

2018

NATIONAL RICE R&D HIGHLIGHTS



PLANT BREEDING & BIOTECHNOLOGY

DIVISION



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PLANT BREEDING & BIOTECHNOLOGY

Division head: Oliver E. Manangkil

EXECUTIVE SUMMARY

The demand in rice is continuously increasing as human population also increased amidst declining production area; hence, it is vital to improve the traits of existing varieties. Essentially, breeding is necessary tool to achieve desired traits such as high grain yield, resistance to abiotic and biotic stresses, and grain qualities acceptable to consumers. Environment and the expression of these traits in the environments are the main differences.

Plant Breeding and Biotechnology Division conducts, monitors, and evaluates 12 national researches, which some were published in scientific papers.

Three varieties bred by the division was released in 2018 while 10 breeding lines was applied for Plant Variety Protection (PVP) to Bureau of Plant Industry (BPI). Method for reference collection digital database and germplasm query software was applied for registration of utility model to Intellectual Property Office of the Philippines (IPOPHL).

The division contributed in increased productivity, cost-effectiveness, and profitability of rice farming in a sustainable manner.

PRE-BREEDING AND GERMPLASM ENHANCEMENT

EV Santiago

Exploration of new and diverse sources of variation is important for the genetic enhancement of crops including rice. Pre-breeding expands genetic diversity, which becomes the foundation for sustainable development of new varieties. This project identified/developed pre-breeding materials necessary to accelerate rice varietal improvement. The studies focused on supporting the current breeding activities for the different favorable and adverse ecosystems. The studies included providing donor germplasm with essential morpho-agronomic traits such as yield, maturity, physiological traits, single or pyramided lines with genes or QTLs for resistance or tolerance to stresses, new parental of hybrids, high quality table rice, and new specialty trait rices with health value.

Induced mutations for quality improvement in rice

LR Pautin, G Avellanoza

Gamma ray irradiation was utilized to induce mutations for quality improvement. Selection of mutants from traditional varieties were initially selected for improved yield and good agronomic traits. Screening was expanded to select for unique and value-added traits.

Among the Azucena mutants, 6 lines have low phytic acid phenotype greater than 2.5 ug Pi. However, results were not validated due to typhoon damages in 2018 WS. Seeds were increased in 2019 DS. Results derived from Ballatinaw mutants with high anthocyanin content (1-diphenyl-2-picrylhydrazyl (DPPH),mg TE/g) will also be validated in 2019 WS.

For the Dinorado mutants, a promising line from the 5kR treatment, *Dinorado* 5kR- 38-3-2-3 produced 7.1t/ha, which is higher than the original parent (3.9t/ha). The chalky character was also significantly reduced from 86.3% to 6.9%.

Gal-ong, a location specific traditional special variety in Benguet, is a popular commercial variety with export potential owing to its aroma and excellent eating quality. Utilizing gamma irradiation, *Gal-ong* generated high frequency and spectrum of desirable mutations including high yield. Two significant variations were selected: 1) aromatic non-glutinous and 2) glutinous or waxy category. Among the non-glutinous, 6 lines showed higher yields from 7.7 to 8.8t/ha than the wild type (1t/ha) and the yield check NSIC Rc 222 (7.5t/ha). The best mutants with more than 8t/ha were GXB405 (8.8t/ha), GXB410(8.7),GXB 311-2 (8.4), and GXB 407(8t/ha). Among the waxy mutants, only GXB 313-2 produced an equally high yield of 8t/ha significantly better than the check IMS *Malagkit Sungsong* producing only 2t/ha. Further phenotyping for grain quality traits is on-going on all selected mutants. DNA fingerprinting will be conducted on the promising mutants of *Azucena*, *Ballatinaw*, *Dinorado*, and *Gal-ong* to establish and determine the degree of similarities of these selected putative mutant lines from their wild types.

The following findings were also derived from the mutated modern varieties::

- PR40346-4-2-1, a progeny of PSB Rc10 targeted for very early maturity, performed better than PSB Rc10 in terms of yield and stability index under transplanted method. PR40346-4-2-1 exhibited premium milling and head rice recovery, physical attributes of less chalky trait, long and slender grains, and excellent grain quality. PR39485-PSB Rc10-25kR-1-27 also had significant better yield than PSB Rc 10 at 5t/ha. It also outperformed the variety in terms of milling yield(69.0%), head rice(50.8%), and amylose content (17.3%).
- PR39487-RC150-20kR-2-15 (18.8%) and PR39488-Rc152-25kR-24 (17.1%) had less amylose content than the original PSB Rc150 and Rc152, respectively.
- PR37913-PSB Rc72H-20kR-6-19 and PR37913-PSB Rc72H-20kR-6-41 were mutant lines derived from gamma irradiated seeds of a 3-line F1 hybrid PSB Rc72H or Mestizo treated with 20kR gamma rays. These mutants had comparable yield, better bacterial leaf blight resistance, slightly later maturity, retained aroma, and eating quality comparable with the parent variety PSB Rc72H. Based on the similarity coefficient values, they were validated to be Mestizo 1 mutants at .75% (Source 3), .51% (Source 1) and 0.67% (Source 2). They were nominated to the Plant Variety Protection Board and are now under final evaluation.

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

TE Mananghaya

Ten traditional varieties were identified having blast resistance using 20 differential blast isolates. Six SSR markers for blast resistance were used to determine the presence of blast resistance alleles. Dinorado 12798-B and Mimis possessed three alleles while most of the traditional rice varieties have Pi9 allele. None of the 6 rice blast R genes were detected in *Dinorado* (13914), *Kalinayan* (Mono) 12383, *Inumay* (ORIG), and *Tomindog*, implying that different novel rice blast R genes are controlling their blast resistance reaction. In genetic analysis of *Malay 2* for blast resistance, 6 potential QTLs were identified using 101 polymorphic markers distributed throughout rice genome. Seventeen breeding lines introgressed with blast R gene were evaluated in two NCT rice blast nurseries. Results showed that most of the breeding lines introgressed were resistant to rice blast pathogen present in blast nursery experimental areas.

General evaluation of donor germplasm

JF Pariñas

One of the most difficult tasks in carrying out a successful breeding program is choosing 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 that meets the increasing market demands and to safeguard the environment through a creation of diverse germplasm pool. In selecting the parent materials, grain type and shape, plant height, and resistance to biotic and abiotic stresses are highly considered. Hence, this study was implemented to ensure availability of select pre-breeding materials in the PhilRice crossing block for breeding programs and evaluation of rice germplasm accessions. About 500 rice accessions were established in the crossing block every season in two staggered batches to allow greater chance of flowering synchronization. From 2015, the characterization of selected

rice accessions was based on grain length, grain shape, and days to maturity. Qualified rice accessions were ranked and top three accessions were recommended to breeders working on yield improvement.

Multiparent Advanced Generation Inter Crosses (MAGIC) in PhilRice Genetic Resources

JBM Alvarino

Using MAGIC (Multi- advanced generation inter crosses) method in breeding generates natural allelic variants that can be sources of novel quantitative trait loci (QTL). Eight donor lines were identified with important traits such as aromatic, high yielding, intermediate amylose content, and resistant to major rice insects/pest and diseases (bacterial leaf blight, green leaf hopper, stemborer, rice tungro, blast, brown planthopper, sheath blight), and saline tolerance. The selected founder lines are elite and released rice varieties recommended by rice breeders. Phenotyping and DNA analysis using functional markers of selected founder lines were conducted to validate and discover important traits. Based on physiochemical properties evaluation of parentals, NSIC Rc 218 and Rc 298 had low amylose content of 15% and 15.5% respectively. NSIC Rc 346, PR37951-3B-37-1-2, Rc 226, PR34358-5-POKKALI-AC-37-M5R-15-Dr93, and Rc 342 showed intermediate amylose content. Four functional markers were used in detection of molecular traits. Rc 298 and Rc 226 were found to have submergence gene. NSIC Rc 218 was observed medium tolerance to salinity and also has xa5 gene for bacterial leaf blight. Most of the entries showed moderately tolerant to salinity while PR34358-5-POKKALI-AC-37 M5R-15-Dr93 was significantly highly tolerant. Eight founder lines exhibited negative allele to Xa4 for BLB and ART 5 markers for sub1 gene. Phenotypic evaluation showed that Rc 354 has resistance to blast among the parental lines.

This project will be discontinued in 2019 for lack of staff who will continue the study. Materials were kept in a safe place for a possible future studies.

Development of New Cytoplasmic Male Sterile Source Using Nucleus Substitution Approach

IG Pacada

Currently, most of the developed three-line hybrids and hybrids already in the pipeline are based on one cytoplasmic source, the wild abortive (WA) cytoplasm. Extensive use of one type of cytoplasm narrows the cytoplasmic diversity and may also result in disease vulnerability. Exploration for new cytoplasmic source using Philippine germplasm and modern varieties was investigated thru this study. Three nucleus substitution approach were used: inter-varietal (primitive landraces/traditional cultivars x modern varieties), inter-specific (wild rice derived lines x modern varieties), and inter-subspecific (primitive indica varieties x japonica/javanica varieties). Among the three-nucleus substitution approach, the inter-varietal and inter-specific provided higher pollen sterility from BC6F1 progeny, which exhibited 80% pollen sterility. Obtaining higher sterility depends on the genetic similarity and dissimilarity of parent used. The more diverse the parents, the more successive backcrossing is needed. However, conduct of more basic research is highly recommended to understand the genetics of traits and possible existence of chromosomal and female sterility among generated BC progeny from three approaches.

DEVELOPMENT OF IRRIGATED LOWLAND RICE VARIETIES

EC Arocena

This project aimed to develop appropriate rice varieties with high and stable yield with average of 8-10t/ha or $\geq 10\%$ yield advantage over the check varieties, resistant to major biotic and abiotic stresses, good grain quality, and better resiliency to changing climate and shifting production constraints. It also aimed to implement a systematic approach for early generation screening and selection and test suitable to transplanting and/or direct seeding method of establishments.

Component studies included Hybridization and Pedigree Nurseries, Early Seedling Vigor, Anaerobic Tolerance and Lodging Resistance Evaluation, Marker-Assisted Selection for Pest and Disease Resistance Genes in Inbred Variety Development and Field Performance Trials. The first three studies deal on trait discovery, and line development while the last study deals on rigid phenotyping and quantitative evaluation of the desired traits identified.

Hybridization and Pedigree Nurseries

EC Arocena

This study aimed to generate crosses, develop early to medium maturing lines that possess high yield potential, high seedling vigor with anaerobic tolerance, lodging resistance, high milling and head rice recovery, acceptable grain appearance and eating quality, and resistance to rice tungro virus (RTV) and bacterial leaf blight (BLB) diseases. It also aimed to select plants with the desired phenotypic characteristics and kernel quality in the segregating generations for further evaluation in the performance yield trials. In hybridization, use of superior donor parents with target traits is very important to generate new superior F1s. There were 298 crosses generated with backgrounds of high yield, biotic and abiotic tolerance using released varieties and breeding lines. In the F1 nursery, 322 entries were evaluated, generating 108 populations for F2 nursery in 2018 WS and 145 for 2019 DS. In 2018 DS, 3,884 plant/line selections and 48 bulk with phenotype based on breeding objectives were selected in the F2-F4 nurseries. From F5 to F9, 1,485 lines were established in 2018 DS and evaluated under direct seeded and transplanted methods. Selection among and within lines based on phenotype, maturity, uniformity, reactions to abiotic and biotic stresses, and kernel quality was conducted. There were 490 lines for advance evaluation and 265 uniform lines selected for performance trial. Selections from the 2018 WS in the pedigree nursery after rigid kernel quality evaluation produced 443 lines and 38 uniform lines.

Early Seedling Vigor, Anaerobic Tolerance and Lodging Resistance Evaluation

OE Manangkil

During crop establishment, germination and seedling survival are affected by flood when sowing coincides with the rainy period or when field is not well-leveled. The effects of flooding during crop establishment and lodging at flowering to maturity limit farmers in the adoption of direct-seeding especially during rainy season. Early seedling vigor, anaerobic tolerance, and

lodging resistance are important traits in direct seeding. The study aimed to develop breeding lines with high seedling vigor, anaerobic tolerance, and lodging resistance which are pre-requisite for a direct-seeded variety. It also aimed to identify promising lines as potential donor parents or entry for multi-location trials.

During line development, F₂ populations (P) and advance breeding lines (ABL) were screened for desired traits. There were 216 F₂ P and 180 breeding lines (BL) submerged in wet seedbed producing 10 P and 4 BL with excellent early seeding vigor and anaerobic tolerance while other 13 P and 4 BL had good rating. Continuous and heavy rains occurred during 2018 WS field screening, causing low survival of entries but a happenstance in naturally screening of materials. Exactly 11 ABL had intermediate anaerobic tolerance under controlled condition and 12 BL were lodging resistant. Promising lines PR45297-42-2-1-1-3-1-B and PR45295-17-1-3-1-1-1-B had early seedling vigor and intermediate anaerobic tolerance under wet bed and controlled conditions. Selected P and BL were advanced to pedigree nurseries and performance trial while selected potential donors for these traits were nominated to the hybridization block. The three important traits in direct seeded environment is equally important in transplanted system as nurseries of transplanted seedlings are sown directly in the field, which could also be damaged by continuous rain.

Marker-Assisted Selection for Pest and Disease Resistance Genes in Inbred Variety Development

AA dela Cruz

This study provided opportunity for effective control of BB and RTD by developing rice with different combinations of BB and tungro resistance genes. Individual plants were genotyped using molecular markers tightly linked to *Glh14*, *tsv1*, *Xa4*, *xa5*, *Xa7*, and *Xa21* and phenotyped by forced inoculation of tungro viruses and three PXoo races. ELISA was used to quantify tungro viruses in rice. In 2018 DS, 273 MAS-bred rice were selected based on presence of target resistance genes and included in the materials established in the field in the wet season. In 2018 WS, the introgression of at least 1 tungro+2 BB resistance genes in 21 F₁s, 10 F₂s, 21 F₃s, 81 F₄s, 24 F₅s, and 36 elite plants was verified; while F₁, F₂, and F₃ plants introgressed with *Glh14+tsv1* and 3-4 BB resistance genes were also identified. Twelve more F₂ and 5 elite plants with at least 3 BB resistance were selected for further improvement with tungro resistance. Moreover, 15 promising advanced rice lines originally bred to serve as common sources of *Glh14* and *tsv1* were also verified carrying *Xa4+xa5*. Despite the added stress inferred by unnecessary infestation of plants with rice blast, most of the MAS-bred plants still expressed resistant (R) to moderately resistant (MR) reactions to *PXoo79* and *PXoo340*, though all were susceptible to *PXoo99*. Upon genotyping of advanced rice lines with a panel of single nucleotide polymorphism (SNP) markers, the presence of favorable resistant allele for *xa5*, *Pita* and *Pi9*, chalkiness, and *BADH* were established. Meanwhile, unfavorable alleles for genes *Xa13*, *Xa21*, *Pi5*, and *salT* were detected. All the 15 advanced rice lines were nominated to ON, while ten rice lines pyramided with 2 tungro+ 3-4 BB resistance genes were shared in the PBBD crossing block for use as common donors of tungro and BB resistance.

Field performance trial of advance breeding lines

EC Arocena

In the ON-TPR and DSR, 41 promising test entries passed the 10% yield advantage over the corresponding maturity check varieties. Notable performers were PR45297-42-2-1-1-3-1-B and PR45295-17-1-3-1-1-1-B with high yield, intermediate anaerobic tolerance under controlled

and wet bed conditions, and good disease resistance; but with hard and soft cooked rice, respectively. In the PYT-TPR and DSR, 38 promising entries were identified that passed the yield standard.

Low yields were recorded during the WS due to the effect of typhoons *Ompong* and *Rosita* during heading to hard dough stage, which caused severe lodging and poor grain filling. Severe hopper burn was also recorded in some plots because of high population of brown plant hopper at vegetative stage. In the GYT, 31 test entries passed the 10% YA over the corresponding maturity checks. Similarly, low yield was observed during the WS due to high lodging incidence caused by typhoon *Ompong* during heading to soft dough stage and *Rosita* during hard dough to maturity stage. Moderate to severe infestation of stem borer and brown plant hopper was also observed in some test entries. Based on overall field performance, 10 promising test entries were nominated to MET 2019 DS evaluation. These are potential entries to the National Cooperative Test.

BREEDING OF SPECIALTY RICE

EC Arocena

The project aimed to develop improved specialty rice: aromatic, glutinous, pigmented, and zinc/iron dense varieties through conventional breeding. However, marker assisted selection was used in the early segregating progenies of aromatic crosses to increase selection efficiency.

Breeding efforts generated 185 new crosses. There were 167 true F1s, 115 F2s for single plant selection, and 59 F2s developed for generation advancement. After rigid kernel evaluation, 4,170 individual plants from hybrid populations and 4,060 pedigree lines were selected for further line evaluation. Exactly 366 uniform lines from the pedigree nursery with good to excellent kernel qualities were elevated to AON. Field performance trials identified 60 AON uniform lines for advancement to PYT, 38 PYT lines to General Yield Trial GYT. Among the specialty types rice evaluated in the GYT, five zinc-dense lines were nominated to MET in 2019 DS. Rice Technical Working Group started to evaluate pigmented lines in the NCT in 2019 DS; hence, nine promising pigmented test entries were nominated. Two aromatic, three glutinous, and three zinc-dense test entries in the NCT will complete its three-season evaluation by 2019. Moreover, three elite pigmented lines were applied for plant variety protection and were included in NCT evaluation.

Marker assisted selection using Bradbury fragrance markers on the aromatic segregating populations identified 1,012 plants with fragrant trait while 493 lines were detected with possible another fragrant allele using INS3 markers. These marker-selected aromatic lines will be further screened for aroma using KOH method.

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

EC Arocena

The study project aimed to develop high-yielding specialty type rice to attract farmers to diversify cultivation and increase their income as special rice command higher price in the market. Special rices and micronutrient-dense varieties are also being developed to improve Filipino's nutrition.

Exactly 159 parentals were evaluated to identify donors with the desired specialty and agronomic traits generating 185 new crosses. There were 167 true F1s, 115 F2s for single plant selection, and 59 F2s developed for generation advancement. Selection during the DS resulted in 3,414 lines while in WS, 756 lines were selected. In the pedigree nursery during DS, 1,811 plants were selected and 132 uniform lines were elevated to AON. In wet season, 2,249 lines for further evaluation and 234 uniform lines for AON advancement were selected after rigid kernel evaluation. Forty-nine AON lines were elevated to PYT and 15 PYT lines were advanced to GYT in the dry season.

Test entries were affected by severe lodging incidence in WS, which resulted in significant yield reduction. Only the 11 5-tonner AON entries were elevated to PYT and 23 PYT to the GYT in 2019 DS. Among the specialty types rice evaluated in GYT, five zinc-dense lines were

nominated to MET 2019 DS. The red non-glutinous line, PR43172-2B-19-1-2, was nominated to NCT-SP Pigmented Group 2019 DS. The three elite glutinous lines nominated to NCT-SP 2018 WS will complete its 3-season evaluation by 2019 DS including the aromatic lines. Moreover, the three elite pigmented lines applied for plant variety protection completed the evaluation awaiting certification.

Evaluation and Utilization of Fragrance Markers for High-Yielding Aromatic Breeding Materials

TE Mananghaya

This study focused on the evaluation of molecular markers linked or associated with fragrance trait in rice and the establishment of molecular marker system for marker assisted selection approach to be used in aromatic rice breeding. Of 2,023 segregating populations evaluated, 1,012 (50) plants have fragrant trait using Bradbury markers. Exactly 562 plants were found to have aromatic trait using Bradbury markers while 493 possibly carried another fragrant allele identified thru INS3 markers. DNA polymorphism of popular 23 traditional rice was conducted using Bradbury fragrance markers and seven (30.43 %) had 580bp and 257bp diagnostic allele for homozygous fragrant trait, 1 (4.35%) with 580bp, 355bp and 257bp for heterozygous, and 15 (65.22%) with 580bp and 355bp for homozygous non-fragrant trait. This molecular information is useful to validate genetically fragrant trait on segregating populations and identification of potential parents for aromatic rice breeding.

DEVELOPMENT OF RICE VARIETIES ADAPTED TO RAINFED AND STRESS ENVIRONMENTS

NL Manigbas

Traits for stress tolerance are quantitative in nature. This means that traits are controlled by more than one gene, with each gene controlling a relatively small effect. Finding new genotypes harboring these genes is very viable in developing new varieties. New sources of novel genes were identified through induced mutations and phenotyping of mutant lines, released varieties and traditional varieties through screenings conducted in the field, greenhouse and glasshouse for various stresses. In this study, 5 IVC4 Lastog-derived lines and 19 Traditional Rice varieties were screened for drought tolerance. Plant recovery data from 21 days after rewatering ranged 2-86%. Two tolerant lines and five moderately tolerant lines were identified. For submergence tolerance, 100 TRVs were evaluated at vegetative stage and identified 16 as potential gene sources. Similarly, 30 elite mutant lines of *Y Dam Do* and *Jepun* were evaluated for comparative field performance under submergence stress in 2018 DS. Grain yield, under favorable condition ranged from 5.7-8.4 t/ha, while 1.5-6 t/ha under submergence condition. Six mutant lines were identified as potential gene source.

Identification of new sources of novel genes as well as confirmation and validation of presence of tolerant trait require specific screening protocols were conducted in the field, greenhouse, and glasshouse. Screening at seedling to early vegetative stage identified 147 advance lines and 5,427 segregating lines tolerant to drought. These segregating populations are composed of IVC-derived Lastog lines, TRVs, and F2 populations. For reproductive stage drought, 150 stable lines were selected putatively tolerant. Seedlings were also screened for salinity and submergence tolerance. Three hundred ten advance lines and 2,966 segregating lines were evaluated tolerant to salinity, while 158 advance lines and 1,125 segregating lines were tolerant to submergence. Lines with dual and multi-trait tolerance were also identified. Thirty-two have salinity and submergence tolerance, 178 with drought and salinity tolerance, 33 with drought and submergence tolerance, and 57 with drought, salinity, and submergence tolerance. In addition, 464 NSIC Rc 222-derived lines putatively tolerant to drought stress were screened for submergence and salinity tolerance. One hundred seventy-eight lines were identified tolerant to salinity and 33 with submergence tolerance. Among the putatively drought tolerant lines, 57 were positive to salinity and submergence tolerance. For high temperature tolerance, 495 advance lines and 73 stable lines were identified tolerant at flowering stage with spikelet fertility that range from 60-99%.

For breeding line development using conventional breeding method, 167 crosses were made to improve abiotic tolerance. Parents used in the crosses were newly released varieties, high yielding elite inbred lines, and breeding lines with tolerance to single or multi-abiotic stresses. There were 5,637 breeding lines established in dry season and 6,859 in wet season for phenotypic acceptability evaluation and generation advance. Of these lines, 5,194 breeding lines were selected for 2019 DS abiotic stress evaluation.

Field evaluation of stable breeding lines determines performance under both stress and non-stress conditions. For 2018 drought field evaluation, 231 breeding lines from various breeding strategies, composed of 39 lines from conventional breeding, 111 lines from in vitro culture (IVC), and 81 lines from seed mutation (SM) were evaluated. Evaluation for growth and yield performance under irrigated (ILD) and managed drought (DRD) was conducted during dry

season, and irrigated (ILW) and simulated rainfed (RFW) during wet season. In comparison with irrigated condition (ILD), grain yield under managed drought (DRD) had 0.4-98% yield reduction. Breeding lines under ILW yielded 0.9-8.2t/ha while breeding lines under DRD yielded 0.1-3.6t/ha. Forty-seven lines with grain yield of 6.2-8.2t/ha out-yielded the highest yielding check variety IR64 (6.2 t/ha) under ILW. PR42837- NSIC Rc 222-27-B-RTD-1-1-DRT3 was the highest yielding line. Under DRD, 135 lines with grain yield of 0.8-3.6 t/ha out-yielded the highest yielding check IR64 (0.8t/ha) with PR40060-Y Dam Do-IVC2008DS 19-1-DRT3 yielding the highest. Selected lines will be evaluated in multi-location trials.

In addition, 52 fixed breeding lines were subjected to comparative field performance trial under submergence stress and favorable condition. Grain yield of fixed breeding lines ranged 4.9-8.8t/ha averaging 7t/ha. As affected by submergence stress, grain yield ranged 1.1-6.2 t/ha, averaging 3.3t/ha. Thirteen breeding lines with yield threshold of 6t/ha under favorable conditions, and 4t/ha under stress conditions were selected. Data for 2018 WS field trial is still in progress. For high temperature tolerance, 20 MET-ready elite breeding lines with spikelet fertility (SF) of 62-95% and yield potential of 6.5-9.1 t/ha were identified. Moreover, 22 uniform lines with yield potential of 6.8-10.6 t/ha were selected and will be evaluated under high temperature condition in 2019 DS.

Development of Rice Varieties Adapted to Stress Environments

JM Niones

The study identified new drought tolerant lines as novel source of genes for tolerance and generated tolerant promising lines with acceptable agronomic characters and grain yield. Twenty-six lines from different breeding strategies were identified and selected for multi-environment trial in different rainfed-drought prone locations in 2018 WS.

Mass screen for abiotic tolerance

JM Niones

Different strategies were used to generate breeding materials resilient to climate change through conventional breeding, mutation breeding, double haploid breeding, and Molecular Aided Backcrossing (MAB). Breeding lines were evaluated for abiotic stress tolerance (drought, salinity, and submergence) at seedling to early vegetative stage to minimize bulk number of materials and identification of tolerant lines at early generations. All 346 breeding lines were evaluated to validate their drought tolerance at seedling to early vegetative stage. The evaluation resulted in the identification of 140 (40.5%) lines. Another set of screening was established for 5 selected in vitro culture-derived Lastog lines, 19 TRVs, and 16 F2 segregating population, composed of 11,724 plants, which provided possible new source of genes. Screening of 85 stable advance breeding lines for salinity stress confirmed 64 lines positively tolerant. Evaluation of 10,420 plants generated from 13 F2 segregating population produced 2,966 (28.5%) plants putatively tolerant. Complete submergence tolerance screening of stable breeding lines identified 20 lines tolerant. From 4 crosses of early generation, 2,498 plants screened generated 1,125 (45.0%) plants putatively tolerant based on phenotypic evaluation. The screening and evaluation of in vitro culture (IVC) and in vitro mutagenesis (IVM)-derived lines identified dual tolerance, 32 lines salinity and submergence, 178 lines drought and salinity tolerance, 33 lines with tolerance to drought and submergence, and 57 lines with multiple tolerance (drought, salinity, and submergence). Identified tolerant lines from early generation will proceed to field evaluation for agronomic traits, phenotypic evaluation, yield performance, and other targeted traits for improvements.

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

JM Niones

Multi-environment trials are conducted to identify both stable and high yielding genotypes in a wide range of environments. In this study, yield performance, stability of breeding lines and check entries across rainfed testing environments, location-specific adaptations were evaluated and identified. Fifty-eight breeding lines: 31 from PhilRice CES, 27 breeding lines from PhilRice Los Baños, and five released varieties were evaluated in four test locations: Nueva Ecija, Ilocos Norte, Negros Occidental, and Midsayap. In 2018 DS, five entries with yield of 0.69-1.46t/ha out-performed the best performing check IR64 (0.66t/ha) at PhilRice CES.

In 2018 WS, 58 breeding lines and 31 test entries were evaluated in five PhilRice stations. Twelve breeding lines out-performed the best performing check with 2.2 -29.8% yield advantage over PSB Rc68 (2.6t/ha). However, only in-station data is available, data from three stations are currently being processed.

Pyramiding Salinity and Submergence Tolerance into High Yielding Varieties

NV Desamero/ JM Niones

New gene sources are being identified from Philippine Traditional Rice Varieties (TRVs) and elite mutant lines for submergence, saline, and stagnant water stress. One hundred TRVs were evaluated for submergence stress at vegetative stage, wherein 16 were identified as potential gene source. Similarly, 30 elite mutant lines of *Y Dam Do* and *Jepun* backgrounds were evaluated for comparative field performance under submergence stress in 2018 DS. Grain yield under favorable condition ranged 5.6-8.4 t/ha and 1.5-6.0 t/ha under submergence. Six mutant lines were identified as potential gene source or NCT entry based on yield threshold. For line development, 1,229 breeding lines from 23 crosses in F3-F8 generation were evaluated in 2018 DS. All 319 (26%) lines from 10 crosses at F3-F5 generation were selected of which 189 (15%) lines from 10 crosses at F4-F6 generation were selected in 2018 WS. Another 50 fixed breeding lines were identified in 2018 DS and WS from the uniformity and stability evaluation, which will be compared in 2019. Fifty fixed breeding lines were subjected to comparative field performance trial under submergence and non-stress conditions. Survival ranged from 5.56% to 85.71%, averaging 48%. Grain yield of fixed breeding lines in 2018 DS ranged 4.8- 8.8 t/ha, averaging 7.2t/ha. Grain yield ranged 1.1-6.1t/ha, averaging 3.3t/ha under submergence. Thirteen or 25% breeding lines were selected with yield threshold of 6t/ha and 4t/ha under favorable and stress conditions, respectively.

Breeding for Heat-Tolerant Rice

NL Manigbas

Breeding for heat-tolerant lines in the Philippines was conducted to develop rice genotypes that can tolerate and adapt heat. Breeding lines generated were screened, evaluated, and selected in Cagayan and Nueva Ecija where temperature reached >35°C. Breeding lines were planted staggered so that their flowering will all coincide with the hottest period of the year, which is between April and May. Thousands of breeding lines were screened under high temperature conditions in Nueva Ecija and Cagayan. Of these lines, 22.4% were intermediate tolerant and 77.6% were tolerant. Advance lines developed had yield range of 5.6-10.6t/ha and spikelet fertility of 43.9-95.1%.

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

With a "Rice-Secure Philippines" vision, we want the Filipino rice farmers and the Philippine rice industry to be competitive through research for development in our central and seven branch stations, coordinating with a network that comprises 59 agencies strategically located nationwide.

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).

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