



2019

PHILRICE R&D HIGHLIGHTS

PLANT BREEDING AND BIOTECHNOLOGY DIVISION

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Plant Breeding and Biotechnology

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Executive Summary

The Plant Breeding and Biotechnology Division (PBBD) develops rice varieties adapted to different agro-ecosystems through conventional and modern technologies and related technologies. It contributes to the strategic outcomes of the Institute, specifically on increased productivity, cost effectiveness, and profitability of rice farming in a sustainable manner; enhanced value, availability and utilization of rice, diversified rice-based farming products, and by-products for better quality, safety, health, nutrition and income; and advanced rice science and technology as continuing sources of growth. Essentially, breeding done at PBBD is directed to achieve desired traits such as high grain yield, resistance to abiotic and biotic stresses, and grain qualities acceptable to consumers.

Four out of the six projects lodged in the division are focused on the development of elite lines for the stressed and unstressed environments. These projects contributed to the development of rice varieties for different ecosystems by incorporating desirable traits to selected elite lines and modern varieties. The fifth project focused on the management and maintenance of the division's laboratory, which complements and supports the breeding activities and implementation of the IMS policy of the Institute. The last project worked on the nucleus and breeder seeds for breeder seed production.

In 2019, PBBD produced eight new varieties recommended for commercialization; registered 10 breeding lines under the Plant Variety Protection (PVP); identified 26 top rice accessions or promising rice germplasms as potential parents from 431 qualified entries; developed 69 elite lines (41 for irrigated lowland and 28 for special purpose rice); identified 89 NCT-ready elite lines with tolerance to either drought, salinity, submergence, high temperature or combinations of these stresses; produced 194 viable and pure seeds of 17 newly inbred released varieties; produced 8,965kg of seeds produced from 36 varieties of irrigated lowland and 2,935kg for 12 adverse and special purpose rice varieties with 72.02 % efficiency in 2019 DS; accomplished preventive maintenance of 11 equipment and calibration of 128 equipment calibrated, and facilitated repair of three equipment; and applied the use of drone technology in breeding.

Pre-Breeding and Germplasm Enhancement

OE Manangkil

Breeding programs must have additional sources of genetic variation aside from what is available within. This is because of the long history of selection in rice that has led to the narrowing of genetic diversity (Tanksley & McCouch, 1997). Additional sources of variation may come from wild rice species, but this is not straightforward because of the possibility of reproductive incompatibilities and the introgression of unwanted traits associated with wild rice species. Search for genes or donors are conventionally being done by screening hundreds of diverse genotypes for particular traits. But natural variations for important traits are not infinite. Relying solely on natural genetic variation may not be enough to address the needs in the future. While it is wise to look for genes in the landraces and traditional varieties, it may take some more time to incorporate the trait into modern cultivars. Geneticists and breeders therefore look for other alternatives of increasing genetic diversity of their breeding programs and one of these alternatives is through this project. The project aimed to broaden the base of germplasm resources by identifying new gene sources or by developing new sources and increase the access and utilization of desirable traits and/or genes existing in the rice germplasm.

The project had implemented four studies that focused on improving quality characters in rice through mutation breeding, search for durable and novel blast resistance genes to identify other sources of novel genes using the differential blast isolates, general evaluation of donor germplasm to identify suitable donors of target traits from a wide range of rice accessions, and development of new cytoplasmic male sterile source using nucleus substitution approach. Each study compliments with each other by widening the genetic diversity of existing materials through the use of other sources with high genetic differences with parents kept in the Crossing Block (CB).

Results of these interrelated studies will ensure availability and accessibility of diverse rice lines/accessions useful as pre-breeding materials in the CB which will serve as the common source of materials for use of breeders/researchers working on various breeding programs. Sharing of pre-breeding materials among various groups is being encouraged to maximize their utilization. To be able to broaden the genetic base of the CB materials, studies under the project continuously strive to develop/identify new breeding lines/accessions with unique or improved traits that can be used directly in breeding or provided to researchers as materials for further studies, such as molecular characterization

to identify underlying genes and gene mapping. For the general evaluation of germplasm, information about agronomic traits and reactions to prevalent pest and diseases of the CB materials are gathered and provided to rice breeders for use as reference. Through this, the project will help address the gap between genetic resources.

Mutational Improvement of Quality Characters in Rice Contributing to Food Security in the Philippines

LR Pautin, TF Padolina, RC Bracerros, and ES Avellanoza

Mutation-based breeding is one strategy to increase trait variation and to improve well adapted plant varieties by modifying one or two major traits to increase productivity and utilization. Mutation techniques were used to diversify the morphological, physicochemical, and nutritional characteristics of different germplasm to boost the economic value of rice. The parent varieties used in this study were commercial modern varieties. It aimed to improve their weak traits, including that of the traditional varieties with potential for high yield and enhanced nutritional content.

Induced mutation was provided by the Philippine Nuclear Research Institute (PNRI) with their gamma radiation facility and their expertise in handling chemical mutagens. In this study, the rice seeds were exposed to physical agent or chemical mutagens. The physical agent used was gamma radiation from radioactive cobalt (Cobalt-60) with a predetermined treatment dosage that will provide high variations. The chemical mutagens include ethyl-methyl sulfonate (EMS) or ion beam treatments. Selection will proceed based on the breeder's selection eye in pinpointing the best entries with good morphological and agronomic traits, including yield. The specific target traits were selected based on appropriate screening procedures. For example, on general grain quality parameters, a standard protocol is followed and the specific traits are identified, while on nutritional traits, a specific chemical analysis is used in identifying those with high anthocyanin or low phytic acid content. Foremost, therefore, the general yielding ability and good agronomic traits were ensured on the mutant products followed by the selection and validation of specific target traits.

Three groups of relevant mutants derived from modern and traditional varieties were selected. Group 1 was composed of 27 lines from modern varieties, namely, PSB Rc 10 (5 lines with reduced amylose), NSIC Rc 134 (11 with improved yield and early maturity, long grain), Rc 150 (3 with reduced amylose), Rc 152 (1 with reduced amylose, improved texture), Rc 240 (3 with long grains and consistent grain size), and MS 16 (4 with improved yield, resistance). Group

2 were from PSB Rc 72H converted into two inbred mutant lines, PR37913-PSB Rc72H-20kR-6-19 and PR37913-PSB Rc72H-20kR-6-41, which both retained the quality trait of good eating quality and aroma of the original hybrid. These lines were nominated for PVP in 2018 and was granted certification on October 19, 2019. The last group consisted of 8 mutant lines from traditional germplasm: *Azucena* (2 with lower phytic acid), *Dinorado* (2 with higher yield), and *Ballatinaw* (4 with higher anthocyanin content). A special traditional glutinous cultivar, *Gal-ong*, also produced 67 diverse mutants: 9 non-glutinous lines with excellent eating quality, 42 high yielding non-glutinous, 16 glutinous, and 14 new putative non-glutinous lines.

Finding Durable and Novel Blast Resistance Genes Effective Against Philippine's *Magnaporthe Griseae* Pathogen Population

JM Niones, TE Mananghaya, JT Niones, JP Rillon, and RP Mallari

In the Philippines, rice blast disease has been frequently reported in upland rice growing areas where the condition is more favorable for disease development and rainfed lowland environments that are prone to drought. However, incidence of rice blast has been also recently reported in lowland areas, bringing more concern for its spreading threat to rice production. Our objective is to identify novel gene(s)/quantitative trait loci (QTL) blast resistance effective to Philippine's rice blast fungal pathogen. Traditional rice varieties, modern released, improved and breeding lines were evaluated for blast resistance in identified blast hot spot areas and in the established National Cooperative Test (NCT) screening sites for major rice diseases. Upon examination of the spectrum of blast resistance, NSIC Rc 152, Rc 160, Rc 240, and Rc 402 demonstrated 1-3 major R genes responsible for controlling blast resistance in these varieties. Specifically, *Pi20*, *Pii*, and *Pita* genes are estimated to be present in Rc 160; *Pita-2* gene in Rc 240; *Pi12*, *Piz-t* and *Pi11* genes in Rc 152; and *Pik-s* and *Pita* genes in Rc 402. A total of 94 BC2F3 plants from the NSIC Rc 160/*pi21* cross and 32 BC1F3 Rc 240/*pi21* were subjected to blast resistance screening at PhilRice-CES blast nursery using selected differential blast isolates. Most of the selected plants showed blast resistance (0-1 lesion type), while 20% of the selected plants exhibited blast intermediate reaction (2-3 lesion type). Advanced lines, parents, traditional rice varieties and selected mapping population plants were established in identified leaf blast hotspot areas. Fifteen advanced lines with

introgressed blast resistance genes were established for agro-morphological characterization. In genetic analysis of resistance of US2/Malay2 cross combination, two blast resistance QTL were identified located in chromosome 4 and 11 with LOD of 2.591 and 3.113, respectively.

General Evaluation of Donor Germplasm

JF Pariñas, PAC Canilang, and TF Padolina

One of the most difficult tasks in carrying out a successful breeding program is the choice of germplasm. Rice breeders need to be sure that the source germplasm has desirable genetic variability to be able to develop a variety with a set of desirable characteristics that meets the increasing market demands, as well as to safeguard the environment through a creation of diverse germplasm pool. In selecting the parent materials, consideration on characteristics such as grain type and shape, plant height, and resistance to biotic and abiotic stresses are of primary importance. Hence, this study was implemented to ensure availability of selected pre-breeding materials in the PhilRice crossing block for use in various breeding programs and conduct general evaluation of rice germplasm accessions as needed. In 2019, 588 rice accessions were established in the crossing block every season, in two staggered batches to allow greater chance of flowering synchronization. The selected rice accessions was characterized based on standard criteria, grain length, grain shape, and days to maturity. Qualified rice accessions were ranked: three derived from TCN ranged 31.4-32.1 for 1000g wt, 1 TCN and 2 PRHY ranged 187.4-216.2 in grain/panicle, and PR44576-HY-R, PR40063-Jepun-SCRL2008DS-18-5-Sal3-Sub2, and TCN-227 ranged 172.2-187.8 for percent filled spikelets. These were recommended to breeders working on yield enhancement. All data gathered in the characterization, however, were provided to rice breeders as reference in identifying potential donors in rice improvement. By showcasing the potentials of available pre-breeding materials, their utilization in rice breeding will thereby increase. This can lead to exploitation of new and diverse sources of variation needed to develop new gene pools for genetic enhancement of rice with a high frequency of useful genes, wider adaptability, and a broad genetic base. Among the profiled accessions, there were 431 selections based on the set criteria.

Development of New Cytoplasmic Male Sterile Source Using Nucleus Substitution Approach

IG Pacada, AG Pascua, and CA Blacer

The exploration and use of PhilRice genetic resources strengthen the foundation of pre-breeding program. This study aimed to develop new cyto-sterility source for three-line breeding, identifying new cyto-sterility source is essential to prevent vulnerability of future three-line hybrids to disease or insect epidemics. Three nucleus substitution approaches were used: inter-varietal (primitive indica x modern varieties), inter-subspecific (Javanica x modern varieties), and inter-specific crosses (wild rice derived lines x modern varieties). Nucleus substitution is a cross of two germplasm with diverse background that undergo successive backcrossing to produce complete sterile plants. The generated BC1Fn progeny or the bred cytoplasmic hybrid has nucleus and cytoplasm that differ in origin. The corresponding female has cytoplasmic factor-inducing male sterility or the A-line while the male parent is a nuclear donor or the maintainer line. In BC8F1 progeny, plants with 75% sterility was observed and came from the cross combination of primitive Indica Sadri and NSIC Rc 300.

Development of Irrigated Lowland Rice Varieties

EC Arocena

The irrigated lowland areas comprising 71% of the total harvest area is the most reliable ecology for developing new intensive-culture rice crops, be it transplanted or direct seeded. With the advent of modern and innovative technologies, variety development based on genetic enhancement and extensive phenotyping allows development of the future's rice ideotypes. This project aimed to: (1) develop appropriate rice varieties with high and stable yield, resistance to major biotic and abiotic stresses, good grain quality, better resiliency to changing climate and shifting production constraints in highly intensive production systems; and (2) implement a systematic approach for early generation screening and selection, and yield performance testing for multi-location trial. There were four studies conducted under the project. Study 1 aimed to produce crosses and desirable breeding lines for transplanting; Study 2 targeted to produce desirable breeding lines for direct seeding; Study 3 intended to produce desirable breeding lines using molecular markers for bacterial leaf blight and tungro resistance. Lines developed with the desired traits from these three studies were evaluated in Study 4 and identified promising lines with higher yield than the check varieties and better agronomic performance to produce advanced lines for national multi-location trials.

Hybridization generated 85 new crosses. Line development using conventional method started from the 89 F1s and successive selection resulted to 2,758 breeding lines for further selection in the pedigree nurseries. For direct seeding under field condition, 29 populations and 14 breeding lines were identified to have early seedling vigor (SV), and anaerobic germination (AG). Moreover, 1,414 advanced breeding lines were designated for further line selection and 345 uniform lines were selected for advancement to the Observation Nursery (ON) of the Performance Trial. Under greenhouse condition, 25 breeding lines exhibited tolerance to anaerobic germination and seedling vigor. Four were positive to SSR markers for anaerobic tolerance using Marker-Aided Selection (MAS). For lodging resistance, 10 resistant lines were identified using push resistance devise. Three advanced lines with 7-ton yield, good to excellent SV and AG, lodging resistant and with blast and BLB resistance were identified for multi-location trials and potential donor parents. Using MAS for resistance, 85 advanced lines pyramided with the desired BLB and RTV resistance genes combinations will be further screened for disease resistance and line advancement.

In the performance trials, 60 ON uniform lines were elevated to the Preliminary Yield Trial (PYT), 32 PYT selected for advancement to the General Yield Trial (GYT), and 41 GYT lines ready for Multi-Environment Trial (MET). Previous nominations in MET identified nine advanced lines as new entries to the NCT-IL Phase I this 2020 DS.

Hybridization and Pedigree Nurseries

EC Arocena, OE Manangkil, TF Padolina, WV Barroga, SB Estrada, and PNM Marcelo

Rice breeding uses conventional and non-conventional methods to develop a new variety. Components of variety development include trait discovery, line development, and performance trials. Success of variety development depends on how rigid are the evaluation and selection based on breeding objectives. The study covered trait discovery and line development. Generation of new superior crosses and breeding lines for advance evaluation under irrigated lowland ecosystem was done. Eighty-five new crosses were generated using released varieties and breeding lines with backgrounds of high yield, and biotic and abiotic tolerance. In the F_1 nursery, 99 crosses were evaluated and 89 F_1 s were found as true hybrids and superior over their female parent for F_2 nursery. Pedigree lines were established and evaluated under direct seeded (DSR) and transplanted (TPR) methods. Selection among and within lines was based on phenotype, maturity, uniformity, reactions to abiotic and biotic stresses, and kernel quality. In 2019 DS, 4,309 entries were established and 2,334 plants/lines were selected in the F_2 to F_4 nurseries with phenotype based on breeding objectives. From F_5 to F_{10} , 424 lines were selected for advance evaluation and 184 uniform lines for performance trial. In 2019 WS, 4,739 entries were evaluated with 609 selections from direct seeded F_2 to F_4 , 805 from F_5 to F_7 nurseries for advance evaluation, and 161 uniform lines for performance trial in 2020 DS. Uniform selections from DSR nurseries survived from anaerobic screening during F_2 evaluation and are potential anaerobic tolerant lines. Kernel quality evaluation of selections from transplanted nurseries is in progress. Line selections are potential donor parents or advanced lines for multi-location trial.

Early Seedling Vigor, Anaerobic Tolerance, and Lodging Resistance Evaluation

OE Manangkil, WV Barroga, AB Rafael, and PNM Marcelo

Early seedling vigor, anaerobic tolerance, and lodging resistance are important traits in direct seeding. During crop establishment, flooding affects germination

and seedling survival when sowing coincides with the rainy period or when field is not well-leveled. Strong wind causes lodging of rice plants which affects the color and flavor of rice grain. 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. This study identified breeding lines with high seedling vigor (SV), anaerobic tolerance (AG) under field and screenhouse condition, and lodging resistance. Under screenhouse screening, the use of MAS for anaerobic tolerance using two SSR markers was also employed. Ninety seven F_2 populations and 193 breeding lines were screened. There were 14 populations and 6 breeding lines with excellent early seeding vigor and anaerobic tolerance, while 15 populations and 8 breeding lines with good rating were identified. Nine advance breeding lines had intermediate anaerobic germination tolerance and 12 had resistant anaerobic seedling tolerance under screenhouse condition. Four breeding lines showed intermediate seedling tolerance in screenhouse condition and positive to two SSR markers for anaerobic tolerance. PR47851-17-1-1-2-1-B and PR 49573DSR-14-1-3-B had excellent early SV and AG tolerance under field condition with 7,301 - 7,566kg/ha yields in dry season, intermediate resistance to lodging and resistant to blast. PR 49575DSR-5-1-B had good SV and AG, 7,116kg/ha yield and intermediate resistance to lodging and BLB. Ten breeding lines were lodging resistant in dry season with pushing resistance of 1.35-1.6kg/cm². These are potential donor parents for hybridization and/or entry for multi-location trials.

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

RC Bracerros, MJC Duque, MJ Yapchiongco, and TF Padolina

In 2019, various combinations of bacterial blight (BB) resistance genes (*Xa4*, *xa5*, *Xa7*, and *Xa21*), tungro resistance gene (*tsv1*), and GLH resistance locus (*Glh14*) were introgressed into originally disease-susceptible irrigated lowland rice lines. Based on polymerase chain reaction amplification of target resistance genes/ locus, candidate plants with homozygous or heterozygous genotypes were selected among 150 MAS-bred rice lines that were screened.

Fifty-three elite MAS-bred rice lines (17 F_5 , 27 F_6 , and 9 F_7), which were pyramided with at least three BB resistance genes and *tsv1* and/or *Glh14* were evaluated for reaction to BB pathogen, *Xanthomonas oryzae* pv. *Oryzae* (*Xoo*) under screenhouse or field conditions. Of these, four exhibited resistance against *PXoo79* and *PXoo99*. The others were only resistant to *PXoo79*. The uniformity and yield of the four promising rice lines will be evaluated further

in the ON in 2020. Meanwhile, rice lines useful as common donor of BB and tungro resistance genes will be shared in the PBBD hybridization block for use in breeding. Thirty-two individual plants that were also pyramided with *Glh14*, *tsv1*, *Xa4*, *xa5*, and *Xa7/Xa21* were selected, but their reactions to BB and tungro are yet to be evaluated.

New F₁ plants were also generated this year from crossing susceptible elite breeding lines and MAS-bred donor lines with BB and tungro resistance. The true hybridity of each plant was determined by genotyping using molecular markers. True F₁ plants from 6 different cross combinations were selected during the dry season. The putative F₁ plants generated during wet season from 10 more cross combinations were planted in the screenhouse for DNA extraction and genotyping. The resulting F₂ seeds from all true F1 plants will be collected for further selection and advancement.

Field Performance Trial of Advanced Breeding Lines

EC Arocena, OE Manangkil, GM Osoteo, WV Barroga, HT Ticman, MV Chico, PNM Marcelo, PS Ramos, Jr., and SB Estrada

Yielding ability is one of the major bases of selection in every breeding program aside from the special traits of the breeding lines developed. However, the genetic make-up of the selected lines coupled with the biotic abiotic stresses and other factors during the cropping seasons contribute to the full expression of this trait.

The field performance trials aimed to develop promising lines with $\geq 10\%$ higher yield than the maturity checks and to identify promising lines for MET. It consisted of three interrelated activities: the Observation Nursery (ON), Preliminary Yield Trial (PYT), and General Yield Trial (GYT). The ON and PYT were established under both transplanted (TPR) and direct seeded (DSR) methods, while the GYT was under TPR method only. Promising lines identified based on yield performance and agronomic traits from each of the ON, PYT, and GYT advanced to subsequent trials.

In the ON-DSR and TPR, 49 promising test entries were identified for PYT with $\geq 10\%$ yield advantage (YA) over the maturity check varieties. Among the 20 top performers identified for PYT-DSR were PR48589-4-2-1-3-B, PR49581DSR-1-1-3-B, and PR48628-14-1-1-B, which had 7,856 - 8,315kg/ha yield, were resistant to blast, had Grade 1 milling recovery, and with intermediate amylose

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content. Another 11 uniform lines with 85-95 DAS maturity were selected for PYT. PR43675-B-VEM-1-1 and PR46588-B-VEM-3-1 were identified as donor for earliness, high yield, and BLB resistance. In the PYT-DSR and TPR, 26 promising entries with $\geq 10\%$ YA over the checks were identified for GYT. Of these, 13 entries had intermediate to resistant (R) reaction to blast. PR47310-13-1-B-1-2 and PR50227TPR-6-3 had intermediate reaction to bacterial leaf blight, and PR47340-23-3-B-1-1 had intermediate reaction to sheath blight. In the GYT, 38 promising lines advanced to MET in 2019 WS. Overall performance resulted to 41 promising entries with $\geq 10\%$ YA over the checks and are potential entries for nomination to the MET.

Breeding of Specialty Rice

EC Arocena

The development of specialty rice, such as glutinous, aromatic, pigmented, and zinc/iron-dense varieties has been carried out in the past decade owing to the increasing demand for this kind of rice. These specialty rices are generally low yielding, susceptible to pests, with unstable and occasion-driven demand, which limits its wide production. However, these rices command higher price in the market. Hence, the project aimed to develop high-yielding specialty rice to lure the farmers to expand its cultivation. The project focused on the development of improved aromatic, glutinous, pigmented, and zinc-dense varieties through conventional breeding. The other study on the use of marker aided selection for aroma was done to facilitate and increase selection efficiency for aromatic breeding lines.

Breeding efforts resulted to 113 new specialty type crosses. Line selection in the segregating generation identified 6,010 breeding lines for further line selection and 307 uniform lines for advancement to ON. In the performance trials, promising lines for each type were identified for advancement. There were 118 ON promising lines for PYT, 38 PYT lines for GYT, and 23 GYT lines as potential entries for MET evaluation.

The study on fragrance markers found 914 breeding lines as aromatic. Out of the 2,250 aromatic progenies evaluated, there were 947 non-aromatic that were found. Optimization also showed that aside from Bradburry, Shao, and INS3 markers could also be used as marker systems to determine other fragrant locus in rice.

Three modern-type pigmented lines were already PVP-certified. These can now be seed produced by the BDD for sale as black and red rices, which are good sources of antioxidants.

Development of Aromatic, Glutinous, Pigmented and Iron/Zinc-dense Rice Varieties

EC Arocena, MV Chico, HT Ticman, and GM Osoteo

Specialty rices, including aromatic (A), glutinous (G), and pigmented (P) rices, command higher price in the market. However, cultivation is limited owing to low yield, susceptibility to biotic stresses, and low and occasion-driven demand, especially for the glutinous and pigmented types. Recently, the demand is

increasing for these types of rice because of its excellent eating quality and aroma, the extensive promotion of products made from glutinous rice through the One-Town-One-Product program of the government, and the increasing awareness of Filipinos on the importance of antioxidants and micronutrients derived from rice. Hence, there is a need to develop higher yielding specialty rice, with resistance to biotic stresses and good grain quality to lure farmers to expand its cultivation. The study was composed of breeding activities from the selection of parentals, to line development from the segregating generations, to the evaluation of advanced lines in the performance trials, and to MET or NCT.

There were 143 parents used in the hybridization. From these, 113 new specialty type crosses were generated. Seventy-one true F1s and 97 hybrid populations for single plant selection were identified. Line selection in the hybrid populations and pedigree nursery resulted to 5,866 specialty type lines for further selection and 261 uniform lines for advancement to ON. From the performance trials, majority of the test entries outyielded the corresponding check by at least 10% and the top promising lines for each type were identified for advancement. Of the ON test entries with at least 10% YA, the following yield ranges were recorded: 8.1-9.8t/ha (DS) and 3.7-5.5t/ha (WS) for aromatic; 7.1-9.1t/ha (DS) and 3.1-4.3t/ha (WS) for glutinous; 6.0-8.1t/ha (DS) and 3.1-4.3t/ha (WS) for pigmented; and 7.4-8.6t/ha (DS) and 3.3-5.0t/ha (WS) for Zn/Fe. The yield of the check varieties were 5.9t/ha (DS) and 2.2t/ha (WS) for Rc 218 (A); 4.9t/ha (DS) and 2.4t/ha (WS) for Rc 13 (G); 4.1t/ha (DS) and 2.8t/ha (WS) for Rc 19 (P); and 6.4t/ha (DS) and 3.0t/ha (WS) for Rc 460 (Zn/Fe). The same 10% YA over the corresponding check standard was applied for the entries evaluated in the PYT and GYT. There were 40 A, 27 G, 25 P and 26 Zn/Fe ON promising lines identified for PYT. There were also 15 A, 12 G, 10 P, and 1 Zn/Fe PYT lines for GYT; while 10A, 10G, 3 P, and 1 Zn/Fe GYT lines were identified for MET evaluation.

The most tangible output of this study was the certification of the three pigmented lines for PVP. These were PR37042-B-1-1-2-6, a black glutinous line with 120 days after sowing (DAS) maturity and with a potential yield of 4.6t/ha; PR38170-B-13-2-3-2-2-1, a black non-glutinous line with 113 DAS maturity and potential yield of 5.2t/ha; and PR35034-B-3-2-1-1-4-1-2-1-1-2-1, a red non-glutinous line with 115 DAS maturity and potential yield of 8.4t/ha.

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

TE Mananghaya, JBM Alvarino, HT Ticman, MV Chico, and DR Arceo

Fragrance in the grain is one of the highly valued grain quality traits in rice. However, this trait is recessive and thus, breeding of aromatic rices needs extensive labor and has to involve large numbers of breeding materials to develop and identify a progeny with the target aromatic trait. Molecular markers associated with fragrance trait will assist rice breeders to develop a high-yielding variety with excellent grain quality in a simple and inexpensive method. This study evaluated a marker system to be used in marker assisted selection for fragrance trait in rice, and consequently, in the aromatic breeding program. The breeding materials were established in the field, plants were individually tagged, and leaf samples were collected prior to deoxyribose nucleic acid (DNA) analysis using selected fragrance markers. Nine cross combinations with aromatic parent were used in DNA analysis. The DNA polymorphism analysis of 2,250 aromatic breeding materials was conducted using Bradbury fragrance markers. Of these, 914 were aromatic, 947 are non-aromatic, and the remaining 389 entries are for validation. In addition to Bradbury, Shao, and INS3 markers were used to identify fragrant trait. Twenty-three selected traditional rice varieties (TRVs) were screened using three marker systems, wherein six were positive to Bradbury, while eight TRVs showed fragrant trait for Shao and INS3 fragrance markers. Hence, Shao and INS3 markers could also be used as marker system in detecting aroma. Additional six markers were optimized to determine other fragrant loci in rice.

Development of Rice Varieties Adapted to Rainfed and Stress Environments

NL Manigbas

The rainfed ecosystem, representing about 1.5 million hectares of harvested area nationwide is prone to stress conditions, such as drought, flooding or submergence, salinity, high temperature, and biotic stresses (i.e., pests and diseases). These are seen to worsen with changing climate patterns. As one of the mitigating measures against the negative impact of adverse conditions associated with climate change, genetic improvement of rice to become resilient to abiotic stresses must be conducted. Breeding better varieties is one of the most efficient and effective ways to address mitigation and adaptation as far as climate change is concerned. The variety development, particularly for rainfed and stress environments, focused on developing adaptable and high yielding varieties in these adverse environments. There were five studies implemented that focused on variety development with traits for drought tolerance; mass screening for abiotic stresses; and multi-environment and adaptability test for drought, submergence and salinity tolerance, and high temperature. Each stress is unique and thus, screening breeding lines is separate. These studies are harmonized by combining 1-3 traits that can be present in the breeding lines being developed through breeding procedures at hand (molecular and conventional).

The general approach of the project is to identify genetic sources being one of the most important considerations in breeding for stress environments. Natural and induced genetic variations were utilized as primary source of genotypes for developing tolerance to abiotic stresses. Hundreds of TRVs, elite breeding lines, cultivars and varieties, mutants, and in-vitro derived lines were mass screened in the field and greenhouse. Molecular markers were employed to validate tolerance to different abiotic stresses. Results from MAS (Marker Assisted Selection) showed that 119 genotypes were identified as possible sources of genes for multi-abiotic stress tolerance that can be utilized for hybridization.

New breeding lines were developed through conventional methods with application of biotechnological tools. Using tissue culture techniques, in-vitro mutagenesis, and seed mutation of NSIC Rc 222 and TRVs, 231 breeding lines were developed with tolerance to different abiotic stresses. Hundreds of lines with validated tolerance by conventional methods were advanced in field trials

under stress and non-stress conditions. To ensure that elite lines will perform in the target environment(s), multi-environment tests for drought-prone rainfed environments were conducted. From these tests, three elite lines were identified as stable and high-yielding.

The project had identified 89 NCT-ready elite lines with tolerance to either drought, salinity, submergence, high temperature or combinations of these stresses. Several elite lines were nominated to 2020 MET and NCT. As final output of the project, one saline-tolerant elite line and four rainfed dry seeded rice were released as new varieties in 2019. These are NSIC Rc 558 (saline tolerant), Rc 568, Rc 572, Rc 574, and Rc 578.

Development of Rice Varieties Adapted to Stress Environments

NV Desamero, CC Cabusora, KRP Balmeo, RMM Sumabat, and RD Buluran

Adaptation to climate change-related environmental stresses such as water deficit resulting in drought, excess precipitation causing floods, and increase in seawater level salinizing coastal rice areas warrants the development of rice varieties with multiple tolerance to stress, while maintaining yielding ability at acceptable level. The PhilRice breeding program for stress environments employs various breeding strategies such as classical hybridization and selection, mutation breeding and doubled haploid breeding to generate and develop climate-resilient rice varieties.

In search of novel gene sources, 102 TRVs were screened for drought tolerance at seedling stage, 41 TRVs were identified as putatively drought tolerant, 3 were distributed as highly tolerant, 11 were tolerant, and 27 were moderately tolerant. PSB Rc 14 and IR 64 were used as resistant and susceptible checks, respectively, in the mass screening for drought tolerance at seedling stage. Mass screening for saline tolerance at seedling stage of 649 TRVs yielded 55 (8.5%) putatively tolerant entries composed of 38 (5.9%) moderately tolerant, 14 (2.2%) tolerant and three (0.5%) highly tolerant genotypes. FL478 and IR29 were used as the resistant and susceptible checks, respectively.

Through line development and successive selection, 64 fixed recombinant inbred lines (RILs) are ready for stress tolerance screening in 2020. Of the 94 fixed RILs selected in 2018, stress tolerance screening identified 38 RILs as tolerant to drought at seedling stage, 10 as saline tolerant at seedling stage, and 14 as tolerant to both stresses. RILs with stress tolerance will be evaluated for

field performance in 2020. In field performance evaluation in 2018, 11 lines were identified as candidate for MET by 2020 WS based on STI values and rYSI rank.

To date, there are 74 NCT-ready breeding lines composed of 58 RILs, 13 anther culture-derived, and 3 seed culture-derived lines, with 5-10kg genetically pure seeds. The breeding lines have tolerance to either drought, salinity, submergence, or combinations of these stresses.

Mass Screen for Abiotic Stress

NV Desamero, CC Cabusora, RD Buluran, and RMM Sumabat

Breeding climate change (CC)-resilient rice varieties warrants simple, reliable, efficient, and effective phenotyping facility and protocol. Adaptation to CC-related abiotic stresses, such as drought or flooding, and increasing salinity level across coastal rice areas includes the use of tolerant varieties. Mass screen for abiotic stress tolerance is a vital component of rice variety development program targeting adoption in CC vulnerable rice areas.

In 2019 mass screen for drought tolerance at seedling to early vegetative stage covered 326 test entries composed of tissue culture-derived lines from traditional rice varieties (TRVs), seed mutation-derived lines from commercial variety, RILs and TRVs. Across test entries, 128 (39.3%) exhibited tolerance to drought, distributed as 1.2% highly tolerant (HT), 7.4% tolerant (T), and 30.7% moderately tolerant (MT). Tolerance was expressed in terms of plant recovery rate, which was 2-133% more plants recovered compared with the tolerant check PSB Rc 14, which had a recovery rate of 42% after releasing from drought stress.

Salinity tolerance mass screen at seedling stage covered 603 entries composed of 143 advanced breeding lines from various sources and 463 TRVs from PhilRice Genebank. Across test entries, 220 (36.5%) exhibited tolerance to salinity distributed as 0.8% HT, 16.1% T, 19.6% MT.

Complete submergence tolerance screen of 764 entries (composed of advance mutant lines, fixed RILs, and TRVs) identified 23 (3.0%) entries expressing tolerance, 17 of which were putatively drought tolerant and one has combined salinity and drought tolerance. These breeding materials are possible novel sources of genes for multi-abiotic stress tolerance and will be studied further.

Consolidating the responses of 231 tissue culture, in vitro mutagenesis and seed mutation-derived 181 (78.4%) lines from *Y Dam Do* and *Jepun* have combined tolerance to drought and salinity, 41 (17.7%) lines from *Salumpikit* have salinity and submergence tolerance, and 9 (3.9%) lines from NSIC Rc 222 were tolerant to drought, salinity, and submergence. These lines warrant confirmatory performance on-site under field conditions to evaluate their yielding ability under abiotic stress of interest.

Mass screen for abiotic stresses of early segregating populations at F_2 and $F_{2:3}$ identified putative tolerant plants which were grown to maturity, and seeds retrieved for use in further evaluation and development of multi-abiotic stress tolerant breeding lines.

Multi-environment and Adaptability Tests of Breeding Lines in Drought-Prone Rainfed Lowland

JM Niones, NV Desamero, and VAC Marcelo

Rainfed lowland rice environment is more complex than most other rainfed crops because it is grown in bundled fields without water control leading to submergence and/or drought stress. Also, genotype by environment interaction complicates the selection of superior genotypes within such a diverse environment. Thus, early MET of fixed lines are economical and one of the best strategies in developing location-specific varieties in the target population environment (TPE). This study aimed to improve rice productivity in selected TPE by evaluating the performance of elite lines across various testing environments and identify lines with stable yield performance across these diverse testing sites. Forty-three elite lines and five check varieties were evaluated under a rainfed lowland ecosystem in the PhilRice CES and three PhilRice branch stations: Batac, Negros, and Midsayap. Yield data from Batac station is currently being processed and hence was excluded from the analysis. GxE analysis identified two mega environments, the 1st mega-environment is the PhilRice CES, while the 2nd environment is succeeded by the Murcia and Midsayap sites. NSIC Rc 222 recorded the highest yield across sites at 2.5t/ha and is most adapted to the 2nd mega-environment with a yield of 3.2t/ha, while PR38537-B-2-2-1 (RF-37) recorded a yield of 3.2t/ha in the 1st mega-environment. PR38537-B-2-6-1 (RF-31), PR48425-ACRL-2013DS 2-6-2 (RF-36), and PR38537-B-7-3-2 (RF-45) were identified as high yielding and stable using yield stability index and AMMI stability value.

Combining Submergence, Stagnant and Salinity Tolerance into High Yielding Rice Varieties

NV Desamero, RGB Cadiente, RMM Sumabat, RD Buluran, and KRP Balmeo

One of the ill effects of climate change (CC) is the projected one-meter rise in sea water level, which will salinize through intrusion the vast coastal rice areas. Water overflow and excessive rainfall may result in flooding of low-lying and with poor drainage rice areas. The compound effects of salinity and flooding aggravate the low productivity in CC-vulnerable rice areas. The use of varieties with tolerance to stresses caused by salinity and flooding is a viable and sustainable adaptation mechanism. Five crosses were made in 2019 DS combining salinity-submergence tolerance into high yielding varieties, for establishment in 2020 DS.

The breeding activity generated 76 elite RILs from 23 crosses and 34 tissue cultured- and seed mutation-derived lines which were evaluated in 2019 DS for field performance under managed submergence stress and non-stress conditions. FR13A, IR64-Sub1, and PSB Rc 68 were the resistant checks, while IR42 and IR64 were the susceptible checks used in the trial. PR47476-B-BIs2-2-2-Sub1 recorded yield under non-stress condition of 6.5t/ha and 4.3t/ha at submergence stress condition and had the lowest percentage yield reduction and highest STI value.

Breeding for Heat-Tolerant Rice

NL Manigbas, LB Madrid, and FB Enriquez

Due to climate change, air temperature is continuously rising. Because of this, rice becomes vulnerable to heat stress especially at 35°C during reproductive stage. High temperature leads to incomplete fertilization that results in increased spikelet sterility and eventually decreased yield by 15%. Breeding for heat-tolerant rice in the Philippines was implemented to develop rice genotypes that can tolerate and adapt to high temperatures. Breeding lines generated were screened, evaluated, and selected in Cagayan and Nueva Ecija where temperatures can reach up to 38-40°C. Breeding lines were planted in staggered manner so that flowering will coincide with the hottest period of the year, which is between April and May. Micro-meteorological Instrument for Near Canopy Environment in Rice (MINCER) and Automatic Weather Station were used to mainly monitor temperature and relative humidity. High temperature tolerance

PROJECT 4

was evaluated based on spikelet fertility. Hundreds of breeding lines were screened under high temperature conditions in Nueva Ecija and Cagayan. Out of these lines, 75% of the selected early segregating populations and 78.5% of the advanced lines had $\geq 60\%$ spikelet fertility. Uniform lines had yield range of 5.5-8.8t/ha under high temperature condition and spikelet fertility of 60.1-85.7%. Fifteen promising lines were submitted to MET for 2020 evaluation and another six lines for NCT.

PBBD Research and Analytical Laboratory Systems and Maintenance

FP Waing

To fast-track and increase precision of breeding and line development, laboratories have served varied support functions in the breeding operation. As these activities require high-throughput equipment and accurate measurement, there is a need to continuously improve and maintain the current laboratory facilities through preventive maintenance, repair and services, and calibration. Thus, this project aimed to provide assistance in the improvement of the laboratory facilities for better quality research output, establish equipment and chemical inventory database and other IMS related laboratory management system, and ensure the proper acquisition of chemicals and equipment and disposal of chemical wastes and unserviceable equipment.

Basic Seed Production

EV Santiago

Basic seed production is an integral part of varietal improvement and it is an inherent support to the NCT. It is the main source of quality seeds for the performance trials and breeder seed of the National Seed Industry Council (NSIC). This project aimed to generate passport data of promising NCT entries; ensure availability of pure, viable seeds as initial breeder seed stock for newly released variety; provide sufficient panicles of nucleus seed for breeder seed production; and provide breeder seed requirements of Business Development Division (BDD) for distribution under RCEF and meet the target passing rate as stated in the Strategic Plan in accordance to NSQCS seed certification and standards. Basic seed has three major studies: (1) Distinctness Uniformity Stability Test (DUST), which serves as the quality control of all varieties released through the NCT to ensure purity of all varieties released since 1990 up to present for seed production ; (2) Nucleus seed as source of breeder seed production facilitates the rapid release and continuous availability of the original phenotype; and (3) Breeder Seed Production, wherein PhilRice CES serves as the main source of planting materials for seed production of BDD and Branch Stations, National, Regional, Provincial, and Accredited Seed Growers, and Universities. Foundation and registered varieties developed and bred by PhilRice, UPLB, and IRRI were reproduced in larger areas by PhilRice through BDD from PhilRice CES and Branch Stations located in Luzon, Visayas, and Mindanao. Currently, varieties developed and bred by PhilRice, UPLB, and IRRI are grown in the PBBD through the Distinctness Uniformity and Stability Test (DUST).

Distinctness Uniformity and Stability Test

JF Pariñas, CA Oliva, and TF Padolina

Distinctness Uniformity and Stability Test (DUST) serves as the quality control to generate passport data of promising NCT entries and ensure availability of pure and viable seeds as initial breeder seed stock of released varieties. All entries in the NCT under irrigated lowland, special purpose, upland, rainfed, and adverse ecosystems are evaluated through DUST for two WS and one DS to establish the identical characteristics of each promising line prior to release. Agro-morphological and other 42 agronomic traits using the IRRI Descriptor for Rice,

Union for the Protection of New Varieties of Plants (UPOV) guidelines, and ISTA at all growth stages were gathered to identify the distinguishing characteristics, uniformity, and stability of the promising lines. The PVP National and/or International Standards was also used to harmonize with the existing entries. A total of 515 entries from different ecosystems were characterized in 2019 (263-DS and 252-WS). Passport data of these lines were generated following the 56 UPOV and IRRI Descriptor for Rice for quantitative and qualitative traits in all growth stages. The passport data will serve as reference once the line is approved and released as a new variety.

Nucleus Seed Production

OE Manangkil, WV Barroga, MT Garcia, and SB Estrada

Nucleus seed is the highest form of seed coming from breeders and are later used to reproduce breeder and foundation seeds. Farmers can access certified seeds produced by accredited seed growers. This study provided sufficient panicles of nucleus seed for Breeder Seed Production (BSP). One hundred gram seed stock of each of the recommended rice varieties were withdrawn from the storage. At maturity, individual uniform and identical plants were selected and five panicles each from the selected plants were processed properly. Eight hundred panicles for the highly demanded varieties and 400 for other varieties per season were submitted for BSP. In 2019 DS, 122 varieties were established and 31 varieties with 13,600 panicles were submitted. Fifty-two varieties were established in 2019 WS, 22 of which have 10,800 panicles, together with 14 varieties produced in 2019 DS, will be established in 2020 DS for BSP. Varieties submitted for 2020 DS are the required varieties to be produced under the seed component of the Rice Competitiveness Enhancement Fund – Seed Program (RCEF-Seed).

Breeder Seed Production

EV Santiago, RC Bracerros, TF Padolina, and OE Manangkil

This study aimed to provide the breeder seed requirements of the BDD and the branch stations, for distribution under RCEF-Seed, and meet the target passing rate as stated in the Strategic Plan in accordance to NSQCS seed certification and standards. Newly released varieties were produced in the second season after approval. Highly demanded varieties per region were recommended by the Rice Seed System and BDD and were considered in the seed production targets. Panicles from nucleus seed production plots were used as planting materials. All panicles were subjected to DNA Analysis 2-3 weeks before seeding to check the

authenticity of all planting materials. Extra panicles were stored in cold storage for further planting for the next cropping seasons. Eight hundred panicles for highly demanded varieties and 400 pre-germinated panicles of other varieties were sown directly on wetbed, with 350 m² allocated per variety. List of varieties were submitted to the NSQCS 20 days after transplanting for field inspection and certification following the seed certification standards. For irrigated lowland varieties passing rates for breeder seed of 70% for irrigated lowland and 60% for other ecosystem varieties.

To ensure genetic purity of rice seeds, roguing was done from vegetative to maturity stage to facilitate removal of all possible mixtures and diseased plants before harvesting. Crops were harvested when 85% of the grains were golden yellow. The ideal moisture content for harvesting range from 20- 24%. Cut panicles were taken out of the plot to minimize drop off seeds during threshing operation. Threshing was done immediately after harvesting to maintain quality of the seeds. The seeds were dried to 11-14% Moisture Content (MC) after threshing, as one or two days of seed storage without proper drying will spoil the seeds, resulting to seed discoloration and reduced seed viability and vigor. Dried seeds were cleaned using blowers or grain cleaners to remove empty, light, and diseased seeds, weed seeds, soil particles, and other contaminants. Breeder seeds were packed in laminated sacks (5 and 10 kg/pack). Four sacks of 5kg/pack represent Lot-1A, 1B, 1C, and 1D, and the remaining seeds were 10kg/pack (Lot-2A, 2B, 2C, etc). The seeds for immediate planting or distribution were stored in an ordinary room condition. However, seeds for planting in the next season were stored in an air-conditioned room with dehumidifier in order to maintain viability and vigor.

In 2019, 66 varieties were planted in the seed production area of PBBD, with a total yield of 13,730kg for both irrigated and adverse environments. During 2019, efficiency of 72.02% and 87.125% in DS and WS, respectively, were obtained from irrigated and adverse varieties based on the results of certification of the NSQCS. The seed production component is intended to speed up the identification and utilization of genotypes that can contribute to removing rice production constraints.

Abbreviations and acronyms

AYT - Advanced Yield Trial	GIS - Geographic information system
ABE - Agricultural and Biosystems Engineering	GEMS - Germplasm Management System
AEW - Agricultural Extension Worker	GAS - Golden apple snail
ATI – Agriculture Training Institute	GL - Grain length
AESA - Agro-ecosystem Analysis	GQ - Grain quality
AC - Amylose Content	GW - Grain Weight
BLB - Bacterial Leaf Blight	GY - Grain Yield
BLS -Bacterial Leaf Streak	GLH - Green Leafhopper
BCA - Biological Control Agent	GOT - Grow Out Test
BS - Breeder Seeds	HR - Head Rice
BPH -Brown Planthopper	HRA - Heat Recovery Attachment
BPI - Bureau of Plant Industry	HIPS – Highly-intensified Production System
CGMS - Cytoplasmic Genic Male Sterility	HQS - High-quality Rice Seeds
COF - Commercial Organic Fertilizer	HON - Hybrid Observational Nursery
CDA - Cooperative Development Authority	HPYT - Hybrid Preliminary Yield Trial
DAS - Days After Sowing	ICT - Information and Communication Technology
DAT - Days After Transplanting	IEC - Information Education Communication
DF - Days to Flowering	IBNM - Inorganic-based Nutrient Management
DM- Days to Maturity	ICM - Integrated Crop Management
DAR - Department of Agrarian Reform	IPM - Integrated Pest Management
DA-RFOs - Department of Agriculture-Regional Field Offices	JICA - Japan International Cooperation Agency
DoF - Department of Finance	IRRI - International Rice Research Institute
DOLE - Department of Labor and Employment	IA - Irrigators’ Association
DTI - Department of Trade and Industry	KP - Knowledge Product
DSR - Direct-seeded Rice	KSL - Knowledge Sharing and Learning
DS - Dry Season	LCC - Leaf Color Chart
FBS – Farmers’ Business School	LFT - Local Farmer Technicians
FC - Farmers’ Cooperative	LGU - Local Government Units
FSM - Farming Systems Models	LPS - Low Pressure Steam-operated
FAA - Fish Amino Acid	SB - Stemborer
FGD - Focused Group Discussion	LE-CYPRO - Lowland ecotype Cyperus rotundus
FSP - Foundation Seed Production	MFE - Male Fertile Environment
FRK - Farm Record Keeping	MSE - Male Sterile Environment
GABA - Gamma-aminobutyric Acid	MAS - Marker-assisted Selection
GT - Gelatinization Temperature	MRL - Maximum Root Length
GAD - Gender and Development	MR - Milled Rice
GYT - General Yield Trial	MER - Minimum Enclosing Rectangle
GCA - Genetic Combining Ability	MOET - Minus-one Element Technique
	MC - Moisture Content

MAT - Multi-Adaptation Trials	RTV - Rice Tungro Virus
MC RTP - Multi-crop Reduced Till Planter	RBFHS - Rice-based Farming Household Survey
MET - Multi-environment Trial	KQ - Kernel Quality
MYT - Multi-location Yield Trial	SV - Seedling Vigor
NAAP - National Azolla Action Program	ShB - Sheath Blight
NCT - National Cooperative Test	ShR - Sheath Rot
NFA - National Food Authority	SMS - Short Messaging Service
NRAM - National Rice Awareness Month	SNP - Single Nucleotide Polymorphism
NSIC - National Seed Industry Council	SWRIP- Small Water Reservoir Irrigation Project
NSQCS - National Seed Quality Control Services	SRB - Stabilized Rice Bran
N - Nitrogen	SUCs - State Universities and Colleges
NBSP - Nucleus and Breeder Seed Production Project	SB - Stem Borer
NFGP - Number of Filled Grains Panicle	TESDA - Technical Education and Skills Development Authority
ON - Observation Nursery	TDF - Technology Demonstration Farm
OSIS - One Stop Information Shop	TRV - Traditional Rice Varieties
OBNM - Organic-based Nutrient Management	TOT - Training of Trainers
PL - Panicle Length	TPR - Transplanted Rice
PW - Panicle Weight	URBFS - Upland Rice-Based Farming
PVS - Participatory Varietal Selection	WS - Wet Season
PWD - Person with Disabilities	WCV - Wide Compatibility Variety
PhilMech - Philippine Center for Postharvest Development and Mechanization	YSB - Yellow Stemborer
PRISM - Philippine Rice Information System	
PhilRice - Philippine Rice Research Institute	
PSA - Philippine Statistics Authority	
PTC - PhilRice Text Center	
P - Phosphorus	
PVS - Plant Variety Selection	
K - Potassium	
QTL - Quantitative Trait Loci	
RCBD - Randomized Complete Block Design	
RSP - Registered Seed Production	
RBB - Rice Black Bug	
RCEF - Rice Competitiveness Enhancement Fund	
RCEP - Rice Competitiveness Enhancement Program	
RCM - Rice Crop Manager	
RHGEPS - Rice Hull Gasifier Engine Pump System	
RPH - Rice Planthopper	
RSTC - Rice Specialists' Training Course	

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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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