Quality Rice. Quality Life.

2017
National Rice R&D
Highlights

CROP BIOTECHNOLOGY CENTER

Philippine Rice Research Institute
Central Experiment Station
Maligaya, Science City of Muñoz, 3119 Nueva Ecija

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Crop Biotechnology Center

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Executive Summary

The Crop Biotechnology Center was established through Administrative Order 21 to implement a rationalized, effective, and efficient AgBiotech R&D agenda for the Department of Agriculture. It was created to generate improved agricultural technologies, productivity, and commercial potential value. The Center aimed to contribute to national food self-sufficiency and to contribute in reducing malnutrition. Specifically, it aimed to 1) increase productivity, 2) improve quality of rice (value-adding), and 3) enhance varietal development for grain quality and abiotic and biotic tolerance.

The Center implemented two projects on rice, one of which is continuing, with studies dealing with molecular biotechnology techniques and approaches to improve research results. The project on gene discovery and marker development for agronomically important traits examines the genetic composition of rice to accelerate genetic dissection of simple or complex traits (such as agronomic, quality, or resistance to biotic or abiotic stresses) and other beneficial organisms to assess species identity. Another project involved the molecular characterization, diversity analysis, and utilization of crop germplasm. One of its studies aimed to identify a set of sequence tandem repeat (STR) markers for rice identification and develop allele ladders that will be used in standard profiling of cultivars.

The Center established the protocols and methods for DNA fingerprinting and rice varietal identification—a major accomplishment in rice breeding in the Philippines. Protocols for DNA extraction, gene amplification, and DNA sequencing were also started with available specimens for bacteria, blue-green algae, and fungi.

Quantitative trait loci (QTLs) associated with root plasticity were also identified at different soil depths under soil moisture fluctuation stress. These are useful in improving rice adaptation and yield under rainfed lowland production systems. The whole genome of one rice mutant, which can be used as source of BLB resistance, was also sequenced. Several PTRV accessions were also identified as potential sources of either Glh14 or tsv1 genes, or, possibly, other resistant genes aside from the two existing genes. For grain quality traits, QTLS associated with crack resistance have been identified and fine mapping is ongoing. Likewise, a marker system for bacterial leaf blight and rice tungro disease in hybrid rice was also established. Markers are important because it give dimensions to breeding and marker-aided selection that can reduce the time span of developing new and better varieties containing the traits of interests.

The Center made big leaps in rice research on identifying novel QTLs and/or genes relating to, among others, crack resistance, yield under drought, root plasticity and functional stay green under water stress, pest and disease resistance, qrain quality, which are being used for developing genetic markers for improving plant performance and quality under favorable and unfavorable production environments, which is very essential in plant breeding.

I. Molecular Characterization, Diversity Analysis, and Utilization of Crop Germplasm

Verna G. Dalusong

Molecular characterization and diversity analysis are important to design effective breeding strategies and obtain yield advantage particularly under biotic and abiotic stress environments. This project has two major studies that generally aimed to utilize the availability of diverse crop germplasm. It examined important agronomical traits applying new biotechnology tools necessary to help advance the crop breeding program.

DNA fingerprinting using molecular tools is important to establish the genetic identity of crop germplasm. Traditionally, agro-morphological characterization based on distinctness, uniformity, and stability (DUS) is being done to establish the genetic characteristics of a cultivar. With the evolution of methods, DNA fingerprinting has become significant particularly in cases of intellectual property rights or ownership including plant variety protection (PVP). In rice, sequence tandem repeat (STR)-based DNA profiling system is being developed following the guidelines of the Scientific Working Group on DNA Analysis Method (SWGDAM). This study hoped to identify a set of STR markers for rice identification and develop allele ladders that will be used in standard profiling of cultivars. It established several DNA extraction protocols that can be used to analyze different parts of rice plant for downstream molecular study and DNA markers, which can be used for establishment of genetic identity, diversity, and genetic characterization. Study output provided a system for rice varietal identification and a database, which is important in establishing the genetic identity of rice varieties and resolving varietal dispute.

The second study focused on the genetic characterization using induced mutation by chemical or gamma radiation, which will enable researcher to study the variation and eventually discover novel genes and traits relevant in rice breeding. This study employed the latest technology in genetic and molecular characterization including molecular marker technology, whole genome sequencing, and use of bioinformatics in conjunction with field testing and disease screening to locate the exact

position of gene and variation of sequences of resistance against bacterial leaf blight, colored pericarp, tungro, and drought.

Establishment of Rice STR DNA Profiling System

Verna G. Dalusong, LH Santos, LM Perez

DNA-based cultivar identification has a great potential in resolving issues on plant variety protection or breeder's right. This method provides unique DNA profile that can serve as genetic identity of the cultivar being explored. Numerous studies on rice DNA fingerprinting and analysis have been done using different types of DNA markers. However, none of these studies has focused on establishing a DNA-based method of cultivar identification based on the Scientific Working Group on DNA Analysis Method (SWGDAM) guidelines (SWGDAM, 2004). SWGDAM is the body that proposes and recommends guidelines for working forensic DNA laboratories. With the advent of intellectual property rights (IPR) and protection of ownership, there is a need to establish methods for the efficient identification of rice varieties using parameters or procedures that can be used as legal evidences in court proceedings.

This study aimed to develop STR DNA profiling system for rice based on SWGDAM guidelines and to create genotype database that will be used as the reference population for comparative purposes. STR markers were selected based on applicable criteria set by the SWGDAM guidelines. Polymorphic STR markers identified from evaluation were subjected to sensitivity, stability, and species specificity. Two hundred ninety-nine STR markers were evaluated in terms of polymorphism information content (PIC), allelic frequency, genetic diversity, and heterozygosity. Forty-one markers spanning the 12 rice chromosomes were selected with 3.4 average number of alleles and PIC values ranging from 0.1889 to 0.7568. The markers showed 0.9609 genetic diversity index indicating a high level of genetic variation detected in the rice cultivars evaluated in the study.

To validate the procedures and establish the methods for DNA analysis, different methods of DNA extraction and tissue sources were evaluated for DNA yield and purity. Results showed that leaves, stems, rice straw, rice hull, seeds, milled rice flours, and boiled rice can be sources of DNA for analysis. Sensitivity and stability tests showed that the selected STR markers produced DNA bands in all tissue sources with DNA templates ranging from 5.0 to 10 ng/µl. DNA bands were faint and were not detected in PCR reactions containing DNA templates lower than 2.5 ng/µl. Meanwhile, 10 ng/µl was found optimum for PCR analysis. Species specificity test showed that STR markers generated PCR amplifications in both target (Oryza sativa) and non-target DNA sources including wild rice species, weeds, corn, rats, and human. The alleles produced and the information

obtained from the analysis is very important in assessing contamination from unknown sources.

Genetic and Molecular Characterization of Rice Mutants and Introgression Lines
Reynante Ordonio, X Caguiat, RT Miranda, RT Aguilar, JC Yabes

Rice mutants are regarded as powerful tools for genetic research. This is because their phenotypes can explain the function of their mutated gene, and at times, such mutants can be directly used for breeding. This study characterized the genetic and molecular profile of rice mutants, analyzed the sequence and expression of their mutant alleles, and identified their molecular function and mechanism. Interesting lines were screened from a gamma ray-induced mutant population derived from NSIC Rc 144, which included two Short lesion (SL) mutants (MSL37 and 40; sister lines) that both showed resistance to BLB. Aside from phenotyping for BLB resistance, DNA sequence of MSL40 was compared with the source variety (NSIC Rc 14), and found that they differ in the promoter region of the gene OsSweet14. Fine sequencing the OsSweet14 promoter in NSIC Rc 144, MSL37 and MSL40 showed that the SL lines had a 2-bp insertion, which lengthens a conserved tandem repeat. In literature, such changes in tandem repeats usually affect gene expression; therefore, necessitating further study of OsSweet14 function in the SL mutants.

II. Gene Discovery and Marker Development for Agronomically Important Traits
Arlen A. Dela Cruz

This project aimed to accelerate the genetic dissection of simple or complex traits and various genetic compositions and find nucleotide polymorphisms in rice and other beneficial organisms from the rice environment that are responsible for phenotypic variations. To help facilitate the advancement of plant breeding, studies under this project elucidated the molecular genetics of traits toward identification of important genes or quantitative trait loci (QTLs) in root plasticity in response to drought stress, fissure/crack resistance, functional stay green trait, salinity and drought tolerance, tungro resistance, and TGMS. Using genomic and molecular information, this project will support rice breeding towards development of rice varieties with enhanced stress and disease resistance, improved yield potential, and superior grain quality. Underlying candidate genes will be marked out and corresponding molecular markers and pre-breeding rice lines for marker-assisted breeding will be developed. The project also worked

on establishing genetic profiles of selected beneficial organisms useful for development of agricultural products such as biofertilizer or biopesticide.

Validation and Fine-Mapping of Root Plasticity QTLs on Lateral Root Development in Response to Water Stress in Rice
Jonathan M. Niones, RR Suralta, MCJ Cabral, MDM Banting, LM Perez, AS Cruz

Series of studies have shown that promoted lateral root (LR) development as key traits for maintaining root system, dry matter production and yield under soil moisture fluctuations and progressive drought stresses contributed to greater water uptake and biomass. Many analyses of QTLs associated with LR production have been reported. The ultimate application of this QTL approach is the development of rice cultivars suitable for soil moisture fluctuating and drought-prone environments via marker-assisted selection (MAS). Therefore, this study aimed to localize the candidate genomic region of QTLs associated with L-type lateral root development through fine-mapping. Specifically, it aimed to develop recombinant inbred line (RIL) mapping population of DHL96 backcrossed with IR62266 and CSSL47 introgressed into IR64 (F3 and BC1F2) and to develop RIL mapping population of DHL96 and CSSL47 crossed with NSIC Rc160 as background. Two hundred thirty-eight BC1F5 lines of IR62266*2/DHL96 and 160 BC1F5 lines of Nipponbare*2/CSSL47 and their respective parents were evaluated for root phenotype using rootbox method. The progenies were subjected to transient waterlogged to drought (W-D) or soil moisture fluctuation (SMF) stress. For control, the parents were grown to continuously waterlogged (CWL) treatment. In SMF, the parents were waterlogged from 3 to 14 DAS. Thereafter, water was drained and allowed to dry up to 10% SMC and maintained at 45 DAS. Watering was done every two days or whenever necessary to maintain the 10% SMC. The three lines identified from the backcross IR62266*2/DHL96, which have increased in shoot biomass production were Line 221, Line 185, and Line 236 relative to IR62266 under SMF. The Line 236 had 60.3% increase in TRL relative to CWL (IR62266) brought about by the promotion of major root components traits such as number of lateral root (LR), total lateral root length (TLRL), and total nodal root length (TNRL). For the 160 BC1F5 lines of Nipponbare*2/CSSL47, only Line 63 had comparable shoot biomass production to Nipponbare under CWL and CSSL47 under SMF conditions.

Detection and Validation of QTL for Functional Stay Green Traits for Rainfed Lowland Environment in Rice

Jonathan M. Niones, RR Suralta, MCJ Cabral, MDM Banting, LM Perez, AS Cruz

Stay green trait is one of the most effective drought resistant traits suggested to be related with leaf traits and roots that absorb water or nutrients of dehydrated plants. Post flowering drought response is associated with stay green, which is basically the retention of green leaf area at maturity (GLAM). Maintenance of stay green trait during grain-filling stage under soil moisture-deficit constitutes an important component of drought tolerance. Functional stay green can be of huge importance for it has been correlated with higher grain filling and increased yield under post anthesis drought. This study aimed to develop doubled-haploid mapping population from the cross NSIC Rc160/Kutsiyam. Specifically, it aimed to identify a DHL with the highest stay-green characteristic and a QTL associated with functional stay-green trait. There were 275 F5 lines generated from the cross NSIC Rc160/Kutsiyam evaluated in the field for initial agronomic data. Each line was planted in 2R x 15H and observed for heading days to determine the maturity, plant height, and tiller. The occurrences of other traits such as lodging, pest, and disease resistance in a certain season were also noted. Most of the progenies were medium maturing, indicating wide variation as the two parents were extremely different in maturity. Generally, most of the lines were in between the height of both parents and have improved tillering ability. Three markers (RM519, RM13502, and RM12460) identified polymorphic were used on mapping population of NSIC Rc160/Kutsiyam. Result showed that there were 23 lines (8.36%) heterozygous in RM1519; 64 lines (23.3%), RM13502; and 7 lines (2.54%), RM12460.

Evaluation of Drought Tolerance QTL Effect in Adapted Genetic Background

Joanne D. Caguiat, FP Waing, AA Palanog, JOS Enriquez, JC Santiago, RA Millas, JV Galapon, XGI Caguiat

Drought stress is still one of the main constraints in global rice production. Three QTLs, qDTY2.2, qDTY2.3, qDTY4.1, and qDTY12.1 were mapped and were determined to be linked to grain yield under drought stress. These four QTLs are being pyramided into popular Filipino varieties, NSIC Rc 160 and NSIC Rc 222, through marker-assisted breeding to develop drought-tolerant varieties with desirable yield and grain quality. In 2017, 123 BC1F2 lines and 27 BC1F5 populations were selected based on molecular genotype data for qDTY2.2, qDTY2.3, qDTY4.1, and qDTY12.1 and phenotypic acceptability and similarity to the respective recurrent parents, NSIC Rc 160 and NSIC Rc 222. Advanced lines generated in this study were screened at PhilRice Isabela and PhilRice Negros. Under reproductive drought stress condition at PhilRice Isabela, PR47201-A102A-29-79-B had the highest yield of at 2.0 t/ha among PR47201 population while the check NSIC Rc 222 only yielded 0.76 t/ha. PR47202-A103A-17-122-1 yielded 2.2 t/ha among PR47202 population while check NSIC Rc 160 yielded only 1.86 t/ha. At PhilRice Negros, PR47201-A102A-3-47-1 had the highest yield at 2.92 t/ha while the check NSIC Rc222 yielded only 0.54 t/ha. For PR47202 population, the highest yielder among entries was PR47202-A103A-18-285-1 with 2.67 t/ha while the check NSIC Rc 160 yielded only 1.70 t/ha. These lines will be established in DS 2018 for further evaluation under reproductive drought stress screening and non-stress set-up at PhilRice Negros. High yielding lines with drought tolerance may be used to combat drought stress without reduction in yield; thereby, helping achieving self-sufficiency and helping farmers increase their income.

Novel Gene Identification for Rice Crack Resistance

Verna G. Dalusong, RP Mallari, TE Mananghaya, APP Tuaño, LM Perez, BO Juliano

Head rice recovery after milling is affected by several factors such as chalkiness, moisture content, and cracking or fissuring of rice grain. Proper post-harvest practices such as drying, storage, and milling can prevent losses due to broken grains. Increasing the resistance to grain cracking by introgression of the gene that controls the trait will also increase the head rice recovery. Recently, 7 QTLs were identified from PSB Rc 52/NSIC Rc 160 located on chromosomes 2, 3, 7, and 9, and one QTL identified from PSB Rc 38/NSIC Rc 160 on chromosome 8. QTLS found on chromosomes 2, 3, and 7 are being fine-mapped to identify the possible gene(s) involved in crack resistance. Activities on genotyping and phenotyping of F2 plants to verify the QTLs in multiple populations are being conducted. For fine-mapping, genotypes of 385 PSB Rc 52/NSIC Rc 160 F2 plants on 66 of the 180 polymorphic SSR markers were obtained. Genotype-phenotype linkage analysis will be implemented following the retrieval of phenotyping results. This will be done to verify the identified QTLs that control the cracking of rice grains and to increase head rice recovery through molecular breeding.

QTL Mapping Analysis with Emphasis on Root Plasticity Traits under Soil moisture Fluctuation Stress

Jonathan M. Niones, RR Suralta, MCJ Cabral, MDM Banting, AS Cruz, LM Perez

Fluctuation of soil moisture and progressive drought at varying degrees are regularly recurring stresses affecting rice production. Rice fields are usually exposed to this continuous cycle of soil moisture fluctuation due to erratic rainfall pattern. Studies have shown that variability in soil

moisture condition adversely affects shoot and root growth and functions on rice crop. This study generally aimed to develop the recombinant inbred lines (RILs) with root plasticity traits in rice under progressive drought and fluctuating soil moisture conditions (transient waterlogged to drought and vice versa). It aimed to develop RIL populations using the high root plasticity genotypes CSSL47 x KDML105 with specific component of root plasticity traits. It also identified the QTL with associated genomic regions and markers that trace plastic root traits. Mapping populations derived from CSSL47 x KDML 105 were evaluated for root phenotype using rootbox system in transient waterlogged to drought (TW-D10) treatment while the parentals were subjected to both transient waterlogged to drought (TW-D10) and continuous waterlogged (CWL). In TW-D10 treatment, root boxes were subjected to waterlogging from 3 to 17 DAS and drained after until it reached 10% soil moisture content (SMC, w/w). Five lines (4.34%) were noted to have good performance among the 115 evaluated lines relative to neither of the parents except in KDML105 under CWL. Lines 81 and 67 had the highest biomass production with 2.26 g and 2.24 g, respectively. Generally, plant statures of the progenies resemble CSSL47. Meanwhile, about 58% of the lines (71-80cm) were intermediate to the height of both parents. Tiller count ranging from 4-7 under water stressed can also be a good indicator that the roots can effectively transport water from deeper soil layer.

Association of GLH and RTSV Resistance to Glh14, tsv1, and eIF4G SNP Type in Selected Popular Philippine Traditional Rice Varieties and Mapping of Novel GLH and RTSV Resistance Genes

Arlen A. dela Cruz, MJC Duque, MM Rosario, RT Aguilar

Traditional rice varieties have higher nutritional values, aromatic, and tasty compared with modern rice varieties. Many are also known to have nutritional and medicinal properties. Though these varieties are generally low-yielding, these are becoming major targets in rice varietal improvement programs. As they are adapted to different agro-ecological conditions, these varieties are endowed with various important traits necessary for crop improvement. Although there are Philippine traditional rice varieties (PTRVs) initially observed with tungro resistance, breeders hesitate to use them in breeding because the useful genes were yet to be determined. Thus, this study generally aimed to diversify sources of tungro resistance genes useful for rice varietal improvement and increase the utilization of PTRVs. Specifically, the study aimed to identify potential sources of GLH, RTSV and/or RTBV resistance genes among PRTVs through systematic examinations of the mechanisms involved. First, varieties were screened for presence of known tungro resistance locus/gene by polymerase chain reaction (PCR), which has led to identification of PTRVs that can serve as alternative sources of Glh14 and tsv1. Results showed that though the tungro resistance

observed among the PTRV were not as strong as in ARC1554, there were accessions that displayed resistance either to GLH, RTSV, or RTBV. These are promising materials for mapping novel tungro resistance genes. By mapping these important genes and pyramiding them into rice plants by marker-assisted selection, rice varieties with durable tungro resistance can eventually be developed for deployment to tungro endemic areas.

However, some PTRVs carrying the tsv1 resistant allele exhibited susceptible reactions to RTSV. To elucidate the ambiguous relationship observed between the molecular marker RM5495 and expression of the desired RTSV resistance, the involvement of another gene coding for a translation initiation factor (eIF4G) was further examined among selected plants. Upon looking at the sequence variants among RTSV-susceptible plants, these were found similar to the SNP type in TN1. It is therefore concluded that RM5495, though had successfully co-segregated RTSV-resistant and RTSV-susceptible plants derived from Indian rice cultivar ARC11554, is not working in some PTRVs. Thus, finding molecular markers appropriate for PTRVs is deemed necessary. To achieve this, detailed examination of gene/s involved and interactions of genes is needed to determine the linkage between markers and traits.

Establishment of Marker System in Developing Thermo-Sensitive Genic Male Sterile (TGMS) Lines with BLB and RTD Resistance

Ronalyn T. Miranda

Hybrid rice can increase production even in less land as it can yield 15-30% higher than inbred varieties. Two-line system or the environment sensitive genetic male sterility (EGMS) is simpler and more efficient hybrid rice seed production and TGMS is one system that is being used in hybrid rice production. However, this technology is faced with the two major rice diseases in the irrigated lowland environment, which may cause significant yield loss: bacterial leaf blight (BLB) and tungro. Resistance genes to these diseases have been known to be linked with molecular markers (such as Xa4, Xa7 and Xa21 for BLB, and RM5495 and RM8213 for tungro) facilitating easier and faster introgression to susceptible varieties through marker-assisted breeding. This study aimed to establish a marker system in developing new improved TGMS lines with resistance to BLB and tungro. In 2017, three generation from cross combination of PRUP 102 S (M20) x Line 27/IR58025B, PRUP 101 S (M19) x Line 27/IR58025B, and PRUP 102 S (M20) x Line 27/IR68897B were subjected to disease (BLB and RTD resistance) screening and pollen sterility assay, which resulted in the selection of 66 plants from six lines with resistance to tungro and BLB and identified sterile in initial evaluation. For the detection of TMS genes conferring pollen sterility, three markers, RM3351, 4039-2,4039-1, were identified to have a distinct banding pattern detected in sterile line of M19 (PRUP 101 S). This

is being validated for their usefulness in tracking down introgressed TGMS genes in succeeding progenies of generated crosses with PRUP 101 S (M19) background through marker assisted selection. Twelve BC1F1 crosses were produced and forwarded for generation advance.

DNA Fingerprinting of Beneficial Organisms for Identification and Product Quality Assessment

Trinidad C. Fernando, AA dela Cruz, RL Ordonio, RT Aguilar, JA Cruz, BM Tabudlong, HX Truong

Biological materials are used intensively in biological and agricultural research. The use of molecular techniques like DNA fingerprinting is still proven to effectively discern the identity of organisms at the DNA level. At PhilRice, beneficial microorganisms intended for soil and plant health enhancement (bacteria) and control of rice pests and diseases (fungi) are being tested for their efficacy. However, the procedure for production of bioinoculants involves identification and mass culture of effective organisms, while handling and processing of mixtures is a critical factor that determines its purity. Moreover, PhilRice is propagating Nostoc commune, a cyanobacteria common to rice paddies, which can be used as food or feed. However, certain strain was reported to potentially cause neurotoxin. Thus, this study generally aimed to safeguard the purity of PhilRice effective organism collections useful for agricultural bioinoculant production and ensure their availability for future use. The protocols for DNA extraction, gene amplification, and DNA sequencing were initially done with the available specimens such as bacteria, fungi, and cyanobacteria. Apparently, the results of identification of species using BioLog Gen III System and DNA fingerprinting showed disagreement on the bacterial isolate pre-identified as B. cibi. Basic local alignment search tool (BLAST) analysis showed that it was 99% identical to partial sequence of Alcaligenes faecalis gene while only 78% similar with B. cibi 16S rRNA gene. Meanwhile, the identity of all other organisms established through use of BioLog Gen III System matched with the results of DNA fingerprinting. Results of this study will be useful in decision-making as this will ensure that only effective organisms of true identity will be incorporated in bioinoculant products while the most suitable strain of N. commune for large-scale on-farm production will be properly identified. This study will further provide a clearing house for ensuring the quality of products and bioinoculant that will soon be released.

Abbreviations and acronymns

ABA – Abscicic acid
Ac – anther culture
AC – amylose content
AESA – Agro-ecosystems Analysis
AEW – agricultural extension workers
AG – anaerobic germination
AIS – Agricultural Information System
ANOVA – analysis of variance
AON – advance observation nursery
AT – agricultural technologist
AYT – advanced yield trial
BCA – biological control agent
BLB – bacterial leaf blight
BLS – bacterial leaf streak
BPH – brown planthopper
Bo - boron
BR – brown rice
BSWM – Bureau of Soils and Water Management
Ca - Calcium
CARP – Comprehensive Agrarian Reform Program
cav – cavan, usually 50 kg
CBFM – community-based forestry management
CLSU – Central Luzon State University
cm – centimeter
CMS – cystoplasmic male sterile
CP – protein content
CRH – carbonized rice hull
CTRHC – continuous-type rice hull carbonizer
CT – conventional tillage
Cu – copper
DA – Department of Agriculture
DA-RFU – Department of Agriculture-Regional Field Units
DAE – days after emergence
DAS – days after seeding
DAT – days after transplanting
DBMS – database management system
DDTK – disease diagnostic tool kit
DENR – Department of Environment and Natural Resources
DH L– double haploid lines
DRR – drought recovery rate
DS – dry season
DSA - diversity and stress adaptation
DSR – direct seeded rice
DUST – distinctness, uniformity and stability trial
DWSR – direct wet-seeded rice
EGS – early generation screening
EH – early heading
EMBI – effective microorganism-based inoculant
EPI – early panicle initiation
ET – early tillering
FAO – Food and Agriculture Organization
Fe – Iron
FFA – free fatty acid
FFP – farmer's fertilizer practice
FFS – farmers' field school
FGD – focus group discussion
FI – farmer innovator
FSSP – Food Staples Self-sufficiency Plan
g – gram
GAS – golden apple snail
GC – gel consistency
GIS – geographic information system
GHG – greenhouse gas
GLH – green leafhopper
GPS – global positioning system
GQ – grain quality
GUI – graphical user interface
GWS – genomwide selection
GYT – general yield trial
h – hour
ha – hectare
HIP - high inorganic phosphate
HPL – hybrid parental line
I - intermediate
ICIS – International Crop Information System
ICT – information and communication technology
IMO – indigenous microorganism
IF – inorganic fertilizer
INGER - International Network for Genetic Evaluation of Rice
IP – insect pest
IPDTK – insect pest diagnostic tool kit
IPM – Integrated Pest Management
IRRI – International Rice Research Institute
IVC – in vitro culture
IVM – in vitro mutagenesis
IWM – integrated weed management
JICA – Japan International Cooperation Agency
K – potassium
kg – kilogram
KP – knowledge product
KSL – knowledge sharing and learning
LCC – leaf color chart
LDIS – low-cost drip irrigation system
LeD – leaf drying
LeR – leaf rolling
lpa – low phytic acid
LGU – local government unit
LSTD – location specific technology development
m – meter
MAS – marker-assisted selection
MAT – Multi-Adaption Trial
MC – moisture content
MDDST – modified dry direct seeding technique
MET – multi-environment trial
MFE – male fertile environment
MLM – mixed-effects linear model
Mg – magnesium
Mn – Manganese
MDDST – Modified Dry Direct Seeding Technique
MOET – minus one element technique
MR – moderately resistant
MRT – Mobile Rice TeknoKlinik
MSE – male-sterile environment
MT – minimum tillage
$mtha^{-1}$ - metric ton per hectare
MYT – multi-location yield trials
N – nitrogen
NAFC – National Agricultural and Fishery Council
NBS – narrow brown spot
NCT – National Cooperative Testing
NFA – National Food Authority
NGO – non-government organization
NE – natural enemies
NIL – near isogenic line
NM – Nutrient Manager
NOPT – Nutrient Omission Plot Technique
NR – new reagent
NSIC – National Seed Industry Council
NSQCS – National Seed Quality Control Services
OF – organic fertilizer
OFT – on-farm trial
OM – organic matter
ON – observational nursery
OPAg – Office of Provincial Agriculturist
OpAPA – Open Academy for Philippine Agriculture
P – phosphorus
PA – phytic acid
PCR – Polymerase chain reaction
PDW – plant dry weight
PF – participating farmer
PFS – PalayCheck field school
PhilRice – Philippine Rice Research Institute
PhilSCAT – Philippine-Sino Center for Agricultural Technology
PHilMech – Philippine Center for Postharvest Development and Mechanization
PCA – principal component analysis
PI – panicle initiation
PN – pedigree nursery
PRKB – Pinoy Rice Knowledge Bank
PTD – participatory technology development
PYT – preliminary yield trial
QTL – quantitative trait loci
R - resistant
RBB – rice black bug
RCBD – randomized complete block design
RDI – regulated deficit irrigation
RF – rainfed
RP – resource person
RPM – revolution per minute
RQCS – Rice Quality Classification Software
RS4D – Rice Science for Development
RSO – rice sufficiency officer
RFL – Rainfed lowland
RTV – rice tungro virus
RTWG – Rice Technical Working Group
S – sulfur
SACLOB – Sealed Storage Enclosure for Rice Seeds
SALT – Sloping Agricultural Land Technology
SB – sheath blight
SFR – small farm reservoir
SME – small-medium enterprise
SMS – short message service
SN – source nursery
SSNM – site-specific nutrient management
SSR – simple sequence repeat
STK – soil test kit
STR – sequence tandem repeat
SV – seedling vigor
t – ton
TCN – testcross nursery
TCP – technical cooperation project
TGMS – thermo-sensitive genetic male sterile
TN – testcross nursery
TOT – training of trainers
TPR – transplanted rice
TRV – traditional variety
TSS – total soluble solid
UEM – ultra-early maturing
UPLB – University of the Philippines Los Baños
VSU – Visayas State University
WBPH – white-backed planthopper
WEPP – water erosion prediction project
WHC – water holding capacity
WHO – World Health Organization
WS – wet season
WT – weed tolerance
YA – yield advantage
Zn – zinc
ZT – zero tillage

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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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