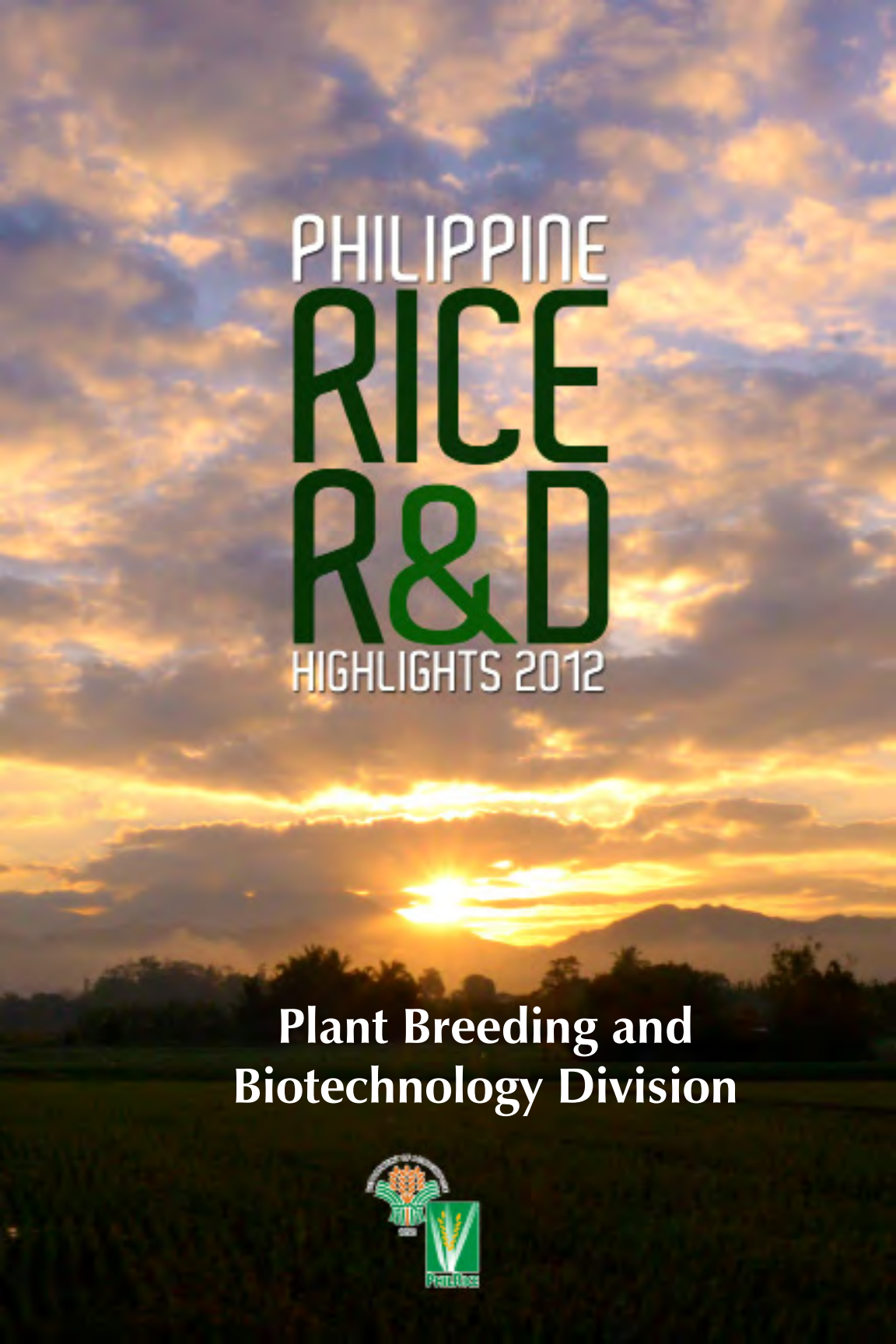

Plant Breeding and Biotechnology Division

TABLE OF CONTENTS

Executive Summary 1

Pre-Breeding and Germplasm Enhancement 1

Induced mutations for rice quality improvement 1

Development of herbicide tolerant and disease resistant rice through induced mutation 8

Breeding for ultra-early maturing rice varieties with high yield 11

Exploring the genetic diversity hidden in wild rice and japonicas to lift the yield barrier 14

Finding durable and novel blast resistance genes effective against Philippines' Magnaporthe grisea pathogen population 19

Elucidating the current physical and milling quality traits in support to breeding 22

Optimization of a rapid screening method against sheath blight (Rhizoctonia solani) in rice and development of sheath blight tolerant breeding lines 28

Plant Breeding and Biotechnology Division

Division Head: Thelma F. Padolina

I. Pre-Breeding and Germplasm Enhancement

Project Leader: Thelma F. Padolina

Genetic enhancement for crop plants has become necessary in recent years to broaden the relatively narrow genetic base of modern crop cultivars selected for higher productivity. Such broadening is needed to supply new kinds of pest resistance, to bring in new levels of productivity and stability of performance, and to provide useful new qualities to food and feed products. With the advent of biotechnology, it will provide essential and innovative support to standard plant breeding to bring in new generic systems, new techniques for selection and identification of genotypes, new ways of making hybrid crops, and, most importantly, deeper understanding of plant gene action, biochemistry, and physiology. In addition to, genetic enhancement and plant breeding in the sense of final cultivar development can be used in two other ways: (1) to develop new crops from heretofore uncultivated species and (2) to change old crops into new crops.

The great challenge for breeders is the search for genetic variability for broadening the gene pool of rice cultivars to develop genetic vulnerability, a direct by-product of successful plant breeding. The resulting new cultivars can display a greater diversity because new gene sources and unrelated breeding materials have been introduced into basic and advanced breeding pools. Non-conventional and innovative techniques are applied for the creation and transfer of variability. Several genes are now being pyramided through molecular marker-aided selection to increase durable resistance. New and better ways of disease diagnostics are also being developed. Studies on the elucidation of the genetic basis of some diseases, yield, and grain quality traits are now underway. The pre-breeding materials developed out of these studies will pave new opportunities for further genetic improvement of our breeding pools.

Induced mutations for rice quality improvement

RC Braceros and LR Pautin

Continuing evaluation of advanced generation mutant lines from

different backgrounds were done in 2012. Different grain quality determination on physical and milling potentials, physico-chemical traits, and some value-adding traits such as low phytic acid screening for all available mutants have been prioritized. Acceptable yield and other morpho-agronomic traits were assured for all the mutant materials. Modern varieties such as PSB Rc10, NSIC Rc152, NSIC Rc150, and MS16 were targeted to reduce chalkiness, improve physico-chemical properties, and improve milling quality. Traditional varieties like Azucena, Dinorado, and Ballatinaw were also chosen for yield improvement while retaining good grain quality. Some advanced mutant lines were also crossed to donor parents possessing resistance/ tolerance to various stresses.

Findings:

- Among the Dinorado mutants (Table 1), Dinorado5kR-38-3-2-3 recorded the highest yield of 5,988kg/ha during the 2012 DS. This is significantly higher by 35% to the parent stock with only 4,461 kg/ha. In 2012 WS, Dinorado5kR-38-3-2-3 also showed high yielding ability with 6,482kg/ha compared to its wild type with only 3,134kg/ha. Percent fertility ranged from 8.0 to 89.2 while the original has only 78.7%. Dinorado5kR-38-3-2-3 remains on the first rank. This line also showed premium milling quality of 70.6%, 40.2% head rice, long and intermediate grain size and shape, 4.2% chalkiness, with low amylose classification, low gelatinization temperature, and soft cooked texture. Higher dose of 20 and 30kR generated extra-long and slender grain types with these two lines: Dinorado 20kR-31-3-1-1 and 30kR-40-2-1. Three entries showed very low amylose and have potential use in confectionary industries. Other traits are shown in Table 3.
- Selected waxy Ballatinaw mutants (Table 2) exhibited higher yields than the low amylose types. Among the waxy types, yield ranged from 6,065 to 7,283kg/ha compared to the low amylose types of only 4,546 to 5,406kg/ha during 2012 DS (not shown). In 2012 WS, these waxy mutants had an average yield ranging from 2,165 to 5,289kg/ha compared to the original type of 2,334kg/ha. Percent fertility ranged from 80.0 to 90.8% while the original had 80.8% only. Majority of these high yielding mutants showed high milling recovery ranging from 66.8 to 70.3%. These lines are being tested for anthocyanin content. Other traits are shown in Table 4.

- Among the 19 Mestizo-converted mutant lines (Table 5), the best in terms of eating quality was PSB Rc72H-20kR-6-19 which already passed the NCT Phase 1 and was elevated to the multi-adaptation trial (MAT) in 2012. This line, ranked third across five sites at NCT Phase 1 and showed highly significant performance than PSB Rc82 in PhilRice-CES, Isabela, BIARC, and CPU. For PSB Rc72H-20kR-6-19 promising mutant, consolidated of the Multi-Adaptation Trials 2012WS is being awaited. Other unique lines with comparable eating quality have extra-long grain shape and earlier maturity. Quality traits of these lines will be explored as Basmati types. Agronomic traits result of these lines during the line development phase is shown in Table 5.Twenty Azucena mutants were selected mostly with reduced maturity from 103 to 117 days as compared to the original with 123 days, better plant types, and higher yielding ability from 4,079 to 8,961kg/ha as compared to 2,300kg/ha of the original Azucena. Further selection is needed to confirm the improved traits.
- Other screening for quality traits were done as follows:
  - ✓ Two hundred seventy four mutants from various irradiated traditional cultivars like Dinorado, Azucena, and Ballatinaw were screened for low phytic acid using the optimized high-inorganic phosphate (HIP) assay; 53 gave positive results and will be subjected to further agronomic and yield screening. Selected ones will become source of good eating quality brown rice with improved mineral bioavailability.
  - ✓ Among the modern varieties, 160 M4 generation derived lines were selected from the mutants of MS16. PSB Rc10 mutants were selected for high yield and disease resistance (BLB and blast). NSIC Rc150 and NSIC Rc152 were selected for intermediate amylose content. Some selected M5 generation of new derived lines were now planted. This will be evaluated in 2013 DS the field performance and grain quality analysis. .

Table 1. Selected Dinorado mutants uniquely different among lines and as compared to the original parent, 2012 DS.

Parent Variety / mutant line	Ave. Yield (kg/ha.) DS	WS	% Brown Rice	% Milled Rice	% Head rice	Grain length, (mm)	Grain Shape (L/W)	% Chalkiness,	Amylose Content	GT type by ASV	Texture
DINORADO -5kR-38-3-2-3	5988	6482	77.2 F	70.6 Pr	40.4 G2	6.7 L	2.6 I	4.2 GI	0.4 L	7 L	Soft
DINORADO -20kR-31-3-1-1	4558	4622	76.3 F	68.1 GI	40.8 G2	7.5 EL	3.2 S	9.5 G2	0.5 L	6 L/I	Soft
DINORADO -30kR-40-1-2-1	4691	4433	75.8 F	69.1 GI	39.8 G2	7.5 EL	3.2 S	5.6 G2	0.5 L	7 L	Soft
DINORADO I-5kR-38-5	4370	3987	76.5 F	70.0 GI	45.5 G2	6.7 L	2.7 I	5.0 GI	0.3 VL	7 L	Soft
DINORADO -20kR-22-2-1-1	4273	3389	75.3 F	69.0 GI	40.9 G2	6.6 L	2.6 I	2.1 GI	0.3 VL	7 L	Soft
DINORADO -30kR-37-2-1-1	5152	2705	77.3 F	71.5 Pr	46.0 G2	6.8 L	2.8 I	33.1 aa	0.1 VL	7 L	Soft
DINORADO ORIG.	4461	3134	76.3 F	68.7 GI	40.1 G2	6.5 M	2.7 I	5.7 G2	0.3 L	5 I	Soft

L-long; EL- extra long; L- low amylose; VL- very low GI- grade 1; G2- grade 2; aa- beyond normal values

Table 2. Selected high yielding waxy Ballatinaw mutants PhilRice CES, 2012 DS.

Patent Variety / mutant line	Ave. Yield (Kg/Ha.) DS	WS	% Brown Rice,	% TMR	% HR	Amylose Content,	GT type by ASV	Cooked texture
BALLATINAW-30kR-1-1-1-1	7283	5085	74.6 P	69.6 GI	38.2 G3	0.4 W	3 HI	Soft
BALLATINAW-30kR-7-2-1-1	6065	2852	74.7 P	68.9 GI	30.8 G3	0.3 W	3 HI	Soft
BALLATINAW-30kR-28-3-1-1	6094	3028	74.7 P	69.9 GI	33.1 G3	0.1 W	3 HI	Soft
BALLATINAW-30kR-14-1-1-1	6551	2423	72.1 P	66.8 GI	34.4 G3	0.1 W	4 I/HI	Soft
BALLATINAW-30kR-8-1-1-1	6297	2165	74.2 P	69.2 GI	35.7 G3	0.4 W	3 HI	Soft
BALLATINAW-35kR-4-2-1-1	6652	4828	74.4 P	69.6 GI	35.0 G3	0.6 W	4 HI/I	Soft
BALLATINAW-25kR-7-4-1-1	6145	3927	75.1 F	70.2 Pr	37.6 G3	0.1 W	3 HI/I	Soft
BALLATINAW-30kR-8-3-1-1	6362	2613	75.4 F	70.3 Pr	38.5 G3	0.0 W	3 HI	Soft
BALLATINAW-35kR-5-5-1-1	6152	3189	74.2 P	69.6 GI	39.0 G2	0.1 W	3 HI/I	Soft
BALLATINAW-35kR-3-3-1-1	6725	5289	75.1 F	70.0 GI	34.7 G3	0.2 W	4 I/HI	Soft
BALLATINAW-30kR-7-1-1-1	6326	3662	74.0 P	68.6 GI	32.1 G3	0.3 W	3 HI	Soft
BALLATINAW-ORIG	5471	2334	75.6 F	70.0 GI	36.4 G3	0.0 W	3 HI/I	Soft

TMR- total milled rice: Pr- premium; GI -grade I; HR- head rice; AC- amylose content; W-waxy

Table 3. Other agronomic traits of selected Dinorado mutants , PhilRice CES, 2012 WS.

Mutant line	PAccp	MAT (DAS)	HT (cm)	TLR (no.)	Grain Fertility (%)	Biotic stress	Remarks
DINORADO SUSI-5kR-38-3-2-3	3	115	103	21	87.6		Uniform, long panicle, heavy grains,
DINORADO SUSI-30kR-37-1-2-1	3	118	109	10	83.7	blb	Uniform, long panicle,, Heavy grains,, w/ awn
DINORADO SUSI-20kR-23-6-1-2	5	106	110	10	82.0	sb	Uniform, long panicle, dense, good
DINORADO SUSI-20kR-11-3-2-1	5	117	113	11	85.2	sb	Uniform, long panicle, dense, heavy
DINORADO SUSI-5kR-38-3-2-1	3	115	111	19	80.2	sb, blb	Uniform, long pan, Long grain, med tall
DINORADO SUSI-20kR-15-10-2-1	5	118	106	10	89.2	bls, blb	NVU, long panicle, w/ awn, heavy grain
DINORADO SUSI-5kR-8-1-1-4	3	115	109	10	85.0	sb	Uniform, long panicle, heavy grn,
DINORADO SUSI-20kR-18-6	3	113	110	18	83.3	sb	Uniform, long panicle, dense,
DINORADO SUSI-30kR-2-4-1-1	3	112	105	13	89.5	blb	Uniform, long panicle, heavy grains, w/ awn
DINORADO SUSI-20kR-22-5-1-1	5	94	111	15	82.3	sb, blb	NVU, long grain
DINORADO ORIG.	5	110	107	17	78.7		Uniform tall

Legend:PAccp-phenotypic evaluation, 3- very good, 5-fair; MAT- maturity in days after sowing;
HT- plant height in cm; TLR- no. of productive tillers:NVU- not very uniform; blb- bacterial leaf blight, bls-bacterial leaf streak; sb- stemborer (whiteheads), small letters mean moderate reaction.

Table 4. Other agronomic traits of selected Ballatinaw mutants, PhilRice CES, 2012 WS.

Mutant line	PA	MAT	HT	TLR	%Fertility	Biotic stress	Remarks
BALLATINAW-35kR-3-3-1-1	3	125	107	18	90.4	sb	NVU, Low panicle, Dark green,
BALLATINAW-30kR-30-4-1-1	5	123	112	13	89.1	blb	Long panicle, Dark green, high dense
BALLATINAW-30kR-1-1-1-1	5	123	110	11	89.2	sb	Short panicle, dense , Dark green, Uniform
BALLATINAW-25kR-24-6-1-1	5	125	109	15	90.5	sb	Low panicle, dense, dark green, Uniform
BALLATINAW-35kR-4-2-1-1	3	126	114	10	83.9	sb	Uniform, good, Low panicle
BALLATINAW-30kR-28-2-2-2	5	125	107	14	89.9	sb	Short panicle, dense , Dark green, Uniform
BALLATINAW-25kR-18-1-1-1	5	127	112	17	86.7	heavy blb, sb	Short panicle, Dark green
BALLATINAW-30kR-19-2-1-1	3	128	103	14	85.1	dense sb	Low panicle, Dark green
BALLATINAW-25kR-7-4-1-1	3	125	112	13	93.1	sb	Uniform, good, Low panicle
BALLATINAW-30kR-30-12-1-1	5	125	109	18	90.8	bls	NVU, Low panicle, Dark green,
BALLATINAW-ORIG	5	127	111	15	80.8	sb	NVU, Dark green, purple margins

Legend:PAccp-phenotypic evaluation, 3- very good, 5-fair; MAT- maturity in days after sowing;
HT- plant height in cm; TLR- no. of productive tillers:NVU- not very uniform; blb- bacterial leaf blight, bls-bacterial leaf streak; sb- stemborer (whiteheads), small letters mean moderate reaction.

Table 5. Mestizo mutants and their agronomic traits, PhilRice CES, 2012.

PARENT VARIETY/ MUTANT LINE	PA	MAT (DAS)	Yield (kg/ha		Ave. Yld (kg/ha)	%Fertility	Biotic stress	REMARKS
			DS	WS				
PSB Rc72H-20kR-6-15 (A)	5	118	4417	3058	3738	68.8		NVU
PSB Rc72H-20kR-6-48 (A)	5	118	5801		5801	59.8		NVU
PSB Rc72H-20kR-6-29 (A)	3	123	8114	6186	7150	64.9		Uniform, late medium tall
PSB Rc72H-20kR-6-29 (A)	3	127	7878	7085	7481	79.7	blb	Uniform scented
PSB Rc72H-20kR-6-29 (A)	3	128	6754	4740	5747	72.5	blb	Uniform, late, scented
PSB Rc72H-20kR-6-29 (A)	3	129	6909	6987	6948	74.0	blb	Uniform, scented
PSB Rc72H-20kR-6-20 (A)	7	119	7961	7971	7966	79.8		NVU
PSB Rc72H-20kR-6-41 (A)	5	129	4882	8355	6618	65.4		
PSB Rc72H-20kR-6-1 (A)	3	124	7448	6868	7158	77.1		Umiform, good
PSB Rc72H-20kR-6-43 (A)	3	126	6759	8422	7591	78.1		NVU
PSB Rc72H-20kR-6-5 (A)	3	127	8208	8489	8349	47.8		NVU
PSB Rc72H-20kR-6-19 (A)	3	129	7182	4378	5780	67.1		Uniform medium early
PSB Rc72H-20kR-6-19 (A)	3	120	8767	6464	7615	81.1	blb	Uniform medium tall
PSB Rc72H-20kR-6-19 (A)	3	117	7365	3842	5604	62.9		Uniform, good
PSB Rc72H-20kR-6-19 (A)	3	127	4362	3479	3920	60.3		Uniform, good, E SNCS
PSB Rc72H-20kR-6-24 (A)	3	129	6857	7014	6936	77.7		NVU, M SNCS
PSB Rc72H-20kR-6-4 (A)	3	123	6759	7930	7345	84.4		Uniform, good, M SNCS
PSB Rc72H-20kR-6-9 (A)	3	119	4966	5859	5413	58.3		NVU, M SNCS , Medium tall
PSB Rc72H-20kR-6-18 (A)	3	129	2597	6352	4474	64.3	BLB	NVU, tall
PSB Rc72H(parent var)	3	120	7993	4942	6468	66.9		Uniform, good

Legend:PAccp-phenotypic evaluation, 3- very good, 5-fair; MAT- maturity in days after sowing; SNCS- senescence rate
HT- plant height in cm; TLR- no. of productive tillers:NVU- not very uniform; BLB(blb)- bacterial leaf blight, bls-bacterial leaf streak; sb- stemborer (whiteheads), Capital letters mean severe infection, small letters moderate reaction.

Table 6. Azucenamutantsand their agronomic traits, PhilRice CES, 2012.

Parent variety/mutant line	PA (1-9)	MAT	Yield kg/ ha	%Fertility	Biotic stress	REMARKS
AZUCENA-30KR-7-6-1		113	8961	88.7		Medium plants, Long grain
AZUCENA-30KR-4-4-5	5	109	8307	89.9		Medium plants, Long grain
AZUCENA-30KR-6-5-2	5	109	6207	80.6		Medium plants, Long grain
AZUCENA-30KR-31-25-1	5	109	6146	82.0	sb	Very tall plants, late Sncs, Segregating plants, Long grain
AZUCENA-30KR-54-10-1	5	117	5974	72.0	sb	Very tall, Long grain
AZUCENA-30KR-7-6-5	5	109	5935	87.3	sb	Medium tall, Medium Sncs
AZUCENA-30KR-10-8-1	5	115	5793	72.4	sb	Medium tall, Medium Sncs
AZUCENA-30KR-30-24-1	5	111	5706	79.4	sb	Very tall plants, late Sncs, Segregating plants, Long grain
AZUCENA-30KR-28-22-1	5	117	5630	82.5	sb	Very tall plants, late Sncs, Segregating plants, Long grain
AZUCENA-30KR-8-7-4	5	103	5477	83.2	sb	Medium tall, Medium Sncs
AZUCENA-30KR-8-7-5	5	109	5464	88.2	sb	Medium tall, Medium Sncs
AZUCENA-30KR-6-5-3	5	109	5334	79.1		Medium plants, Long grain
AZUCENA-30KR-18-14-1	5	106	5332	73.0	sb	Tall plants
AZUCENA-30KR-24-18-1	5	115	5325	82.4	sb	Very tall plants, late Sncs, Segregating plants, Long grain
AZUCENA-30KR-2-2-4	5	106	4914	90.6	blb	Dwarf plants, Very Early maturing,
AZUCENA-30KR-37-28-1	5	111	4876	90.9	sb	Very tall plants, late Sncs, Segregating plants, Long grain

AZUCENA-30KR-65-55-1	5	109	4811	57.6	Sb	Medium Sncs, tall plants, Long grain
AZUCENA-30KR-66-56-1		119	4793	79.2		Late Sncs, tall plants, Long grain
AZUCENA-30KR-29-23-1	5	117	4716	76.7	sb	Very tall plants, late Sncs, Segregating plants, Long grain
AZUCENA-30KR-8-7-2	5	105	4698	80.8	sb	Medium tall, Medium Sncs
AZUCENA-30KR-8-7-3	5	111	4672	88.3	sb	Medium tall, Medium Sncs
AZUCENA-30KR-15-11-1	5	113	4616	86.0	sb	Medium tall, Medium Sncs
AZUCENA-30KR-11-9-1	5	113	4581	67.2	sb	Medium tall, Medium Sncs
AZUCENA-30KR-23-17-1	5	115	4390	83.5	sb	Very tall plants, late Sncs, Segregating plants, Long grain
AZUCENA-30KR-1-1-4	5	106	4113	83.4	blb	Dwarf plants, Very Early maturing, SBGrn
AZUCENA-30KR-2-2-3	5	106	4079	76.8	blb	Dwarf plants, Very Early maturing
Azucena Original	5	123	2300			Very tall plants, late Sncs, Long grain

Ave. Yield (TPR)
Dry Season: 5906 kg/ha.
Wet Season: 5013 kg/ha
Maturity (MAT): 114 DAS
Plant Height (cm):106
Productive Tillers (no. /hill): 14

Field Diseases and insect Pests;
Intermediate reaction- blast, bacterial leaf blight, sheath blight
Moderately resistant to BPH and GLH
Susceptible to RTV and YSB

Grain Quality ;

Milling potential:
Brown rice - 78.8 Fair
Milled rice -70.0.5 Premium
Head rice- 53.6 Grade 1

Physical Attributes:
Chalkiness-0.5 Premium
Grain Length- 7.0 L
Grain Shape- 3.3 S

Physicochemical Properties:
%Crude Protein -7.8
%Amylose content -20.5 intermediate
GT score- 3.0 HI/I

Fig 1 . Yield and other agronomic characters of promising Mestizo mutant [PSB Rc72H- 20kR-6-19 (A)] in the NCT Phase I, 2012.

Development of herbicide tolerant and disease resistant rice through induced mutation

AA Alfonso, RT Miranda, ES Avellanoza, EO Espejo and AML Agustin

Increasing global temperatures and changes in rainfall patterns are two major consequences of climate change. In areas with elevated temperatures and insufficient rainfall, drought is a major concern as it affects crop production. One way to address the water scarcity problem is the adoption of water-saving cultivation practices. Aerobic rice, alternate wetting and drying, and dry seeding are some of the systems being developed to deal with water scarcity for agriculture. However, one major setback in the implementation of these systems is the emergence of weeds that compete with the rice plants for space, nutrients, and sunlight. Controlling weeds by manual weeding can be very tedious and time-consuming.

One viable option is the development of herbicide-tolerant rice. Unfortunately, no natural source of herbicide tolerance has been reported in rice so far. While it is prudent to look for herbicide tolerance in the landraces and traditional varieties, there is no assurance that such trait will ever be found and it would take time to incorporate the trait into modern cultivars. One viable option is to induce mutation in modern cultivars by chemical or physical means in the hope of generating variants that are tolerant to herbicides, but with minimal change in the plant's agronomic traits and overall field performance. Mutation breeding offers a way forward without having prior knowledge on the intricate physiological processes involved in herbicide susceptibility in rice, which is a pre-requisite for transgenic approaches. Furthermore, even if transgenic approaches are possible, it will be subject to rigorous biosafety considerations which may hamper its immediate and full utilization.

The changing temperature and rainfall profiles are also expected to trigger the evolution of new types of pathogens that can overcome current disease resistance genes. Search for new disease resistance genes is traditionally done by combing through hundreds of diverse genotypes (usually landraces and traditional accessions), and screening them for particular diseases. While this has provided much of the disease resistance genes deployed among modern varieties today, the natural variation for disease resistance genes is not infinite. Moreover, the rapid evolution of new pathogen types can overcome resistance genes, especially those that have major/large effect. Relying solely on natural gene variation for disease resistance, therefore, may not be

enough to address the emergence of new pathotypes in the future.

This study aims to develop breeding lines with tolerance to herbicide and resistance to tungro and bacterial blight through induced mutation.

Findings:

- To generate more mutant populations for evaluation, seeds of NSIC Rc192, NSIC Rc272, and NSIC Rc288 were subjected to gamma irradiation and ethylmethylsulfonate (EMS). During 2012 DS, bulk M2 seeds were generated from gamma ray-treated NSIC Rc192 (5kg), NSIC Rc272 (1.7kg), and NSIC Rc288 (1.9kg) using gamma irradiation. During 2012WS, bulk M2 seeds were generated from NSIC Rc192 amounting to 6.5kg (EMS-treated) and 1.10kg (gamma irradiated).
- Mass screening of 4,000 bulk M2 plants from NSIC Rc192 for tungro resistance (modified induced method) during 2012 DS resulted in the identification of 85 putative tungro resistant mutant plants (Figure 2). In wet season, mass screening of M2 plants of NSIC Rc288 and Rc272 and individual screening (forced feed method) of M3 progenies of selected individual resistant plants were evaluated for tungro resistance resulting in the identification of 185 M3 progenies from 19 M2 of NSIC Rc192 (Figure 3) and 225 M2 putative resistant plants from mutant NSIC Rc272 (195 plants) and NSIC Rc288 (30 plants).
- Mass screening of M2 plants coming from a total of 8kg seeds during the dry season and another 5kg bulk M2 seeds during the wet season did not produce any plant resistant to glyphosate.
- For BLB screening during 12 DS, two BLB resistant mutants from NSIC Rc144 were further evaluated using different *Xoo* races. MSL 37 exhibited R to MR reaction to eight races (Races 1, 2, 3, 5, 7, 8, 9, and 10) of BLB and MS reaction to Race 6 and Race 4. MSL 40 was found to have R to MR reaction to all races except Race 6 (Table 7). During 12 WS, MSL 37 and 40 were further evaluated and confirmed to have superior resistance against bacterial blight under field condition (Figure 3). Additionally, a new set of M2 mutants from three rainfed varieties were evaluated against BLB using Race 3 leading to the selection of 10, 19, and three plants with short lesions derived from NSIC Rc192, NSIC Rc272, and NSIC Rc288.

- DNA fingerprinting on MSL 37, MSL 40, and NSIC Rc144 revealed that MSL 37 and MSL 40 are 97.4% similar with each other and both have 94.5 % similarity to NSIC Rc144. This indicates that the two mutant lines were derived from NSIC Rc144.
- Crosses were performed to generate populations for genetic studies including identification of the mutant locus or loci that confers resistance to bacterial blight. Additional crosses were also performed for incorporating BLB resistance from these mutants into elite breeding lines.

Table 7. Reaction of two short-lesion mutant selections (MSL 37 and MSL 40), wild type NSIC Rc144 and R and S controls to different races of *Xoo*.

Test Entries	Race 1	Race 2	Race 3b	Race 3c	Race 4	Race 5	Race 6	Race 7	Race 8	Race 9a	Race 9b	Race 9ac	Race 9d	Race 10
MSL -37	R	R	R	MR	MS	MR	MS	R	R	R	R	R	MR	R
MSL -40	R	R	R	R	MR	MR	MS	MR	R	R	R	MR	MR	R
NSICRc144 (WT)	MS	S	MS	MS	MS	MS	S	MR	MS	MR	MS	MS	S	MR
IR24	S	S	S	S	MS	MS	S	S	MR	S	S	S	S	S
IRBB4	R	MS	MR	S	MR	MR	S	R	MS	MS	S	MS	S	MR
IRBB5	R	R	R	MR	S	R	S	R	R	R	R	MR	R	R
IRBB7	MS	MS	MS	S	MS	MS	S	MR	MS	S	S	S	S	S
IRBB21	MS	R	MR	MS	S	MR	S	MR	MR	MS	MR	MR	MR	MR
IRBB61	R	R	R	R	R	MR	MR	R	MR	R	R	R	R	R
IRBB62	MR	MR	R	MR	MR	MR	S	MR	MR	MS	MR	MR	MS	MS

BLB rating scale: R = 1-5 cm; MR = 5.1-10; MS = 10.1-15; 15 and above

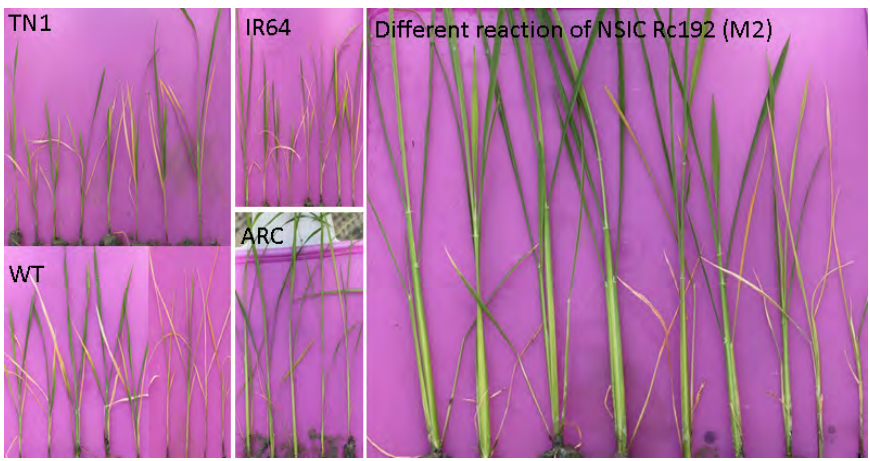

Fig. 2. Reaction of NSIC Rc192-derived M2 plants to Tungro under induced condition. IR64 and TN1- susceptible controls; ARC11554 - resistant control (2012 DS).

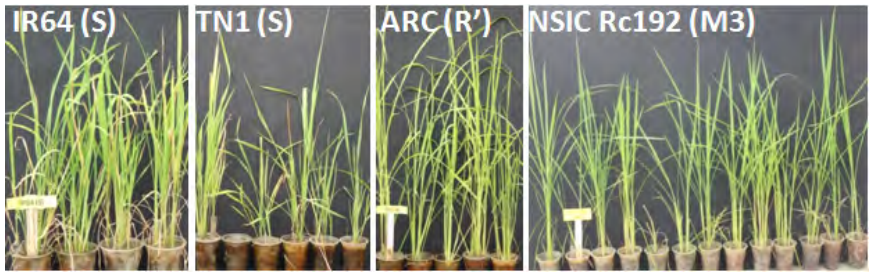

Fig.3. Reaction of selected NSIC Rc192 putatively resistant M3 plants to Rice Tungro Virus under induced condition. IR64 and TN1-susceptible controls; ARC11554 - resistant control (2012 WS).

Fig.4. Field set-up of MSL lines side by side with wild type, NSIC Rc144 and susceptible check, IR24 during 2012 WS.

Breeding for ultra-early maturing rice varieties with high yield
LR Pautin and RC Braceros

The main objective of this study is to develop high yielding varieties that can be harvested in less than 100 days from sowing. Considering the predicted impacts of water availability in the physical rice environment, of climate change on the timing and length of production seasons, and of dwindling lands for cultivation, ultra-early maturing varieties (UEMVs) offer sustainable breakthrough interventions to increase our total productivity for rice.

The practice of a shorter production cycle using UEMVs 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, UEMVs could provide the soil with a longer "rest" period (fallow) for dry matter incorporation. It can also help break the pest cycle.

Findings:

- In 2012 DS, eight advanced lines were elevated to AON for initial yield assessment (Table 8). These lines are crosses with known early maturing varieties such as PSB Rc4 and IR58, which are expected to generate UEM lines. As to reactions to the prevailing diseases, majority of the lines showed field resistance to Blast, BLB, tungro, and bakanae. Only 20 entries were found intermediate to sheath blight.
- In 2012 WS, 581 selected UEMderived lines and 24 UEM new plant types were established in the field for early direction traits.
- A total of 346 lines (F2-F7) were also selected for further evaluation from hybridization work. Nineteen uniform lines in AON were eliminated in 2012 WS. Some of these were the OPM materials that mature early.
- Conduct of characteristic tests was also considered (biotic, grain quality, abiotic stresses).
- A total 294 M3 derived lines from irradiated PSB Rc10 and NSIC Rc134 were selected at 91to 99 days after planting. More lines at radioactive dose of 250 gray or 25kR were selected. In 2012 WS, only 210 selected lines M4 population were established in the field. These M4 derived lines will be grown in pedigree nursery for agro-morphological characterization, screening to seedling vigor, lodging resistance, and reactions to field pests.

Table 8. Selected uniform lines (F6) elevated to AON 2012 (DS)

Pedigree No.	Cross combination	MAT (DAS)	Pacp	Kernel Quality	Grain size/ shape
PR40348-7-1	IR 58 X NSIC Rc 140	98	3	5	medium slender
PR40348-7-2		98	3		
PR40344-3-2	IR 58 X PSB Rc 28	105	3	3	medium slender
PR40344-3-3		105	3		
PR40351-6-3	PSB Rc 4 X PSB Rc 28	100	3		
PR40356-5-1	PSB Rc 4 X NSIC Rc 150	105	3	1	medium grain
PR40389-6-3	NSIC Rc 134 X PSB Rc 28	105	3		
PR40411-7-3	NSIC Rc 150 X PSB Rc 10	105	3		

PAccp-phenotypic acceptability 3- very good; DAS – days after sowing

Fig.5. M2 plants at heading and maturity stage, 2012 DS.

Fig. 6. UEM lines in the F7 generation 2012 WS.

Fig7. UEM lines in the F5 evaluated in the AON, 2012DS.

Exploring the genetic diversity hidden in wild rice and *japonicas* to lift the yield barrier

AT Rigor, MRM Maoirat, DA Tabanao, and MM Rosario

Variation plays a vital role in the success of crop genetic improvement, so plant breeders need to rely on a rich source of genetic variation. The advent of molecular marker technology and the derived quantitative trait loci (QTL) mapping technology have provided strong evidence that despite the inferior phenotype, exotic germplasm is likely to contain QTLs that can increase the yield and quality of elite breeding lines. At PhilRice, improvement of hybrid parent lines relies mainly on crosses within the indica subpopulation. To achieve greater genetic diversity and thus higher genetic variation of germplasm pools currently available at PhilRice, there is a need to infuse more variation from other rice subpopulations like the japonica group as well as rice's wild progenitor, Oryza rufipogon.

The ultimate goal of this study was to enhance diversity of hybrid rice parent lines and eventually increase heterosis in hybrid combinations. Specifically, it aimed to (1) develop *indica* hybrid rice parent lines with *japonica* and wild rice (*Oryzarufipogon*) introgressions; and (2)map QTLs from japonica and wild rices associated with increased yield and heterosis

Findings:

- BC1F1 seeds from crosses between hybrid parental lines (HPLs) and japonicas and wild rice derivatives produced in 2011 WS

were planted and backcrossed to HPLs. Thirty-six (36) lines were generated and 1,213 BC2F1 seeds were produced, which will be planted in 2013 DS in the testcross nursery (TCN) for phenotypic evaluation (Table 9).

- Because of the weedy appearance of the BC2F1 populations, which is a cross between hybrid parental lines and wild rices, further backcrossing was done. Out of the 49 lines, 3,568 BC3F1 seeds were produced. These materials will also be evaluated in the TCN in 2013 DS (Table 10).
- During the 2011DS, BC2F1 population from a cross between Nipponbare and HPL was testcrossed with their corresponding cytoplasmic male sterile (CMS) line. The testcrossed progenies were evaluated in 2011 WS. One line showed a superior quality over the hybrid check Mestiso 1, while two lines with the same parent, IR68897B and Nipponbare, showed different phenotypes. The BC2F2 parent of the three lines were advanced in the 2012 DS and crossed with their corresponding cytoplasmic male sterile (CMS) lines (Table 11). A total of 112 BC2F2 testcrossed progenies were generated and evaluated for yield along with Mestiso 1 in 2012 WS. Of the 112, 16 showed yield superiority over Mestiso 1 with a percent yield advantage ranging from nine to 54 (Table 12). Based on the evaluation, the parent of the selected experimental hybrids will be backcrossed (BC_3) with their corresponding original parents in 2013 DS (Fig 8).
- Leaves were collected from the BC2F2 male parents from the three selected Nipponbare x HPL cross combinations. DNA extraction was done for molecular marker and QTL analysis. So far, the entries were genotyped with 23 SSR markers.

Table 9. List of BC2F1 families and number of F1 seeds produced, PhilRice CES 2011WS.

Line Name	# of F1 seeds produced
97B_AZ-6-2-2	66
97B_AZ-6-2-2	10
97B_AZ-6-3-1	80
97B_MO-1-1-1	22
97B_MO-1-1-2	14
97B_MO-1-1-3	15
97B_MS-1-1-1	8
97B_MS-1-1-2	45
97B_M2-1-1-1	63
97B_M2-1-1-2	8
PR2B_OR57-2-3-1	8
PR2B_OR57-2-3-2	87
PR2B_OR57-2-3-3	14
PR2B_OR57-2-3-4	23
PR2B_OR57-2-3-5	34
PR2B_OR57-2-4-1	9
PR2B_OR57-2-5-1	62
PR3B_IR87220-4-1-1	46
PR3B_IR87220-4-1-2	13
PR3B_IR87220-4-1-3	47
PR3B_IR87220-4-1-4	39
PR3B_OR57-2-1-1	77
PR3B_OR57-2-1-2	20
PR3B_OR57-2-3-1	35
PR3B_OR57-2-3-2	27
PR3B_OR57-2-3-3	46
PR3B_OR57-2-3-4	41
PR3B_OR57-2-3-5	13
PR3B_OR57-4-2-1	13
PR3B_OR57-4-2-2	27
PR3B_OR57-6-1-1	41
PR3B_OR57-6-1-2	26
19R_IFG95-1-2-1	55
19R_IFG95-1-2-2	40
19R_IFG95-1-4-2	39

Table 10. List of BC3F1 families and number of F1 seeds produced, PhilRice CES 2011WS.

Line Name	# of F1 seeds produced	Remarks
25BB_OR77-7-3-3-1	6	BC3F1 seeds will be characterized and evaluated for yield in 2013DS
25BB_OR77-7-3-4-1	127	
25BB_OR77-7-4-1-1	83	
25BB_OR77-7-4-3-1	66	
25BB_OR77-7-4-3-2	109	
25BB_OR77-7-4-3-3	87	
25BB2_OR77-7-1-1-1	23	
25BB2_OR77-7-1-1-2	94	
25BB2_OR77-7-1-2-1	127	
25BB2_OR77-7-1-2-2	63	
25BB2_OR77-7-1-3-1	55	
25BB2_OR77-7-1-3-2	103	
25BB2_OR77-7-1-3-3	23	
25BB2_OR77-7-2-1-1	81	
86RB2_OR24-B-1-1-1	24	
86RB2_OR24-B-1-1-2	170	
86RB2_OR24-B-1-1-3	18	
86RB2_OR24-B-1-1-4	113	
86RB2_OR24-B-1-1-5	31	
86RB2_OR24-B-2-2-1	25	
86RB2_OR24-B-2-3-1	123	
86RB2_OR24-B-2-3-2	209	
86RB2_OR24-B-2-3-3	107	
86RB2_OR24-B-3-1-1	19	
86RB2_OR24-B-3-2-1	12	
86RB2_OR24-B-4-2-1	158	
86RB2_OR24-B-4-2-2	70	
86RB2_OR24-B-4-2-3	158	
86RB2_OR24-B-4-2-4	67	
86RB2_OR24-B-4-2-5	14	
86RB2_OR57-10-1-1-1	98	
86RB2_OR57-10-1-1-2	50	
86RB2_OR77-1-2-1-1	144	
86RB2_OR77-1-2-1-2	137	
86RB2_OR77-1-2-1-3	83	
86RB2_OR77-1-2-1-4	38	
86RB2_OR77-B-1-1-1	256	
86RB2_OR77-B-1-1-2	53	
86RB2_OR77-B-1-1-3	46	
86RB2_OR77-B-1-1-4	115	
86RB2_OR77-B-1-1-5	47	
25BB2_OR77-5-2-1-1	136	

Table 11. Number of F1 seeds produced per BC2F2xA-line cross combination, PhilRice CES 2012DS.

Cross combination	# of plants crossed	# of F1 seeds produced	Remarks
Nipponbare x IR34686R	71	5837	57 progenies evaluated for yield in 2012WS
Nipponbare x IR68897B-1	67	2482	24 progenies evaluated for yield in 2012WS
Nipponbare x IR68897B-2	37	1751	31 progenies evaluated for yield in 2012WS

Table 12. Field performance of BC2F2 testcross progenies (PhilRice CES, 2012WS)

Field code	Cross		1000 grain wt (g)	yield (g)*	%Yield Advantage	Panicle Length (cm)	Unfilled Grains	Filled Grains	Plant Ht (cm)	# of Panicle
TCN 1798	IR68897A	97-1-46	35	169	34	27	-	-	101	16
TCN 1807	IR68897A	97-1-75	33	131	4	27	55	101	115	16
TCN 1812	IR68897A	97-1-86	34	160	27	28	43	122	112	14
TCN 1821	IR68897A	97-2-6	33	190	51	27	34	141	91	17
TCN 1823	IR68897A	97-2-12	31	195	54	30	38	197	111	17
TCN 1829	IR68897A	97-2-24	32	187	48	28	89	127	110	19
TCN 1831	IR68897A	97-2-33	34	172	37	27	54	97	111	18
TCN 1833	IR68897A	97-2-38	35	156	23	29	24	147	110	14
TCN 1834	IR68897A	97-2-39	36	131	4	28	8	142	86	26
TCN 1835	IR68897A	97-2-40	34	142	13	31	96	130	88	21
TCN 1840	IR68897A	97-2-49	40	129	2	28	44	117	112	19
TCN 1841	IR68897A	97-2-50	38	136	8	29	56	113	103	13
TCN 1842	IR68897A	97-2-66	34	177	40	29	28	157	112	20
TCN 1873	IR34686R	86-1-65	34	141	12	31	72	167	110	19
TCN 1891	IR34686R	86-1-91	34	150	19	28	58	119	95	21
TCN 1895	IR34686R	86-1-95		137	9	28	64	124	102	24
Mestiso 1			**31**	**126**	0.00	**26**	**41**	**131**	**110**	**18**

**Based from 5 hills*

Fig. 8. Selected BC2F2 progenies for backcrossing.

Finding durable and novel blast resistance genes effective against Philippines' *Magnaporthe grisea* pathogen population

LM Perez, MER Fabreag, JT Niones, HM Pastor, GB Amar, TE Mananghaya, and VG Dalusong

The pathotypic race diversity of population structure of the fungus *Magnaporthegrisea* and the capability of pathogen to produce new ones could be among the main reasons why rice blast disease is difficult to control. Unfortunately, there is limited information on the characteristics of its population. When gained, this could give direction as to identify the genes and their possible deployment.

The study's goal was 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 were identified. Furthermore, this study also aimed to discover novel and durable resistance genes from traditional and released varieties.

Findings:

- Seventy two blast-infected samples from the provinces of Tarlac, Pangasinan, Benguet and Nueva Ecija were processed. A total of 25 monoconidial isolates were obtained.

- Another round of blast disease resistance evaluation of promising varieties such as Malay 2, Moroberekan, Buluhan, Inarimata, IDSA 6, Azucena M5 R-1, NSIC Rc122, Azucena, Pinas, PSB Rc18, Galaygay, and Kuhoy was set at Benguet State University.

- Assessment of 32 monogenic lines containing 25 blast resistance genes at NCT disease screening sites such as Cagayan Valley Integrated Agricultural Research Center (CVIARC), San Felipe, Ilagan, Isabela; Bicol Integrated Agricultural Research Center (BIARC), Pili, Camarines Sur; Visayas State University, Baybay, Leyte; University of the Philippines Los Baños, Laguna; PhiRice Isabela; PhilRice Midsayap; and PhilRice CES was accomplished. Variation of results across sites was observed (Table 13)

- We requested DOST-PAG-ASA located in BSU, Balili, La Trinidad, Benguet to have a meteorological data of 2011 and January to September 2012. Based on the data presented, Benguet recorded 13.1 to 24.5 degrees air temperature and a relative humidity of 81 to 91% from January to September 2012. This information will help in identifying the time to establish test materials for blast screening evaluation to coincide to the optimum condition for blast disease development.

- On-farm screening for blast resistance in Brgy. Quezon, San Carlos City was conducted. Differential varieties for blast and 25 modern varieties from different ecosystems together with resistant and susceptible checks were established for blast disease screening evaluation and seed multiplication. Agronomic parameters and percentage of blast infection, bacterial leaf blight, and tungro incidence were also collected.

- A total of 78 test entries consisting of monogenic lines, CO 39 NILs (near isogenic lines) and advanced breeding materials of blast were introduced to seven NCT sites for blast screening evaluation for 2013 DS.

- Rice varieties US2, Malay 2, and LTH were genotyped using 94 SSR markers to compare the background of Malay 2 to US2 and LTH. Analysis showed that Malay 2 has a similarity coefficient of 0.54 to US2 and 0.30 to LTH (Table 14). Cluster analysis exhibited that Malay2 and US2 clustered together (Figure 9). This infers that the genotype of Malay 2 is closer to US2 than LTH.

Table 13. Disease reaction of monogenic lines at different NCT disease screening site in 2012 WS.

Entries	NCT DISEASE SCREENING SITE						
	PhilRice CES	PhilRice Midsayap	PhilRice Isabela	CVIARC	BIARC	UPLB	VSU
IRBLa-A	S*	S	R	I	S	S	S
IRBLa-C	S	-	R	R	S	S	S
IRBLi-F5	S	S	R	R	S	S	S
IRBLks-F5	S	-	R	R	S	S	S
IRBLks-S	S	S	R	R	S	S	S
IRBLk-Ka	S	R	R	I	S	S	S
IRBLkp-K60	S	I	I	R	R	S	S
IRBLkh-K3	S	R	-	R	I	R	S
IRBLz-Fu	S	R	I	R	I	R	S
IRBLz5-CA	S	I	R	R	S	R	S
IRBLzt-T	S	S	I	R	S	S	S
IRBLta-K1	S	S	I	R	S	S	S
IRBLta-CT2	S	R	I	R	S	S	S
IRBLb-B	S	S	I	R	S	S	S
IRBLt-K59	S	S	I	R	S	S	S
IRBLsh-S	S	S	R	R	S	S	S
IRBLsh-B	S	S	R	R	S	S	S
IRBL1-CL	S	R	R	R	S	S	S
IRBL3-CP4	S	S	R	R	S	S	S
IRBL5-M	S	S	-	I	S	S	S
IRBL7-M	S	I	I	I	I	S	S
IRBL9-W	S	-	-	R	I	S	S
IRBL12-M	S	R	I	R	S	S	S
IRBL19-A	S	-	I	R	S	S	S
IRBLkm-Ts	S	-	I	R	R	S	S
IRBL20-IR24	S	-	R	R	S	S	S
IRBLta2-Pi	S	-	R	R	S	S	S
IRBLta2-Re	S	-	R	R	S	S	S
IRBLta-CP1	S	-	R	R	S	S	S
IRBL11-Zh	S	-	I	R	S	S	S
IRBLz5-CA-2	S	-	I	I	I	S	S
LTH	S	-	S	R	I	S	S
IR50	S	-	S	-	-	-	-

* S- susceptible, I- intermediate, Resistant, -- no data

Table 14. Similarity coefficient of US2, Malay 2 and LTH.

	US2	MALAY2	LTH
US2	1.000000		
MALAY2	0.543011	1.000000	
LTH	0.311828	0.295699	1.000000

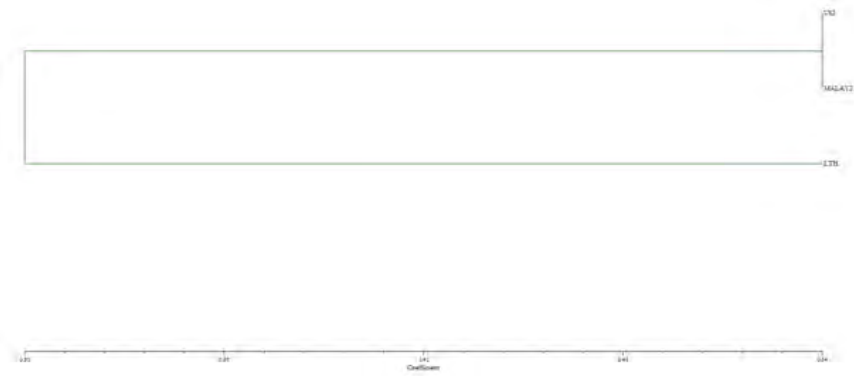

Fig. 9. Similarity tree of US2, Malay 2 and LTH generated in NTSYSpc version2.1.

Elucidating the current physical and milling quality traits in support to breeding

EH Bandonill

Physical attributes of milled rice determines its market price. High amount of broken grains decreases the value of milled rice. Chalkiness, grain cracking due to water absorption, and moisture content of harvested paddy are the known factors which affect head rice recovery. Increasing head rice recovery will increase the value of milled rice and availability of quality table rice. Thus, development of screening methods for crack resistance and grain hardness is essential. Moreover, consumers prefer rice that is transparent and not chalky. Therefore, various environmental factors (i.e temperature, soil and field water pH, elevation) affecting chalkiness of rice have to be documented. Meanwhile, The Philippine Center for Postharvest Development and Mechanization (PhilMech) developed the PhilMech Grain Quality Analysis Software (PGQAS) which aimed to speed up the process of determining the quality of procured milled rice by the National Food Authority (NFA). Its consistency in predicting known

chalky samples has to be assessed and its capability in classifying crack/fissured milled grain samples must be evaluated. This study aimed to develop low-cost and efficient methods for screening crack resistance and grain hardness, and for determining crack and chalkiness of rice, as well as to generate information on factors affecting rice quality. The information from the study will facilitate and fast-track grain quality screening with improved accuracy and delivery.

Development of screening methods for crack resistance and grain hardness

BO Juliano, APP Tuaño, DN Monteroso, AR Agarin, AD Peñaloza, and MG Lansin
Collaborators: TF Padolina, LM Perez, and R Tabien

Findings:

- Rough rice soaking method was improved, validated, and established in the laboratory for the screening of crack resistance and stable head rice yield. Twelve to 14 samples can be screened per day considering an overnight simultaneous air-drying of a batch of samples. SATAKE dehuller and KETT pearlest mill are the equipment needed for the tests in addition to the balance and beakers.
- The brown rice exposure (humidity chamber) method was also employed as primary screening methods for crack resistance. Reducing exposure time that will be enough to effect differentiation between crack susceptible and resistant cultivars shall be continually explored.
- To apply the developed methods to locally released varieties, rough rice soaking method was used in screening 48 and 37 samples of newer released varieties (NSIC Rc110 and above) from WS and DS, respectively , as well as 66 collected traditional rice cultivars from NVP 002-006 study. Twenty two cultivars were identified to have stable head rice yield when compared under stressed and unstressed conditions. These shall be subjected to further analysis using brown rice exposure and Instron-based grain hardness methods.

Evaluation of rice milling potential and chalkiness as influenced by various environmental factors

EH Bandonill, TF Padolina, GG Corpuz, OC Soco, and PA Tibayan
Collaborators: MJ Du, WC Malayao (Bohol), and H Cascolan (PSU)

Findings:

- Data on elevation, soil texture, pH, temperature, and humidity of the sites were gathered. Elevation of Nueva Ecija was 48m above sea level (ASL), 42 m in Pangasinan, and 10m in Bohol. Soil texture in Nueva Ecija and Pangasinan was clay loam while sandy clay in Bohol. DUST-Maligaya, Nueva Ecija had soil pH range of 5-6, PSU-Pangasinan had 6.3, and Bohol had 4.7-5.5. No sample was obtained from direct-seeded method and from MAT-Bohol in 2011 WS. Two typhoons that hit Nueva Ecija affected the grain quality of the samples. Also, no setup was established in 2012 DS.
- Temperature (T) and relative humidity (RH) in Maligaya, Nueva Ecija were higher than Bohol (Figure 10). Likewise, during ripening of rice grains in Nueva Ecija, T and RH were higher in the WS (September and October) than DS (February and March).
- Milling recovery and chalkiness determination of samples revealed that among the 12 MAT-Transplanted (TP) entries, majority of the PSU-Pangasinan samples had higher milled rice (65.9-72.3%) and head rice (19.2-64.5%) recoveries compared to DUST-Maligaya (65.6-71.8% and 20.4-57.0%, respectively). Samples from DUST had higher percent chalky grains (5.8-19.6%) compared to samples from PSU (3.0-14.5%) which may have caused the lower milling and head rice recovery. Chalkiness of samples negatively correlated with milling and head rice recovery (Figure 11).

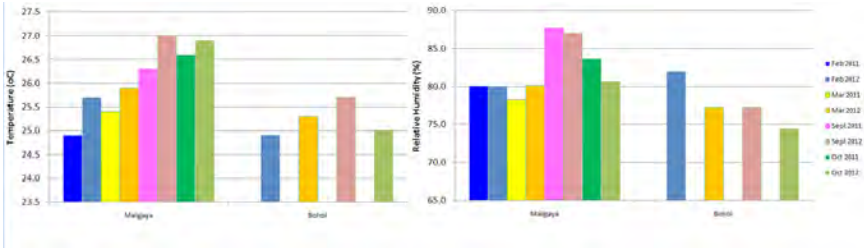

Fig. 10. Temperature and relative humidity during ripening of grains in Maligaya and Bohol.

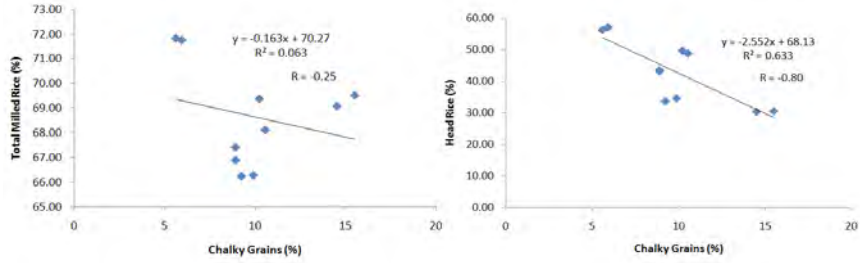

Fig. 11. Correlation between chalky grains and milling recovery and head rice of check rice varieties in 2011 wet season.

Enhancing PGQA software for predicting chalkiness in milled rice and crack in kernels

IG Pacada, EH Bandonill, MC Bulaong, A Tuates, OC Agustin, TF Padolina, APP Tuano, and BO Juliano

Findings:

- Stability and consistency evaluation of PhilMech's PGQA modified software was carried out using various degrees/levels of chalkiness (0 to 100%). Using dump samples: chalky + immature combine algorithm, scatter plot summary (Figure 12), using linear regression analysis of actual and PGQAS value showed no significant difference in 0, 20, and 30% level of chalky grains ($p = 0.0$ to 0.946), while the other degree of chalkiness showed significant difference ($p = \leq 0.001$ to 0.007) . Using paired t-test (Table 15), similar results were obtained except for 30% chalky grain which had a P value of 0.046 (NS).

- Results of consistency analysis (Figure 12), implied that the algorithm of the PGQA software was insufficient in predicting various degree of chalkiness particularly in the commonly used range of <2.0% to 15% classification. Thus, development of software intended for rice breeding must be explored.
- Table 16 showed the other features of PGQAS. This signifies the potential of PGQAS as effective tool for predicting chalkiness specifically in speeding up the classification process with less time and manpower, thus, revolutionizing the traditional chalkiness evaluation in more economical way.
- Assessment for crack/fissuring rice was not yet established due to unavailability of training samples.

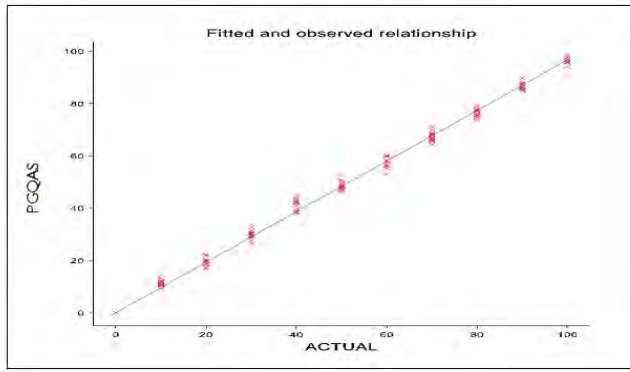

Fig. 12. Summary of relationship of actual value and PGQA predicted value for 11 levels/degree of chalkiness.

Table 15. P value of two statistical analyses for various degree of chalkiness.

% Chalky	Linear regression analysis	Paired t-test
100	< 0.001***	< 0.001***
90	< 0.001***	< 0.001***
80	< 0.001***	< 0.001***
70	< 0.001***	< 0.001***
60	< 0.001***	< 0.001***
50	0.005***	0.005***
40	0.007***	0.007***
30	0.946ns	0.046**
20	0.186 ns	0.186 ns
10	0.001**	0.001**
0	-	* ns

Threshold P values used: >0.05, Not significant (ns); 0.01 to 0.05, Significant (*); 0.001 to 0.01, Very significant (**); <0.001, Extremely significant (***)

Threshold P values used: >0.05, Not significant (ns); 0.01 to 0.05, Significant (*); 0.001 to 0.01, Very significant (**); <0.001, Extremely significant (***)

Table 16. Comparison of visual and PGQAS in evaluating chalkiness in rice.

Parameters	Visual	PGQAS
Maximum no. of samples that can be evaluated in a day	HT, 5 - 10 T, 5 - 7	40
Total hours of evaluation (hour:min)	HT, 4:43 – 5:38 T, 4:43 – 6:22	6:04
Manpower needed to accomplish 40 samples/day	HT, 4- 8 T, 5.5 - 8	2
Requirements to perform the work	Experienced and trained individual	Basic knowledge in windows

Note: HT-highly trained, T-trained classifier

Optimization of a rapid screening method against sheath blight (Rhizoctonia solani) in rice and development of sheath blight tolerant breeding lines

AA Alfonso, RT Miranda, and ES Avellanoza

Traditionally, screening of rice breeding materials for resistance to sheath blight is done under field or screenhouse condition using an "open" system. In these methods, densely planted field plots are inoculated with *Rhizoctoniasolani,* the pathogen is allowed to grow and the entries are rated based on the severity of disease symptoms. Such process entails longer screening time, requires a lot of seeds, and is costly and labor intensive.

A new method of screening the fungal disease was originally conducted in Bangladesh. Called 'micro-chamber' method, it uses soda bottles to effectively trap moisture during incubation period and creates a humid 'micro-environment' for the seedling that favors growth of the pathogen. It requires less seeds, less labor, less screening costs, and shorter plant-growth time needed to come up with a result. It is also conducted under controlled screen house conditions, thus, freeing researchers to the restriction on the timing of planting in the field every season.

Validation and improvement/development of the 'micro-chamber' method of screening against sheath blight under Philippine screen house condition will make it easier for the breeders to fast-track the development of elite lines with resistance/tolerance to the fungal disease. This new method will allow screening for early generation breeding materials with few seeds.

Moreover, an existing method to rapidly screen materials against sheath blight will certainly speed up breeding efforts for the development of lines resistant to the disease. The identification of potential donors for the disease can be achieved in a shorter period of time as well as screening of breeding materials during hybridization.

Findings:

- In the DS, four populations consisting of 886 individual F2 plants from the crosses 10WS-HF3-1 x #9IRGC100898; HF6 x XZ-Xian; MXB 56-2 x IRGC105979, and Rc160 x O.barthii were screened against sheath blight using microchamber method (Figure 13). Based on visual scoring, a total of 213 resistant plants (Table 17) were selected and advanced to F3.

- For second batch, we screened 28 individual plants from two advance lines from the cross MueyNaw Ng x NSIC Rc138 background. Of the 28 plants screened, there were 13 resistant and 10 intermediate plants selected. Other test plants were rated susceptible.
- Using four previously identified sheath blight resistant donors (IRGC77140, IRGC78727, O. nivara/O. sativa, and IRGC 82111) and two high yielding released varieties (NSIC Rc160 and NSIC Rc222), four new F1 populations were generated. Backcrosse of NSIC Rc160 to O. barthii was seed increased for BC1F2 generation.
- For the induced field screening, a total of 247 entries were screened including five IRRI advance lines, four reported sheath blight resistant and six backcross populations (NSIC Rc138 and MueyNaw Ng background) from which 17 resistant and 776 intermediate plants (Table 18) were selected and seed increased. Other entries were rated susceptible.

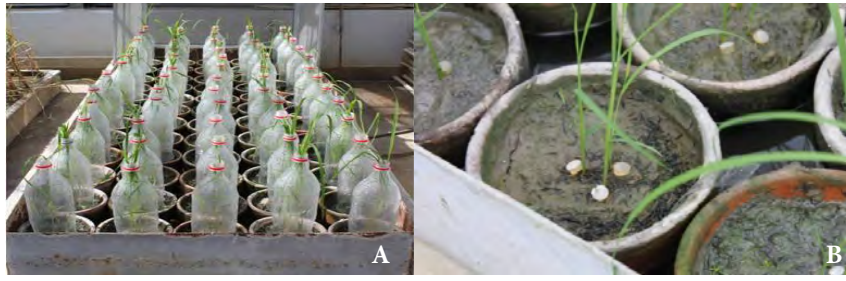

Fig. 14. asdfasdfasdfasdfsdaf

Table 17. Evaluation of F2 population with sheath blight resistance using micro-chamber method.

Cross combination	No. of F2 plants	No. of R plants
10WS-HF3-1 x #9IRGC100898	159	72
HF6 x XZ-Xian	369	65
MXB 56-2 x IRGC105979	94	21
Rc160 x O.barthii	264	55

Table 18. Field evaluation of different advance generation lines for sheath blight resistance

Designation	No of Entries	No of Selected plants	
		Resistant	Intermediate
NSIC Rc138//MueyNaw Ng	222	17	723
Adv. Lines from IRRI	5	0	19
ShB Resistant Cultivar (IRRI)	4	0	34

- In WS, 9 intermediate sister lines wereIdentified from NSIC Rc138 and MueyNaw Ng(ratings from CPD group) and 212 individual plants with intermediate ratings from 55 entries.

Fig. 14. 2012 WS Sheath blight field screening; A) field inoculation; B) Indi-

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

List of Tables

Table 1. Selected Dinorado mutants uniquely different among lines and as compared to the original parent, 2012 DS. 4

Table 2. Selected high yielding waxy Ballatinaw mutants PhilRice CES, 2012 DS. 4

Table 3. Other agronomic traits of selected Dinorado mutants, PhilRice CES, 2012 WS 5

Table 4. Other agronomic traits of selected Ballatinaw mutants, PhilRice CES, 2012 WS. 5

Table 5. Mestizo mutants and their agronomic traits, PhilRice CES, 2012. 6

Table 6. Azucenamutantsand their agronomic traits, PhilRice CES, 2012 6

Table 7. Reaction of two short-lesion mutant selections (MSL 37 and MSL 40), wild type NSIC Rc144 and R and S controls to different races of Xoo. 10

Table 8. Selected uniform lines (F6) elevated to AON 2012 (DS) 13

Table 9. List of BC2F1 families and number of F1 seeds produced, PhilRice CES 2011WS. 16

Table 10. List of BC3F1 families and number of F1 seeds produced, PhilRice CES 2011WS. 17

Table 11. Number of F1 seeds produced per BC2F2xA-line cross combination, PhilRice CES 2012DS. 18

Table 12. Field performance of BC2F2 testcross progenies (PhilRice CES, 2012WS) 18

Table 13. Disease reaction of monogenic lines at different NCT disease screening site in 2012 WS. 21

Table 14. Similarity coefficient of US2, Malay 2 and LTH. 22

Table 15. P value of two statistical analyses for various degree of chalkiness. 27

Table 16. Comparison of visual and PGQAS in evaluating chalkiness in rice. 27

Table 17. Evaluation of F2 population with sheath blight resistance using micro-chamber method. 29

Table 18. Field evaluation of different advance generation lines for sheath blight resistance 30

List of Figures

Fig. 1 . Yield and other agronomic characters of promising Mestizo mutant [PSB Rc72H- 20kR-6-19 (A)] in the NCT Phase I, 2012. 7

Fig. 2. Reaction of NSIC Rc192-derived M2 plants to Tungro under induced condition. IR64 and TN1- susceptible controls; ARC11554 - resistant control (2012 DS). 10

Fig. 3. Reaction of selected NSIC Rc192 putatively resistant M3 plants to Rice Tungro Virus under induced condition. IR64 and TN1- susceptible controls; ARC11554 - resistant control (2012 WS). 11

Fig.4. Field set-up of MSL lines side by side with wild type, NSIC Rc144 and susceptible check, IR24 during 2012 WS. 11

Fig. 5. M2 plants at heading and maturity stage, 2012 DS. 13

Fig. 6. UEM lines in the F7 generation 2012 WS. 13

Fig. 7. UEM lines in the F5 evaluated in the AON, 2012DS. 14

Fig. 8. Selected BC2F2 progenies for backcrossing. 19

Fig. 9. Similarity tree of US2, Malay 2 and LTH generated in NTSYSpc version2.1. 22

Fig. 10. Temperature and relative humidity during ripening of grains in Maligaya and Bohol. 25

Fig. 11. Correlation between chalky grains and milling recovery and head rice of check rice varieties in 2011 wet season. 25

Fig. 12. Summary of relationship of actual value and PGQA predicted value for 11 levels/degree of chalkiness. 26

Fig. 13. asdfasdfasdfasdfsadfasdf 29

Fig. 14. 2012 WS Sheath blight field screening; A) field inoculation; B) Individual plant evaluation of ShB infection conducted by GTL; C) Reading of ShB infection by CPD grp and D) Tillers with infection and without infection 30

Department of Agriculture

PhilRice

PHILIPPINE RICE RESEARCH INSTITUTE

We are a chartered government corporate entity under the Department of Agriculture. We were created through Executive Order 1061 on 5 November 1985 (as amended) to help develop high-yielding, cost-reducing, and environment-friendly technologies so farmers can produce enough rice for all Filipinos.

We accomplish this mission through research and development work in our central and seven branch stations, coordinating with a network that comprises 58 agencies and 70 seed centers strategically located nationwide. To help farmers achieve holistic development, we will pursue the following goals in 2010-2020: attaining and sustaining rice self-sufficiency; reducing poverty and malnutrition; and achieving competitiveness through agricultural science and technology.

We have the following certifications: ISO 9001:2008 (Quality Management), ISO 14001:2004 (Environmental Management), and OHSAS 18001:2007 (Occupational Health and Safety Assessment Series).

Central Experiment Station
Maligaya, Science City of Muñoz, 3119 Nueva Ecija
Trunklines: (044) 456-0277, -0285 • Telefax: (044) 456-0141
Email: pri@email.philrice.gov.ph

PhilRice Agusan
Basilisa, RTRomualdez, 8611 Agusan del Norte
Tel/Fax: 343-0768; 343-0778
Email: agusan@email.philrice.gov.ph

PhilRice Batac
MMSU Campus, Batac City, 2906 Ilocos Norte
Tel/Fax: (77) 792-4702; 670-1867
Email: batac@email.philrice.gov.ph

PhilRice Bicol
Batang, Ligao City, 4504 Albay
Cell: 0908-884-0724

PhilRice Isabela
San Mateo, 3318 Isabela
Tel: (78) 664-2954 • Fax 664-2953
Email: san_mateo@email.philrice.gov.ph

PhilRice Los Baños
UPLB Campus, Los Baños, 4030 Laguna
Tel: (49) 536-1917
Email: los_banos@email.philrice.gov.ph

PhilRice Midsayap
Bual Norte, Midsayap, 9410 North Cotabato
Tel: (64) 229-8178 • Fax 229-7242
Email: midsayap@email.philrice.gov.ph

PhilRice Negros
Cansilayan, Murcia, 6129 Negros Occidental
Cell: 0928-506-0515
Email: negros@email.philrice.gov.ph

PhilRice Field Office
CMU Campus, Maramag, 8714 Bukidnon
Tel/Fax: (88) 222-5744

PhilRice Liaison Office
3rd Flr, ATI Bldg., Elliptical Road,
Diliman, Quezon City
Tel/Fax: (02) 920-5129
Cell: 0920-906-9052

PhilRice Farmers' Text Center
0920-911-1398

PinoyRice Knowledge Bank
www.pinoyrkb.com

PhilRice Website
www.philrice.gov.ph