
ON	–	72	In the 72 entries, 57 from F4, 8 F5, & 7 from F6
PYT		111	Entries came from 2014 WS ON

Figure 49. Field evaluation of breeding materials under upland condition.

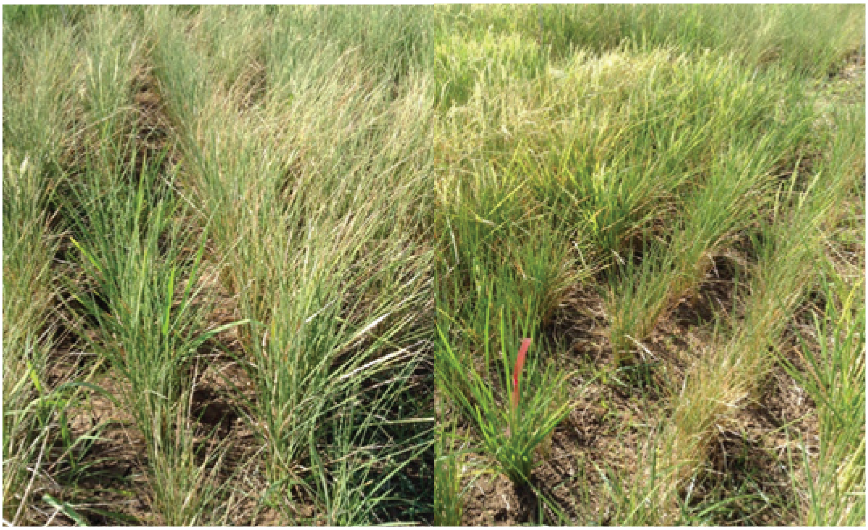


Figure 50. Leaf rolling and drying exhibited by rice plants during drought stress. Selected rice plants withstood drought stress (with arrows).

Breeding of resilient and productive genotypes adapted to water stress environment in Mindanao

JM Niones, SJ Labarosa, JLG Espina, RR Suralta, and LM Perez

Soil moisture deficit at varying degree is a recurring stress that affects rice production. Rice plants in rainfed rice areas are usually exposed to a continuous cycle of transient of drought and waterlogged condition (soil moisture fluctuation) due to erratic rainfall. Rice areas in Mindanao particularly in Regions 9, 10, 11 and 12 which has a combined area of 231,449 ha are highly dependent on the availability of rainfall for irrigation source. These areas do not have fixed cropping calendar and often practice asynchronous rice planting. Variability in soil moisture deficit condition adversely affects shoot and root growth and functions of various crops. In addition to water deficit stress, problems on rice tungro and bacterial leaf blight diseases often arise. The combined effect of abiotic and biotic stresses present in rainfed areas possesses a negative impact on rice production. Breeding activities with emphasis on increasing yield level and drought tolerance thru the mechanism of plastic root development, and incorporation of tungro and bacterial blight disease resistance genes will significantly improve rice productivity in rainfed lowland areas.

Highlights:

- Field performances of advanced breeding lines, Raeline 7 (PR33374-28-1-5), Raeline 6 (PR33381-29-1-2-1-B-B), Raeline 3 (PR33382-25-1-1-B-B) and, Raeline 10 (PR3395-27-1-B-B-B) were evaluated at the rainfed areas in the municipalities of Aleosan and Libungan,North Cotabato and in Bukidnon.

- In Bukidnon, farmers preferred Raeline because of its high milling recovery.

- 4,700 individual plants were selected from 47 THM entries from CES which survive RTV and in rainfed condition.

- 81 F6 segregating lines showed good phenotypic acceptability and field resistance against RTV and will be elevated to observational nursery.

- Out of the 56 entries in observational nursery 39 were selected and will be elevated to advance observational nursery. The unselected entries will be retained in the observational nursery.

- Out of the 11 entries in advance observational nursery 6 were selected and will be elevated to Preliminary yield trial (PYT) with three replications.

- Among the 11 Raeline entries subjected to GYT, Raeline 10 showed the highest yield of 5.96 tons/ha. However, grain yield of Raelines 3, 5, 6, 8 9, 11 are comparable NSIC Rc222 (6.0t/ha) and NSIC Rc226 (4.6t/ha. On the other hand, Raeline 1 showed the lowest yield of 4.6 tons/ha. In addition, it is comparable to Raelines 2, 4, 7 and to check NSIC Rc298 (3.7 tons/ha) based on ANOVA. Results of ANOVA also showed that yield of Raelines 3, 5, 6, 8, 9, 10 and 11 are significantly different from NSIC Rc298 (Figure 52 and Table 68).

- Results of ANOVA showed that the yield of B11598C-TB-21-B-7, DRS 768 (Raeline 7), DRS 14 (Raeline 3), BP1976B-2-3-7-TB-1-1, IR82912-B-B-16 and RAELINE 3 showed no significant difference to check varieties NSIC Rc226 (4.92 tons/ha) and NSIC Rc222 (3.89t/ha). In addition, B11598C-TB-21-B-7 (4.52t/ha) showed the highest yield among the 8 entries subjected to PYT. It is numerically lower than the check variety NSIC Rc226. On the other hand, B11577E-MR-B-12-1-1 has the lowest recorded yield of 0.93t/ha under rainfed condition. It is however comparable to the yield of IR83142-4-4 (IR07G 104), Dinorado and check variety NSIC Rc298 (2.52t/ha) (Table 69 and Figure 53).

- Field performances of Raeline 6, Raeline 7, and Raeline 10 were evaluated at the rainfed areas in Libungan and Aleosan, North Cotabato during the wet season.

- Raeline 6 was preferred over Raeline 10 by the cooperating farmer in Libungan, North Cotabato because of its resistance to lodging, good grain quality and its late and slow leaf senescence.

- Raeline 7 was preferred over Raeline by the cooperating farmer in Aleosan, North Cotabato because it yields higher than Raeline 10, more resistant to shattering, more resistant to diseases and matures early than Raeline 10. In addition, he observed that when water is scarce Raeline 10 shows spotted symptoms whereas Raeline 7 seems unaffected. In terms of eating quality, Raeline 10 has good eating quality than Raeline 7 and comparable with that of Masipag variety.

- 22 of 207 entries under the observational nursery (ON) showed interemediate phenotypic acceptability and has intermediate reaction to rice tungro disease were initially selected.

- 11 of 39 entries under the advance observational nursery (AON) showed intermediate to good phenotypic acceptability and exhibited intermediate reaction to rice tungro disease have been initially selected.

- 88 of 3630 THM entries were initially selected that showed acceptable plant stand during the vegetative stage.
- Three PYT entries (Jasmin 1, Raeline 6 and Raeline 7) and 3 GYT entries (IR83142-4-4, Raeline 7 and Raeline 3) were harvested with <100 g yield due to heavy rice black infestation.

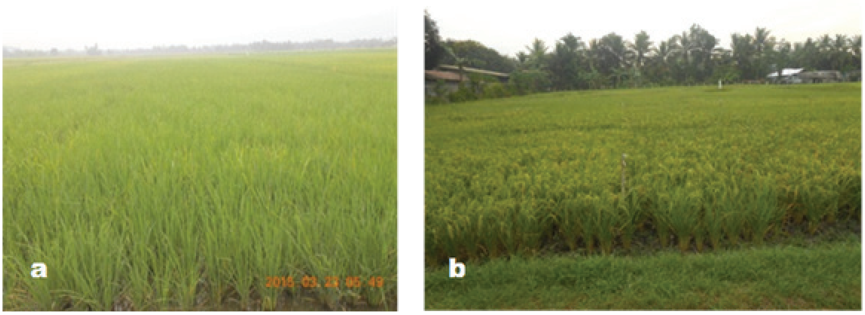


Figure 51. The rainfed entries under simulate rainfed conditions in 2015 dry season.

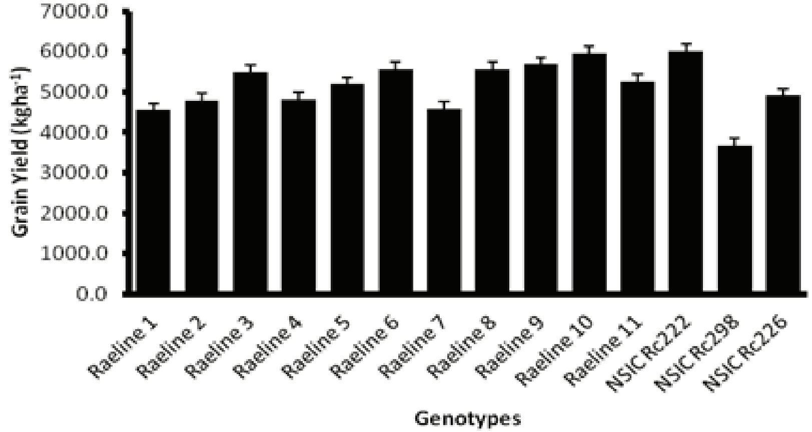


Figure 52. Grain yield of 11 advanced breeding lines and 3 check varieties in general yield trial nursery under rainfed area at PhilRice Midsayap Experimental station.

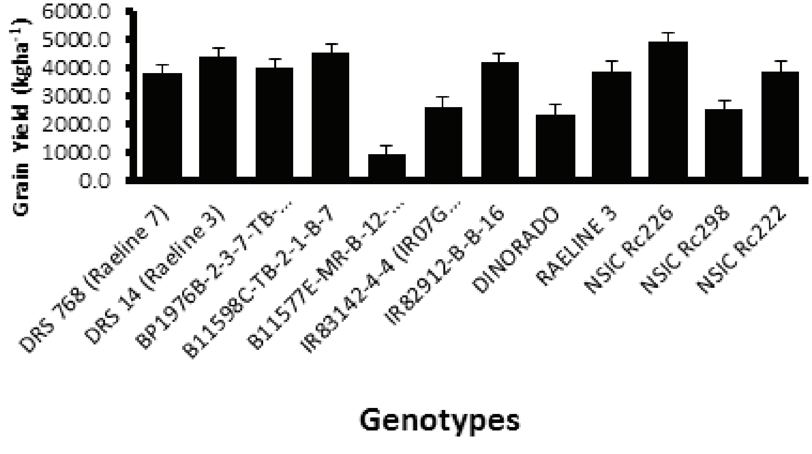


Figure 53. Grain yield of 9 breeding lines and 3 check varieties in preliminary yield trial nursery under rainfed area at PhilRice Midsayap Experimental station.

Table 68. Yield and yield components, shoot dry weight, plant height and number of productive tillers of 14 general yield trial entries under rainfed condition 2015.

PLOT No. 15 DS	Designation	PR code	Grain yield (kg/ha)	Yield Components					No. of productive tillers	Shoot dry weight^{-1} (g)	Plant height (cm)
				No.of grain panicle^{-1}	No.of filled grain panicle^{-1}	No.panicles plant^{-1}	Spikelet fertility (%)	Grain weight (g)			
GYT 101	Raeline 1	PR33381-29-1-2-B-B	4547.6	81.7	64.4	14.7	78.9	25.3	13.1	115.8	88.6
GYT 102	Raeline 2	PR33382-28-2-1-B-B	4794.2	99.7	72.3	15.0	72.5	26.9	13.6	130.4	91.7
GYT 103	Raeline 3	PR33382-25-1-1-B-B	5488.9	91.1	70.7	16.2	77.6	24.7	14.0	124.1	89.1
GYT 104	Raeline 4	PR33481-B-1-B-B-B	4816.0	72.7	53.1	13.8	73.0	25.1	11.1	108.3	87.6
GYT 105	Raeline 5	PR33481-B-2-B-B-B	5199.8	66.9	49.2	14.8	73.5	25.3	14.2	102.6	89.5
GYT 106	Raeline 6	PR33381-29-1-2-1-B-B	5565.6	92.0	67.9	14.5	73.9	25.2	13.3	115.2	85.2
GYT 107	Raeline 7	PR33374-28-1-5-B-B	4581.3	106.2	86.9	15.0	81.8	25.3	13.7	127.8	88.6
GYT 108	Raeline 8	PR33382-25-1-3-B-B	5577.4	86.5	65.5	15.2	75.7	24.6	14.4	116.2	92.5
GYT 109	Raeline 9	PR33393-25-2-B-B-B	5687.7	83.5	60.4	16.5	72.3	25.1	14.1	108.8	86.1
GYT 110	Raeline 10	PR33395-27-1-B-B-B	5956.1	93.5	76.8	15.3	82.1	24.6	13.1	128.4	84.3
GYT 111	Raeline 11	PR33481-B-1-B-B-B	5259.4	96.7	81.4	14.5	84.2	28.5	12.8	125.0	88.5
GYT 112	NSIC Rc222	-	6008.0	86.7	65.0	15.0	75.0	29.1	13.2	136.7	97.1
GYT 113	NSIC Rc298	-	3676.6	82.3	63.9	14.8	77.6	24.4	12.7	114.5	86.9
GYT 114	NSIC Rc226	-	4914.5	100.4	64.9	17.2	64.6	23.9	12.6	137.1	91.3

Table 69. Yield and yield components, shoot dry weight, plant height and number of productive tillers of 12 preliminary yield trial entries under rainfed condition 2015.

PLOT No. 15 DS	Designation	Grain yield (kg/ha)	Yield Components					No. of productive tillers	Shoot dry weight^{1} (g)	Plant height (cm)
			No.of grain panicle^{-1}	No.of filled grain panicle^{-1}	No.panicles plant^{1}	Spikelet fertility (%)	Grain weight (g)			
PYT 101	DRS 768 (Raeline 7)	3793.8	96.9	79.9	15.8	82.5	25.1	13.3	142.4	87.5
PYT 102	DRS 14 (Raeline 3)	4383.9	88.6	74.0	16.7	83.5	23.2	11.6	128.9	87.9
PYT 103	BP1976B-2-3-7-TB-1-1	3979.2	112.8	90.7	10.5	80.5	23.6	8.6	116.0	111.0
PYT 104	B11598C-TB-2-1-B-7	4522.6	148.8	120.3	8.8	80.8	26.0	8.7	121.4	109.0
PYT 105	B11577E-MR-B-12-1-1	934.1	101.3	67.2	15.2	66.3	28.7	9.4	141.1	105.4
PYT 106	IR83142-4-4 (IR07G 104)	2605.0	67.9	54.2	15.3	79.8	25.8	9.4	119.7	90.9
PYT 107	IR82912-B-B-16	4170.1	112.6	94.0	13.3	83.5	25.4	11.5	159.1	92.9
PYT 108	DINORADO	2333.8	167.0	146.0	6.0	87.4	24.4	5.9	105.5	124.2
PYT 109	RAELINE 3	3881.8	96.5	76.6	12.8	79.4	24.4	11.6	118.9	89.5
PYT 110	NSIC Rc226	4917.3	119.7	87.0	11.3	72.7	22.1	11.3	125.5	91.2
PYT 111	NSIC Rc298	2521.8	64.9	48.5	14.7	74.8	23.5	12.8	109.9	86.0
PYT 112	NSIC Rc222	3890.0	85.6	63.9	13.3	74.6	27.9	10.5	124.1	93.1

Figure 54. GYT entry shows symptom of rice tungro virus infection at 30 (left) and 35 (right) days after transplanting (DAT).

Figure 55. Infestation of rice black bug on the yield performance trial at 91 DAT.

Identification of high-value traits (grain quality and nutrition) and population improvement of upland rice cultivars in Mindanao

SE Abdula, AY Cantila and JL Balos

Traditional cultivars far exist in the upland; these traditional cultivars were known thru the years to stand biotic and abiotic stress and are believed to be of higher quality than lowland rice. To date, 14 varieties were released for upland production. Thus, this study aims to the improvement of preferred and adapted upland cultivars in Mindanao. It will improve farmers' productivity in the upland ecosystem. The study used recurrent population improvement and screening high-value traits like grain quality and nutrition (Zinc and Iron) through hydroponics. It will also use soil-media for further screening of Fe/Zn problems and grain content analyses.

Highlights:

- Survey and collection of preferred traditional, improved and elite breeding lines of upland rice cultivars was done at provinces of South Cotabato, North Cotabato, Sarangani and Maguindanao was done. Among the cultivars found, the preferred cultivars are Dinorado Kasagpi, Awot, Makiraga, Hinomay, Karutak, Kutibos, Palawan, Maland and Azucena. These germplasm were seed increased and used in population improvement.

- Among the 816 upland cultivars sent by PhilRice CES, 38 cultivars (Figure 56) were most adapted in Midsayap despite heavily infested of rice black bug and infected of tungro on its early stages. These were Arabon, Aritao-cagayan, Aryos, Awot, Balibod, Batangueno (Glut), Binatang, Binernal White, Binisaya, Buntot Kabayo, C2, C22, C43, Camuros, Chumi-i-tinawon , Dalagang Bukid, Dinorado, Dukpayon, Guinata, Hinomay, Hinumay, Inamos, Inipot-ibon, Kawatil Gold, Kinaboag, Kutibos (Opi), Linangka, Magsanaya, Maligaya 2, Milbuen 3, Milpal 18, Minarugon, Murado, Parorutong, PE-2, Pinalwa, Pinursigi and Wagwag. For early maturing trait, 30 had flowered 50% in a range of 37 to 55 days after transplanting (DAT). These cultivars were Epis, Kinalansing, Inipot-ibon, Putang-lansong-A, Azucena, Ag-oyong, Mindanao, Inaguiw, Kinanda, Maluit, Singguyan, Diket (Pilis), P2-7-2, P1-2-4, Triveni, P9-2-1, Fortuna, P2-7-2, Kamros, Euran, Kamuros, Awot, Azmil 82, Balatinao, Malagkit Kinato, Palawan, Kawatil, Lubang White, Union, Binacone And Kinaruray.

- An on-going field characterization for 177 experimental units (57 entries including 2 checks with 3 replication under RCBD) for the morphological characterization and thorough genetic variability analyses of Upland cultivars in Midsayap condition (Figure 57).

- For the Fe toxicity screening (Figure 58), the protocol used was a modification from Platten (2011) of IRRI using SNAP hydroponics. The most adapted cultivars were used as test materials along with 10 preferred upland cultivars. For Fe toxicity, 12 showed tolerance to Fe toxicity: Binatang, Binernal White, C2, Chumi-I-tinawon, Dalagang bukid, Maligaya 2, Milbuen 3, Milpal 18, Parirutong, Pinalwa, Kalinayin and Karutak.

Figure 56. Upland cultivars evaluated under Midsayap field condition with infestation of rice black bug on dry season 2015.

Figure 57. Field evaluation of 57 upland cultivars with 2 checks at Midsayap condition, Dec 2015 WS to date.

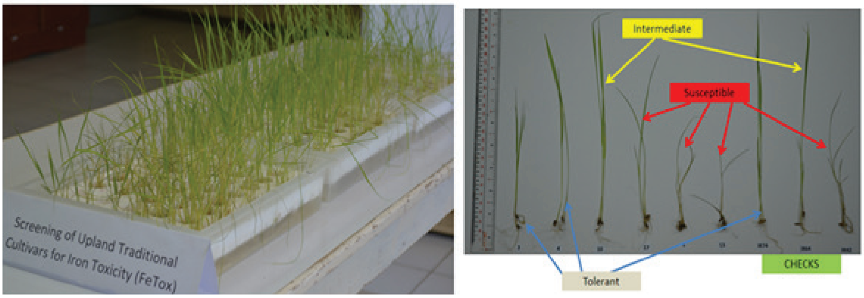


Figure 58. Screening of Upland germplasm under Iron toxicity and sample cultivars showing tolerance and susceptibility.

Utilization of wild rice species as gene sources for drought tolerance and other traits

CFS Te, RT Miranda and NRL Sevilla

Drought is the single most important abiotic factor that hinders productivity in rainfed areas. With modest increases in productivity and decreasing physical area for favorable rice production, increasing production in the vast rainfed areas in the country is crucial in achieving rice self-sufficiency. Increased production, however, can only be achieved by developing technologies such as appropriate rice varieties and water-saving technologies that will address water-related stresses that become more and more severe due to changing climate patterns.

The wild relatives of rice are a rich source of important genes that can be transferred into cultivated varieties through wide hybridization. Although drought tolerance is a very complex trait and, therefore, quite challenging to achieve through breeding, the availability of drought-tolerant wild and cultivated germplasm offers opportunities to develop modern varieties that can withstand water stress.

While direct selection for drought tolerance may become difficult due to unpredictable weather condition that may affect field selection, selection for several secondary traits associated with drought has been shown to yield some gains. Similarly, genetic tools are available to mark loci associated with these traits making it feasible to select genetic loci in segregating populations using DNA markers.

This study aimed to: (1) acquire wild rice accessions and evaluate them for tolerance to drought and other important traits; (2) transfer drought tolerance and other important traits from wild rice donors into elite background through wide hybridization and; (3) evaluate the comparative performance of derived elite breeding lines under field condition.

Highlights:

- Four hundred forty five breeding lines composed of 56 Preliminary Yield Trial (PYT) (including 3 checks: PSB Rc14, IR64 and NSIC Rc276), 58 Pedigree Nursery (PN), 119 Observational Nursery (ON) and 268 Advance Observational Nursery (AON) were screened for drought tolerance on 2015 DS.

- Performance evaluation of PN last 2015 DS identified four lines out of 58 lines with yield range of 4.33 to 6.40 t/ha under drought-stressed condition. These lines also belong to the top 30 lines that performed well last 2014 DS drought screening with yield of >3.20t/ha. They were uniform in terms of agro-morphology and were advanced to PYT of 2015 WS for seed increase and generation advance.

- Out of 119 ON lines evaluated under drought-stressed condition, six lines were identified with putative drought tolerance with yield range of 4.41 to 6.45t/ha. These lines were crosses of drought-tolerant varieties and Nam Sa Gui 19. These lines were forwarded to PYT of 2015 Wet Season for seed increase and generation advance.

- Ten AON entries obtained yield with range of 4.07 to 9.03t/haThese lines were added as new entries for PYT of 2015 WS.

- Significant difference in grain yield was observed among different genotypes. Performance evaluation under drought condition showed that among the 56 elite breeding lines, PYT 43 obtained the highest yield of 7.02t/ha which is significantly higher over the tolerant checks PSB Rc14 and NSIC Rc276, and the susceptible check IR 64 with 4.07t/ha, 3.98t/ha and 3.64t/ha respectively.

- PYT 16, 39, 54 and 7 had yield ranging from 3.88 to 6.16 t/ha which were comparable to that of the checks.

- Two lines PYT 39 and 40 were identified to be less responsive to drought as seen on the leaf rolling (LR) score (7) as compared to the rest of the lines with score of 9.

- Three entries had leaf drying (LD) score of 3, indicating less response to drought.

- PYT 16 and 39 obtained promising results with high yield and low leaf drying score.

- Significant differences on the number of days to maturity were observed among entries. The earliest entry to mature was PYT 38 at 111 days and the NSIC Rc276 was the most late to mature at 134 days.

- Grain yield was found negatively correlated with leaf rolling. Strong positive correlation was observed between panicle length, number of filled spikelet, total spikelet, plant height and biomass. Negative linear relationship on the other hand, was observed between panicle length, leaf rolling, lead drying and days to maturity. This implies that panicle elongation and grain filling is affected by the plant's drought response (green leaf retention and delay in leaf rolling).

- Correlation values may imply that low leaf drying score can be an indicator of good response of plants to drought, as seen in its inverse relationship with panicle length and number of filled spikelet. Thus, leaf drying would likely result to unfilled spikelet.

- Three elite breeding lines were forwarded for Multi-Environment Trial.

- Germinated and regenerated 5 seeds of 40 wild rice accessions.

- Seed-increased ten accessions of Oryza australiensis, one O. alta, one O. glumaepatula, one O. punctata, one O. ridleyi and one O. eichingeri.

- Five wild rice accessions is undergoing reproductive drought screening under screenhouse condtions with IR64 as susceptible check and PSB Rc14 as drought tolerant check.

Figure 59. Field set-up (a.) 13 days and (b.) 39 days after drought imposition.

Table 70. Drought response and agronomic traits of breeding lines under drought stress conditions, 2015DS.

Entry	GY	LR	LD	PL	FS	UFS	TS	PH	PT	TT	PPT	MAT	BM	TGW
PYT-43	7.02	9.0	7.0	25.33	50.87	29.00	79.87	77.87	10.00	11.93	85.94	130.33	30.81	19.53
PYT-7	6.16	9.0	7.0	21.68	46.95	19.12	66.07	69.20	10.87	15.27	70.62	117.33	36.32	15.67
PYT-54	5.11	9.0	7.0	24.43	45.10	18.70	63.80	75.07	10.73	12.73	85.89	129.00	37.51	25.33
PSB Rc14	4.07	9.0	7.0	27.97	53.73	19.60	73.33	66.40	13.27	15.13	88.05	131.00	42.53	16.07
PYT-39	3.98	7.0	5.0	35.95	72.80	13.70	86.50	80.07	14.47	16.53	86.50	119.00	40.79	16.57
NSIC Rc276	3.98	9.0	7.0	14.00	7.10	44.30	51.40	64.27	6.60	7.67	86.68	133.67	25.99	15.07
PYT-16	3.88	9.0	5.0	23.57	51.60	9.13	60.73	69.00	14.87	17.73	85.80	118.00	44.61	16.40
IR64	3.64	9.0	7.0	22.49	41.67	18.27	59.93	67.53	12.20	14.13	87.27	122.67	38.74	16.23
PYT-24	3.61	9.0	7.0	26.37	48.80	18.40	67.20	70.07	14.80	18.93	80.42	127.33	44.53	25.43
PYT-40	3.58	7.0	3.0	31.55	58.00	26.27	84.27	91.73	11.07	12.53	88.43	118.00	46.03	19.23
PYT-22	3.45	9.0	7.0	23.23	50.87	16.67	67.53	76.33	31.80	34.20	88.40	132.33	45.66	25.10
PYT-13	3.42	9.0	3.0	29.40	58.13	17.27	75.40	73.73	14.73	16.07	91.88	125.67	48.20	18.53
PYT-6	3.10	9.0	7.0	27.75	57.13	13.87	71.00	71.93	13.20	18.00	75.53	122.67	36.97	24.37
PYT-17	3.06	9.0	5.0	35.15	77.20	6.30	83.50	70.07	13.80	15.67	88.21	118.67	48.05	22.07
………. .														
PYT-25	2.87	9.0	7.0	27.03	50.90	9.80	60.70	72.40	14.20	15.93	90.25	131.67	36.86	18.83
PYT-20	2.83	9.0	7.0	24.60	43.00	11.20	54.20	76.20	14.47	17.13	84.33	126.33	34.96	25.90
PYT-15	2.56	9.0	5.0	29.17	67.47	9.27	76.73	84.87	15.40	18.80	82.08	116.33	42.72	23.87
PYT-49	2.35	9.0	3.0	22.11	54.90	21.57	76.47	87.33	14.00	16.40	84.01	127.00	36.35	25.30
PYT-52	2.32	9.0	7.0	25.69	46.27	17.27	63.53	74.40	10.67	11.13	95.77	117.67	36.17	21.37
PYT-46	2.31	9.0	7.0	31.00	57.13	29.13	86.27	81.53	10.87	12.87	85.22	132.33	31.33	17.43
PYT-35	2.29	9.0	7.0	28.17	46.67	17.07	63.73	77.80	13.33	17.00	77.57	116.33	44.25	21.70
PYT-8	2.17	9.0	5.0	23.78	48.00	14.40	62.40	69.00	13.40	17.40	77.06	120.00	45.62	20.73
PYT-55	2.14	9.0	7.0	25.30	58.67	23.13	81.80	70.73	10.80	11.33	95.50	119.00	38.25	19.37
PYT-1	2.08	9.0	7.0	31.12	74.87	41.88	116.75	86.40	14.20	15.73	90.43	125.67	46.33	19.57
PYT-23	2.05	9.0	7.0	22.56	45.12	21.40	66.52	68.60	13.53	15.00	90.71	133.67	39.05	23.07
PYT-18	1.93	9.0	7.0	21.07	39.80	7.27	47.07	69.10	12.70	15.90	79.82	120.00	40.25	21.03
PYT-5	1.89	9.0	7.0	25.29	55.00	13.93	68.93	73.80	13.20	17.93	75.31	123.33	43.11	19.23
PYT-44	1.84	9.0	7.0	29.92	64.16	17.09	81.24	78.47	11.27	13.20	84.50	130.33	44.11	20.33
PYT-11	1.78	9.0	7.0	34.45	71.00	10.60	81.60	78.40	10.33	12.53	82.57	125.00	55.09	20.80
PYT-3	1.70	9.0	7.0	21.43	45.73	22.67	68.40	72.80	12.13	13.40	90.36	131.00	33.99	20.93
PYT-2	1.66	9.0	7.0	23.48	51.77	10.85	62.62	73.73	14.00	20.73	68.55	119.67	38.18	20.93
PYT-48	1.65	9.0	7.0	28.43	56.33	21.80	78.13	92.07	11.53	13.07	88.01	117.67	41.71	21.13
PYT-9	1.64	9.0	5.0	25.70	48.07	29.47	77.53	74.33	11.60	13.20	87.85	125.67	43.60	21.40
PYT-14	1.64	9.0	5.0	36.66	100.40	8.80	109.20	79.47	13.40	16.27	83.45	122.33	39.47	21.07
PYT-12	1.56	9.0	7.0	29.03	66.87	17.53	84.40	80.93	11.67	14.93	77.94	123.00	50.83	22.30
PYT-45	1.55	9.0	7.0	29.79	56.20	19.13	75.33	77.67	11.27	12.80	87.93	132.33	45.04	20.93
PYT-37	1.51	9.0	7.0	34.83	97.40	24.00	121.40	80.27	11.73	13.20	89.46	127.00	46.99	24.53
PYT-30	1.49	9.0	7.0	22.77	38.60	16.27	54.87	76.73	16.07	19.80	81.73	121.00	41.60	30.20
PYT-19	1.48	9.0	7.0	25.09	51.27	15.80	67.07	75.53	14.80	18.40	80.37	124.33	39.62	27.77

Table 70. Drought response and agronomic traits of breeding lines under drought stress conditions, 2015DS. (Con't)

PYT-19	1.48	9.0	7.0	25.09	51.27	15.80	67.07	75.53	14.80	18.40	80.37	124.33	39.62	27.77
PYT-51	1.41	9.0	7.0	26.05	48.65	19.73	68.38	69.80	10.67	11.87	89.74	127.00	34.55	28.60
PYT-38	1.34	9.0	5.0	41.25	83.70	25.30	109.00	146.47	15.27	16.20	93.70	111.00	54.24	22.00
PYT-41	1.27	9.0	7.0	21.67	31.47	28.93	60.40	73.53	10.47	14.00	73.06	113.67	38.41	21.83
PYT-21	1.24	9.0	7.0	24.73	46.20	10.60	56.80	72.00	13.73	15.60	90.94	132.00	43.36	23.87
PYT-36	1.22	9.0	7.0	26.02	47.47	17.73	65.20	80.87	15.67	19.60	79.33	116.33	38.94	22.57
PYT-34	1.22	9.0	7.0	22.47	39.67	12.87	52.53	82.33	13.47	17.20	78.20	122.33	39.86	17.77
PYT-50	1.21	9.0	7.0	23.18	46.40	10.70	57.10	80.87	11.20	13.67	81.61	121.00	40.01	23.50
PYT-47	1.09	9.0	7.0	27.16	49.00	18.80	67.80	85.60	13.53	15.40	88.00	130.67	36.56	22.80
PYT-56	1.08	9.0	7.0	29.41	63.80	17.73	81.53	70.20	13.40	15.00	90.24	132.33	39.42	29.70
PYT-33	1.05	9.0	7.0	25.80	44.33	22.67	67.00	78.18	13.40	17.47	76.58	121.00	35.35	25.47
PYT-4	0.95	9.0	7.0	19.30	50.03	10.62	60.65	71.93	13.73	19.20	73.12	126.33	39.92	26.97
PYT-10	0.88	9.0	7.0	33.87	75.60	10.40	86.00	114.27	14.73	18.40	79.88	121.00	38.09	24.20
PYT-53	0.83	9.0	7.0	27.00	49.30	21.00	70.30	69.00	11.87	12.67	93.56	125.00	34.86	19.80
PYT-31	0.76	9.0	7.0	22.07	35.33	23.27	58.60	80.53	13.27	17.87	75.11	125.33	37.46	20.83
PYT-32	0.73	9.0	7.0	25.92	51.40	19.70	71.10	81.00	12.13	15.13	79.60	127.00	31.16	17.30
PYT-29	0.68	9.0	7.0	22.21	30.07	24.33	54.40	78.13	12.13	16.33	74.33	125.67	35.74	21.43
PYT-42	0.49	9.0	5.0	24.06	32.40	40.67	73.07	79.00	10.47	12.00	86.71	128.33	44.39	19.40
CV	51.87	4.99	17.17	20.18	30.67	37.30	20.37	22.86	32.98	36.74	9.91	5.67	20.59	10.27

Code	**Description**
GY	Grain Yield (t/ha)
LR	Leaf Rolling
LD	Leaf Drying
PL	Panicle length
FS	Filled Spikelets
UFS	Unfilled spikelets
TS	Total Spikelets
PH	Plant height
PT	Productive Tillers
TT	Total Tillers
PPT	Percent Productive Tillers

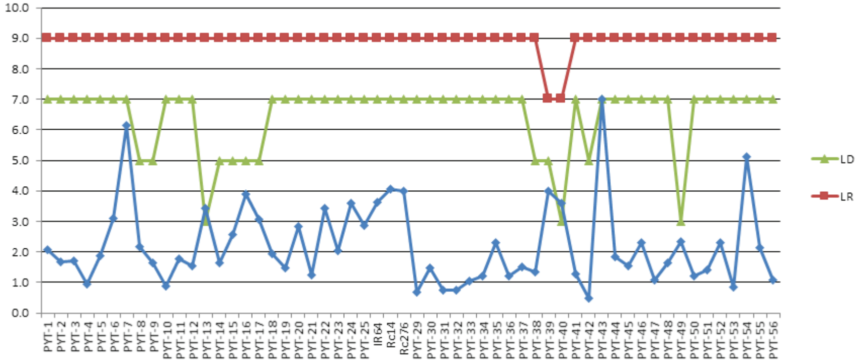


Figure 60. Relationship between grain yield, leaf rolling and leaf drying of 56 entries under PYT of 2015 DS.

VII. Development of selection criteria and strategies for organic rice breeding

Project Leader: AD Palanog

The breeding goals and objectives of conventional and organic rice systems are much alike. Basically, the breeding is directed to achieve desired traits such as high grain yield, resistance to biotic and abiotic stresses, and grain qualities acceptable to consumers. The main differences are the selection environment and the expression of these traits on these environments. Some of the important traits to be considered in organic rice breeding system are not often addressed in conventional breeding systems particularly on traits such as nutrient uptake efficiency, weed competitiveness, high total biomass yield, tolerance to mechanical weed control, and others. These traits are agronomic important traits and are highly cultural management dependent and different traits demands for different selection parameters and criteria in order to achieve maximum genetic gain. The basic requirement for the breeding program to commence is to test different genotypes under organic condition, identify the genotypes that will perform well under this condition, and characterize the traits of the adaptable genotype(s). From these, phenotypic characteristics ideal for adaptation under could be identified and could be the set as phenotypic parameters in selection for ideal genotypes.

Under conventional rice breeding system, it takes 10 years or more from hybridization or crossing of two parents to develop a new variety. To realize varietal improvement for organic farming systems, it is imperative that screening and crossing of ideal genotypes have to make as early as possible (Lammerts van Bueren et al. 2011). To develop an effective strategy of variety, development, the breeder must understand the alternative method that could be utilized and evaluate the genetic improvement that could be realized using this method (Fehr). Selection is always been an integral tool in plant breeding. The efficiency of selection largely depends on the accuracy and precision of selection criteria to the particular target trait and most importantly the ability of the breeder to effectively employ the selection criteria set. Selection criteria and parameter discriminate traits between desirable traits that should be advanced and undesirable traits that should be discarded. Their ultimate goal is to develop varieties that address the criteria and are suited to the target environment.

Evaluation of rice genotypes under low-external input

CU Seville, AD Palanog, IMG Ciocon, and LT Sta. Ines

In support to the declaration of Negros as an organic island, PhilRice Negros Station started its organic rice production and research in the six (6) hectares research and seed production area during the dry season of 2012. Various researches are needed to know the appropriate varieties or rice plant type suitable for organic rice production. It is also essential to know if there is need to have a separate varietal development intended for organic rice production, thus this study. The study aims to assess the performance of genotypes under conventional and organic rice production systems. It also aims to identify ideal plant type suitable for organic rice production.

Highlights:

2015 DS

- Thirty (30) entries (hybrid, modern and special rice) were established in three production systems: organic, zero input and conventional.

- Number of productive tillers, percent fertility, seed weight and harvest index were significantly affected by the production systems. More productive tillers and heavier seed weight were observed under conventional system while higher fertility and harvest index were observed under zero input production system (Table 71).

- No significant differences were observed on average yield; however yield under conventional production system was relatively higher than organic and zero input production systems (Table 71).

- Under organic production system, mean yield ranges from 1.5 to 3.6t/ha-1. Modern released varieties performed well under the organic system. Corocan had also a promising performance under the system (Table 72).

- Correlation analysis for yield showed that yield under organic production system is significantly correlated with the yield under conventional production system. The result is not yet conclusive, thus another field experiment were set-up this wet season.

Table 71. Mean yield and performance of 30 genotypes under three production systems.

	Days to heading	Plant hgt (cm)	Produc-tive tillers	Panicle length (cm)	Spikelet per panicle	Percent Fertility	Seed weight (g)	Harvest index	Yield (t/ha-1)
Organic	80	80	9b	21	104	82a	29b	0.34b	2.7
Zero input	84	71	9b	22	97	86a	27c	0.44a	1.8
Conventional	84	84	13a	23	109	70b	30a	0.29c	3.1
Con x gen	**	**	ns	ns	Ns	ns	ns	ns	**

Table 72. Top 10 best performer varieties under organic production system during the 2015DS under PhilRice Negros field.

	VARIETIES	YIELD (t/ha-1)
1	NSIC Rc204H	3.6
2	NSIC Rc224	3.6
3	NSIC Rc120	3.3
4	NSIC Rc280	3.3
5	Corocan	3.3
6	NSIC Rc19	3.2
7	NSIC Rc214	3.2
8	NSIC Rc240	3.1
9	NSIC Rc222	3.1
10	PSB Rc36	3.0

2015 WS

- Three separate seedbeds for thirty entries were prepared for organic, zero and conventional production systems. Vermicast at 1kg/m2 was applied to the organic seedbed prior to sowing while 1.5kg of 14-14-14 was applied to 30m2 seedbed area at 14 days after sowing (DAS) for conventional system. Organic main field was applied with vermicast at 3t/ha before the 3rd rotovation and conventional system was applied with 100-30-30 NPK, N applied in 3 splits. Pest control includes the used of attractants specifically for the rice bug in organic area while insecticides were applied to control green leaf hopper and rice bug in conventional system.

- During the wet season 2015 establishment, days to heading, plant height, number of productive tillers, panicle length, average spikelet, percent fertility and yield per ha were significantly affected by the production systems. Conventional system had longer days to heading, taller in height, more productive tiller longer panicle length more spikelets per panicle and higher yield than organic and zero input production system. No significant differences were observed on average seed weight and harvest index (Table 73).

- Under organic production system, mean yield ranges from 2.3 to 4.7t/ha. NSIC Rc204H and modern released varieties performed well under the low input system. NSIC Rc120, Rc222, Rc214, Rc280 Rc19 and 218 were consistent to perform from WS2014 cropping season. Corocan (pigmented), the newly released NSIC Rc358 and a promising line Raeline 7 also showed a promising performance under this system (Table 74).

Table 73. Mean yield and performance of 30 genotypes under three production systems.

	Days to heading	Plant hgt (cm)	Produc-tive tillers	Panicle length (cm)	Spikelet per panicle	Percent Fertility	Seed weight (g)	Harvest index	Yield (t/ha-1)
DS 2014									
Organic	82b	102b	8b	26.4a	142ab	68b	32	031	3.3ab
Zero input	81c	97b	8b	24.9b	130b	72a	31	0.37	2.6b
Conventional	84a	114a	12a	26.9a	148a	66b	32	0.33	3.9a
Con x gen	ns	*	ns	ns	ns	ns	**	ns	*

Table 74. Top 10 best performer varieties under organic production system.

	WS 2014	YIELD (t/ha)
1	Corocan	4.7
2	Raeline 7	4.1
3	NSIC Rc204H	4.0
4	NSIC Rc222	3.8
5	NSIC Rc358	3.8
6	NSIC Rc120	3.7
7	NSIC Rc280	3.5
8	NSIC Rc214	3.4
9	NSIC Rc19	3.4
10	NSIC Rc218	3.4

The role of GxE in breeding for superior genotypes for low-external input system

AD Palanog, LG Dogeno, CU Seville, IMG Ciocon, and LT Sta. Ines

Organic agriculture is continuously growing worldwide in more than 160 countries with 132 million hectares of organic agriculture land (including transition stage land) which is mostly in Europe (24.0%), followed by Latin America (23.0%), Asia (9.6%), North America (7.1%), and Africa (2.8%) (Willer and Kilcher, 2011). The unsustainable practice and growing concern on the environmental of conventional high-input system are the core reasons for the increasing popularity of organic agriculture. Organic agriculture aims to achieve optimum yield without depleting the environmental resources. In input aspect, conventional agriculture intensively used commercial inputs produced from fossil-fuel based processes compared to organic agriculture which utilizes resources available within the bio-system. However, the variety used in organic agriculture is still largely dependent on the varieties produced in the conventional system which may or may not suitable to the practice.

The response of varieties to conventional rice production system will be more likely differ to their response to organic rice system which apparently due to the difference on level of inputs applied. Genotype x inputs (environment) interaction contributes largely to the variation of responses. Previous study showed significant genotype-by-fertilizer interaction when modern cultivars and advance lines were used. The genotypes with greater yield potential under fertilizer condition do not yield usually do not yield more than other genotypes high under low fertilizer/no fertilizer condition (Wonprasaid et al.,1996; Romyen et al., 1998; Inthapanya et al., 2000). High genotype x input interaction exhibited would mean that cultivars selected under research station will not perform well in low-input farmer's field. Thus, indirect selection of varieties with higher grain yield under conventional system intended for organic system may not be effective.

Study aims to (a) examine the effect of genotype x environment (input) interaction on grain yield and other agronomic traits; (b) identify genotypes generally- and specifically-adapted to low external input systems; and (c) Investigate the need for breeding for genotypes with general or specific adaptability to low-external input systems.

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Highlights:

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- Established field trials in four sites: (a) Inayauan, Cauyan, Negros Occidental, (b) Tabunan, Bago City, (c) Taloc, Bago City and (d) PhilRice Negros. Each site (farmer) chosen for their considerable differences in cultural management and inputs used to determine if genotypes really respond differently under different management. Thirty different rice genotypes were used for the study. Unfortunately, data from Inayauan, Cauayan was not obtained since it was severely damaged by drought and weeds during reproductive stage and heavily infested by rodents during the ripening stage. On the other hand, experiment in Taloc, Bago City failed when the farmer-partner accidentally harvested the experimental plots. Only data from three sites were analyzed.

- Phenotypic traits with importance to low-external input system (organic production) rice production and farmers preferred traits such as grain yield and above ground biomass, among others were measured. Other agronomic traits measured were productive tillers, plant height, 1000-seed weight, number of spikelets per panicle, spikelet fertility, and harvest index. Average grain yield for two sites was 2476t/ha. Combined analysis of variances (ANOVA) for grain yield in two sites: Tabunan, Bago City and PhilRice Negros was done.

- Bartlett's test of homogeneity showed not significant differences in the variance hence, combined analysis can be done. Combined ANOVA for grain yield showed significant difference ($P>0.0045$) for genotype by environment interaction (GXE) for grain yield. Which indicates that environments (which includes the organic practices) have large influence on the yield performance of different genotypes tested.

- Heritability for grain yield is high in both sites (0.77 and 0.61) indicating that direct phenotypic selection for this trait in the field will be most likely effective. However, for total biomass, values are inconsistent in two sites and for other traits heritability values are very low.

Table 75. Heritability of agronomic traits important for organic rice breeding.

TRAITS	HERITABILITY		
	CAUAYAN	TABUNAN	STATION
Grain yield	–	0.77	0.61
Above ground biomass	–	0.62	*
Productive tillers	–	0.34	*
Plant height	–	0.56	0.40
Harvest Index	–	0.64	0.19
1000-seed weight	–	–	–
No. of spikelets/panicles	–	–	–
Spikelet fertility	–	–	–
Total tillers	–	0.84	*

*- too low values

Table 76. Combined analysis of variance of grain yield for three sites.

Source	DF	SS	MS	F Value	Pr (>F)
Environment	1	88428627.9680	88428627.9680	267.43**	0.0000
Genotype	29	27865164.3200	960867.7352	2.91**	0.0000
GxE	29	10331762.9787	666612.5165	2.02**	0.0045
Pooled error	120	39678668.6933	330665.5724		
Total	179	175304223.9600			

*- significant

**-highly significant

2015 WS

- Established experiments in three sites: 1) PhilRice Negros (on-station); 2) Taloc, Bago City (on-farm); and 3) Tabunan, Bago City (on-farm).

- Field experiments have already harvested and crop cut and panicles samples are currently being processed; data gathering is ongoing.

Abbreviations and acronymns

ABA – Abscicic acid
Ac – anther culture
AC – amylose content
AESA – Agro-ecosystems Analysis
AEW – agricultural extension workers
AG – anaerobic germination
AIS – Agricultural Information System
ANOVA – analysis of variance
AON – advance observation nursery
AT – agricultural technologist
AYT – advanced yield trial
BCA – biological control agent
BLB – bacterial leaf blight
BLS – bacterial leaf streak
BPH – brown planthopper
Bo - boron
BR – brown rice
BSWM – Bureau of Soils and Water Management
Ca - Calcium
CARP – Comprehensive Agrarian Reform Program
cav – cavan, usually 50 kg
CBFM – community-based forestry management
CLSU – Central Luzon State University
cm – centimeter
CMS – cystoplasmic male sterile
CP – protein content
CRH – carbonized rice hull
CTRHC – continuous-type rice hull carbonizer
CT – conventional tillage
Cu – copper
DA – Department of Agriculture
DA-RFU – Department of Agriculture-Regional Field Units
DAE – days after emergence
DAS – days after seeding
DAT – days after transplanting
DBMS – database management system
DDTK – disease diagnostic tool kit
DENR – Department of Environment and Natural Resources
DH L– double haploid lines
DRR – drought recovery rate
DS – dry season
DSA - diversity and stress adaptation
DSR – direct seeded rice
DUST – distinctness, uniformity and stability trial
DWSR – direct wet-seeded rice
EGS – early generation screening
EH – early heading
EMBI – effective microorganism-based inoculant
EPI – early panicle initiation
ET – early tillering
FAO – Food and Agriculture Organization
Fe – Iron
FFA – free fatty acid
FFP – farmer's fertilizer practice
FFS – farmers' field school
FGD – focus group discussion
FI – farmer innovator
FSSP – Food Staples Self-sufficiency Plan
g – gram
GAS – golden apple snail
GC – gel consistency
GIS – geographic information system
GHG – greenhouse gas
GLH – green leafhopper
GPS – global positioning system
GQ – grain quality
GUI – graphical user interface
GWS – genomwide selection
GYT – general yield trial
h – hour
ha – hectare
HIP - high inorganic phosphate
HPL – hybrid parental line
I - intermediate
ICIS – International Crop Information System
ICT – information and communication technology
IMO – indigenous microorganism
IF – inorganic fertilizer
INGER - International Network for Genetic Evaluation of Rice
IP – insect pest
IPDTK – insect pest diagnostic tool kit
IPM – Integrated Pest Management
IRRI – International Rice Research Institute
IVC – in vitro culture
IVM – in vitro mutagenesis
IWM – integrated weed management
JICA – Japan International Cooperation Agency
K – potassium
kg – kilogram
KP – knowledge product
KSL – knowledge sharing and learning
LCC – leaf color chart
LDIS – low-cost drip irrigation system
LeD – leaf drying
LeR – leaf rolling
lpa – low phytic acid
LGU – local government unit

LSTD – location specific technology development
m – meter
MAS – marker-assisted selection
MAT – Multi-Adaption Trial
MC – moisture content
MDDST – modified dry direct seeding technique
MET – multi-environment trial
MFE – male fertile environment
MLM – mixed-effects linear model
Mg – magnesium
Mn – Manganese
MDDST – Modified Dry Direct Seeding Technique
MOET – minus one element technique
MR – moderately resistant
MRT – Mobile Rice TeknoKlinik
MSE – male-sterile environment
MT – minimum tillage
mtha^{-1} - metric ton per hectare
MYT – multi-location yield trials
N – nitrogen
NAFC – National Agricultural and Fishery Council
NBS – narrow brown spot
NCT – National Cooperative Testing
NFA – National Food Authority
NGO – non-government organization
NE – natural enemies
NIL – near isogenic line
NM – Nutrient Manager
NOPT – Nutrient Omission Plot Technique
NR – new reagent
NSIC – National Seed Industry Council
NSQCS – National Seed Quality Control Services
OF – organic fertilizer
OFT – on-farm trial
OM – organic matter
ON – observational nursery
OPAg – Office of Provincial Agriculturist
OpAPA – Open Academy for Philippine Agriculture
P – phosphorus
PA – phytic acid
PCR – Polymerase chain reaction
PDW – plant dry weight
PF – participating farmer
PFS – PalayCheck field school
PhilRice – Philippine Rice Research Institute
PhilSCAT – Philippine-Sino Center for Agricultural Technology
PHilMech – Philippine Center for Postharvest Development and Mechanization
PCA – principal component analysis
PI – panicle initiation
PN – pedigree nursery
PRKB – Pinoy Rice Knowledge Bank
PTD – participatory technology development
PYT – preliminary yield trial
QTL – quantitative trait loci
R - resistant
RBB – rice black bug
RCBD – randomized complete block design
RDI – regulated deficit irrigation
RF – rainfed
RP – resource person
RPM – revolution per minute
RQCS – Rice Quality Classification Software
RS4D – Rice Science for Development
RSO – rice sufficiency officer
RFL – Rainfed lowland
RTV – rice tungro virus
RTWG – Rice Technical Working Group
S – sulfur
SACLOB – Sealed Storage Enclosure for Rice Seeds
SALT – Sloping Agricultural Land Technology
SB – sheath blight
SFR – small farm reservoir
SME – small-medium enterprise
SMS – short message service
SN – source nursery
SSNM – site-specific nutrient management
SSR – simple sequence repeat
STK – soil test kit
STR – sequence tandem repeat
SV – seedling vigor
t – ton
TCN – testcross nursery
TCP – technical cooperation project
TGMS – thermo-sensitive genetic male sterile
TN – testcross nursery
TOT – training of trainers
TPR – transplanted rice
TRV – traditional variety
TSS – total soluble solid
UEM – ultra-early maturing
UPLB – University of the Philippines Los Baños
VSU – Visayas State University
WBPH – white-backed planthopper
WEPP – water erosion prediction project
WHC – water holding capacity
WHO – World Health Organization
WS – wet season
WT – weed tolerance
YA – yield advantage
Zn – zinc
ZT – zero tillage

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