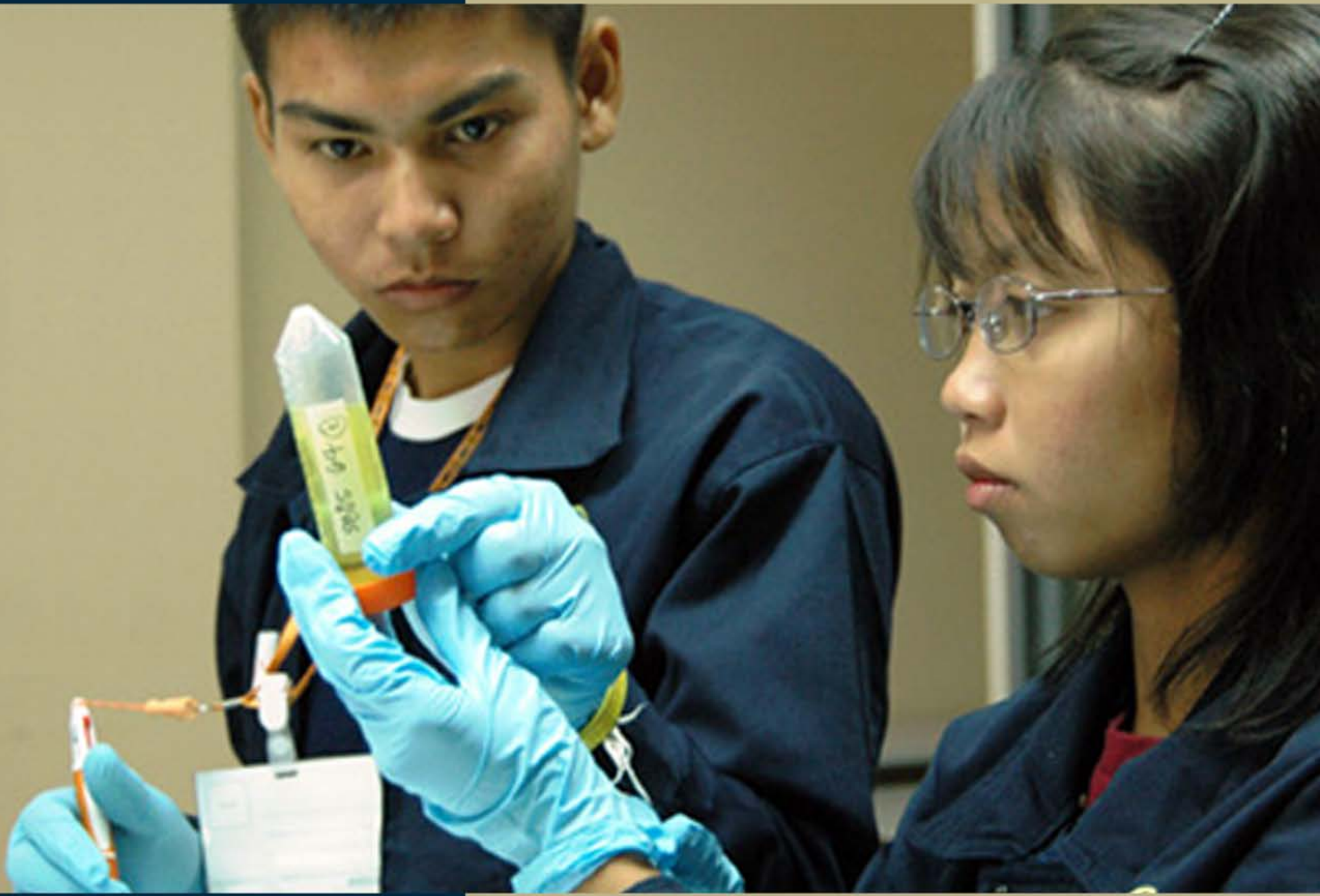
2012 IRRI Young Scientists Conference

SUSTAINING EXCELLENCE IN RICE RESEARCH

Program and Abstracts



8-9 November 2012
International Rice Research Institute
Los Baños, Laguna, Philippines

The International Rice Research Institute (IRRI) was established in 1960 by the Ford and Rockefeller Foundations with the help and approval of the Government of the Philippines. Today, IRRI is one of the 15 nonprofit international research centers supported in part by more than 40 donors: members of the Consultative Group on International Agricultural Research (CGIAR – www.cgiar.org), other government funding agencies, foundations, the private sector, and nongovernment organizations.

The responsibility for this publication rests solely with the International Rice Research Institute.

Copyright International Rice Research Institute 2012

🅭 This publication is copyrighted by the International Rice Research Institute (IRRI) and is licensed for use under a Creative Commons Attribution-NonCommercial-ShareAlike 3.0 License (Unported). Unless otherwise noted, users are free to copy, duplicate, or reproduce, and distribute, display, or transmit any of the articles or portions of the articles, and to make translations, adaptations, or other derivative works under the following conditions:

🅯 **Attribution:** The work must be attributed, but not in any way that suggests endorsement by IRRI or the author(s).

🄏 **NonCommercial:** This work may not be used for commercial purposes.

🄎 **ShareAlike:** If this work is altered, transformed, or built upon, the resulting work must be distributed only under the same or similar license to this one.

- For any reuse or distribution, the license terms of this work must be made clear to others.
- Any of the above conditions can be waived if permission is obtained from the copyright holder.
- Nothing in this license impairs or restricts the author's moral rights.
- Fair dealing and other rights are in no way affected by the above.
- To view the full text of this license, visit http://creativecommons.org/licenses/by-nc-sa/3.0/

Mailing address: IRRI, DAPO Box 7777, Metro Manila, Philippines
Phone: +63 (2) 580-5600
Fax: +63 (2) 580-5699
Email: irri@cgiar.org
Web: www.irri.org.
Rice Knowledge Bank: www.knowledgebank.irri.org
Courier address: Suite 1009, Security Bank Center
6776 Ayala Avenue, Makati City, Philippines
Tel. +63 (2) 891-1236, 891-1174, 891-1258, 891-1303

Suggested citation: International Rice Research Institute. 2012. Program and Abstracts: Sustaining Excellence in Rice Research, Los Baños (Philippines): IRRI. 130 p.

Contents

Message from the IRRI Director General

It is with great pleasure that I write the foreword for the 2012 IRRI Young Scientists Conference abstract book.

With nearly 100 abstracts obtained from a diverse mix of our young scientists, the abstracts represent an excellent range of IRRI's research. I do not envy the committee who had to select the six finalists!

Without a crop of vibrant, intelligent, dedicated, and caring young scientists, IRRI would not have a future. Indeed, the future of rice research and the progression of rice farmers and consumers out of poverty would also be threatened.

Oftentimes, it is at the start of young scientists' careers that some of their exciting research is undertaken. Unburdened with managerial responsibilities and ripe with enthusiasm and the latest technologies, we, time and again, see our young scientists publishing excellent papers and producing high-quality, even world-class, research. This is well reflected in the abstracts presented at the 2012 IRRI Young Scientists Conference.

History tells us that many young people who spend the early part of their career at IRRI go on to achieve other professional successes and continue to contribute to rice science for development in many varied ways. IRRI alumni work all over the world at leading research institutes, heading national agencies, taking senior roles in government and the business sector, and even returning to IRRI.

Armed with the knowledge gained at IRRI, the unique experience they get here, and of course the valuable professional relationships they foster, our current batch of young scientists, I believe, will continue this legacy of contributing to a better world through rice science.

The 2012 IRRI Young Scientists Conference is not only an important activity to support the professional development of our young scientists, it also promotes and showcases the exciting work that they are doing. I commend the organizers for their vision and commitment to the conference and to all the scientists who contributed. I wish you all great success.

Robert S. Zeigler

Robert S. Zeigler, PhD

Message from the IRRI Deputy Director General for Research

Transformations in the agricultural sector are emerging that will change the way food will be grown in the future.

Many of these changes will be driven by processes such as a declining share of agriculture in gross domestic product and employment, rural to urban migration, the rise of an industrial and service economy, and demographic transitions from high rates of birth and death to low rates.

These mega trends will provide new opportunities for the development, adaptation, and adoption of new technologies that could enable an ecological intensification of cropping systems and a more eco-efficient way of food production at high levels of productivity and resource use efficiency and less risk.

Agricultural science needs to be reoriented towards that. We need to anticipate what will be needed by farmers and others in the value chain 10, 20, or 30 years from now, and we need to take full advantage of such new opportunities in agricultural research for development.

Young scientists must play a leading role in such efforts and thus help in shaping a new image for modern agriculture. They have the modern skills and knowledge that will be required to tackle some of the grand challenges in biology and agriculture. Therefore, I am very excited to see this first young scientists' conference happening at IRRI.

This book of abstracts is evidence of the enormous breadth and depth of research done by young scientists at IRRI. It is evidence of innovation, high-quality and strong development orientation of science, and wide-ranging partnerships. These are all essential ingredients to enable IRRI and its partners to fulfill their mission. The future of rice science will be in good hands.

Achim Dobermann

Achim Dobermann, PhD

I am humbled and inspired by the privilege conferred on me to welcome you all to the 2012 IRRI Young Scientists Conference (2012IYSC), the first international conference in IRRI after a long time.

The conference is conceptualized to provide an opportunity for early-career scientists to present their completed and ongoing research on rice. Our aim is to create a cohesive bond and catalyze interactions among scientists who are mostly locked up in laboratories and those who work in rural and remote areas across the world where they have intensive dialogues with farmers.

To understand and acknowledge one another for mutual benefit, there is a need for constant interaction and wholesome debate within the community of young scientists. This platform will also work as the golden bridge between experienced senior scientists and those following their footsteps. There is no substitute for cooperation and no shortcut to collaboration. Foreseen as the next generation of rice scientists, the young scientists should continue to walk together toward the road to a 'rice-filled bowl for all.'

The 2012 IYSC would not have been possible without the help of a lot of people from the different units of the Institute. Support flowed in from all corners, beyond expectations. The preparations were completed before the self-imposed deadlines. From this experience, I firmly believe that there is a huge untapped human resource within the Institute, with eagerness to manifest them given the opportunity to do so.

The year 2012 also marks the golden jubilee of the arrival of the first scholars and trainees in IRRI. On this auspicious occasion, a scholarship fund– the "IRRI-AFSTRI-Alumni Scholarship"–is being launched with contributions from both IRRI staff and alumni. This scholarship will be awarded to needy and committed students who are pursuing degrees in agriculture in various universities.

On behalf of the 2012 IYSC Organizing Committee, I thank you all for your support and active participation in making this conference a successful event and I wish for the same support in other endeavors in the future.

GovindaRizal

Govinda Rizal, PhD

Acknowledgments

The 2012 IYSC Organizing Committee greatly acknowledges the following for their invaluable help and for being instrumental in making this conference possible and successful:

Achim Dobermann and the Office of the IRRI Deputy Director General for Research, and the Association of Fellows, Scholars, Trainees, and Residents of IRRI (AFSTRI) for financial support;

The Abstract Review Committee and conference chairpersons: Akshaya Kumar Biswal, Alex Stuart, Alice Laborte, Amelia Henry, Bhagirath Chauhan, Bo Zhou, Chitra Raghavan, David Raitzer, Elizabeth Humphreys, Endang Septiningsih, Gina Zarsadias, Grace Centeno, Impa Somayanda, Joel Janiya, John Platten, Joong Hyoun Chin, Jung-Hyun Shim, Kshirod Jena, Khondoker Abdul Mottaleb, Kurniawan Rudi Trijatmiko, Lutz Neumetzler, Mallikarjuna Swamy, Michael Thomson, Mohammad Rafiqul Islam, Nancy Castilla, Ricardo Oliva, Roland Buresh, Rosa Paula Cuevas, S.V. Krishna Jagadish, Samart Wanchana, Sarah Beebout, Sigrid Heuer, Stephen Haefele, Takuji Tsusaka, and Valerien Pede;

The judges of the Best Paper Competition: Abdelbagi Ismail, Achim Dobermann, Casiana Vera Cruz, Eero Nissilä, Rakesh Kumar Singh, Ruaraidh Sackville Hamilton, and Samarendu Mohanty;

The conference panelists: Bas Bouman, Jung-Hyun Shim, Ninh Ngoc Ho, Noel Magor, Rowena Oane, Sarah Beebout, and William Paul Quick;

Bruce Tolentino for being part of the awards and recognition ceremony;

The Committee for the Celebration of 50 Years of Scholarship in IRRI (alumni homecoming and scholarship fund raising): Anilyn Maningas, Froilan Fule, Govinda Rizal, Jauhar Ali, Jocelyn Finegan, Joong Hyoun Chin, Judith Galeng, Katrina Evangeline Zapanta, Nelzo Ereful, Ria Anna Dimapilis, Rosa Paula Cuevas, Ruth Ann Felismino, and Tam Dang;

The AFSTRI executive members: Govinda Rizal, Judith Galeng, Kai Wang, Khondoker Abdul Mottaleb, Nurul Hidayatun, Sharifa Sultana Dipti, Tam Dang, Teodora Cabasan, Vivek Thakur, and Zilhas Ahmed Jewel;

The IRRI Communication and Publications Services: Cynthia Quintos, Emmanuel Panisales, Juan Lazaro IV, Teresita Rola, and Bill Hardy;

The IRRI Events and Visitors Office: Ria Dimapilis and Ruth Ann Felismino;

Adonna Robles, Anabel Valdenarro, April Muere, Fiona Farrel, Judith Buresh, Lucia Gamel, Maria Socorro Arboleda, Melanie Quinto, Rosalie Laude-San Antonio, Sylvia Arellano, and Zorayda Menguito for the secretarial and administrative support;

And to all conference participants for their active participation and discussion.

Due to space constraints or to unintentional failure to mention everyone, our personal thanks will reach you.

Program

Time	8 November, IRRI Training Center		2012 IRRI Young Scientists Conference			
8:00	Registration					
	Opening ceremony, MC: Shanta Karki					
8:30	Opening remarks, Govinda Rizal (Head, 2012 IYSC Organizing Committee)					
8:40	Welcome message, Robert Zeigler (IRRI Director General)					
8:55	Message to the young scientists, Achim Dobermann (IRRI Deputy Director General for Research)					
9:15	Ceremonial tree planting and group photo, Ruth Ann Felismino, and Guest and Participants					
9:55	Break					
10:10	Concurrent sessions (The number refers to the one assigned to a specific abstract.)					
	CIM	CP	EMP	ENV	GAG	INA
	CIM: Crop Improvement; CP: Crop Protection; EMP: Extension, Marketing, and Policies; ENV: Environment and Sustainability; GAG: Genetics and Genomics; INA: Innovations and Novel Approaches					
	Moderators					
	R. Gamuyao	J. Ferrater	C. Ye	T. Cabasan	G. Rizal	S. Karki
10:10	Introduction of chairpersons by moderators					
	Chairpersons					
	S.V.K. Jagadish	A. Stuart	V. Pede	S. Beebout	A. Biswal	R. Cuevas
10:15	22	10	13	14	6	9
10:35	31	11	21	23	7	17
10:55	40	12	29	26	15	24
11:15	49	34	38	30	16	33
11:35	53	39	43	35	18	47
11:55	55	5	48	41	20	50
12:15	Lunch					
13:30	Introduction of chairpersons by moderators					
	Chairpersons					
	J.H. Shim	J. Janiya	T. Tsusaka	S. Impa	M. Swamy	B. Chauhan
13:35	56	45	77	46	32	51
13:55	59	64	78	60	36	57
14:15	70	65	81	67	37	61
14:35	72	74	85	68	42	63
14:55	88	79	86	75	52	80
15:15	Break					
15:30	Introduction of chairpersons by moderators					
	Chairpersons					
	J.H. Chin	R.F. Oliva	K.A. Mottaleb	G. Centeno	R.J. Flor	S. Wanchana
15:35	92	89	87	76	66	83
15:55	96	90	94	84	71	93
16:15	97	91	95		73	98
16:35	Free time					
18:00	Banquet					
20:00	End of Day 1					

Program

Time	9 November, IRRI Havener Auditorium	2012 IRRI Young Scientists Conference
8:25	2012IYSC Best Paper Competition, MC: Changrong Ye	
	Introduction of judges and announcement of competition criteria, Rico Gamuyao	
8:30	Gene validation of a major QTL for tolerance of anaerobic conditions during germination, Tobias Kretzschmar	
8:50	Ubiquitous resistance to rice tungro spherical virus is mediated by a gene for translation initiation factor 4G, Genelou Atienza	
9:10	Impact of rice price hike on poverty in Bangladesh, Taznoore Samina Khanam	
9:30	Methane emission and rice yield as affected by elevated temperature, rice straw incorporation and soil properties in lowland rice paddy soils, Yam Kanta Gaihre	
9:50	Transformation of rice with C4 genes and characterization of the transgenic plants, Swati Kamal	
10:10	Introduction of transport proteins into Oryza sativa L. to facilitate installation of the C4 pathway, Ronald Tapia	
10:30	Break	
10:45	Panel discussion	
	Introduction of the program and panelists, Govinda Rizal	
	Moderator, Bas Bouman	
	Panelists, William Paul Quick, Rowena Oane, Sarah Beebout, Jung-Hyun Shim, Ninh Ngoc Ho and Noel Magor	
	Discussion among the participants and panel members	
12:15	Lunch	
13:30	Celebration of 50 years of scholarship in IRRI, MC: Dang Tam and Nelzo Ereful	
	Background and success stories, Anilyn Maningas and Maria Socorro Arboleda	
	Introduction of the scholarship fund raising project, Judith Galeng, Vivek	
15:00	Acknowledgments, Govinda Rizal	
15:20	Awards and Recognition, MC: Bruce Tolentino (IRRI Deputy Director General for Communications and Partnerships)	
16:00	Closing ceremony, Robert Zeigler (IRRI Director General)	
16:05	Preparation for Cultural Night	
18:00	International Cultural Night, AFSTRI Members	
20:00	End of Day 2	

Abstracts
Open Presentation

8 November 2012

IRRI Training Center

Category 1: Crop Improvement

Category 2: Crop Protection

Category 3: Extension, Marketing, and Policies

Category 4: Environment and Sustainability

Category 5: Genetics and Genomics

Category 6: Innovations and Novel Approaches

Category 1

Crop Improvement

8 November 2012 Category 1: Crop Improvement 2012 IRRI Young Scientists Conference

Time	Abstract no.	Abstract title, authors
10:15	22	**Simultaneous improvement of multiple complex traits of rice by BC breeding method** Ying Wang, Lubiao Zhang, Kai Chen, Qiang Zhang, Jianlong Xu, and Zhikang Li
10:35	31	**Diversity and structure of indica collected from multi-continents for exploitation of potential heterotic groups using 384 single nucleotide polymorphisms** Kai Wang, D. Madonna, and Fangming Xie
10:55	40	**Farmers' participatory site-specific nutrient management in the Ganges tidal floodplain for high- yielding boro rice** Fahomida Amin, Deb Kumar Nath, Md. Shahidul Islam, and M.A. Saleque
11:15	49	**Zinc foliar application improves grain zinc quality of rice** Ranee Christina Mabesa, Somayanda M. Impa, Grewal Deepinder, and Sarah E.J. Beebout
11:35	53	**Evaluation of traditional cultivars and wild rice species for reaction to rice ragged stunt virus and rice grassy stunt virus** Minh Tam Dang, R.C. Cabunagan, and I.R. Choi
11:55	55	**Evaluation of biofertilizers in irrigated rice: effects on grain yield at different fertilizer rates** Niño Paul Meynard C. Banayo, Pompe C. Sta. Cruz, Edna A. Aguilar, Rodrigo B. Badayos, and Stephan M. Haefele
13:35	56	**Screening for C3 and C4 photosynthesis types using low CO_2 environment** Kelvin Acebron, Mary Jacqueline Dionora, Julius Rañada, Glenn Dimayuga, Michael Marasigan, Rey Vergara, Michael Orlina, Panopio Isidro, Aris Andaya, Rommel Hibek, Natalia Elayda, Omar Abellera, Govinda Rizal, and William Paul Quick
13:55	59	**Light-directed photosynthesis and leaf anatomical plasticity of *Setaria viridis* (L.) Beauv.** Robert A. Nepomuceno, Anna Mae de los Reyes, Ronilo Bajaro, Ma. April Grace Estonilo, Reychelle Mogul, Glenn Dimayuga, Omar Abellera, Abigail Mabilangan, Mary Jacqueline Dionora, and William Paul Quick
14:15	70	**Connecting the dots from amylose content to cooked rice texture** Jeanaflor Crystal Concepcion, Rosa Paula Cuevas, Artemio Madrid, Jr., Teodoro Atienza, Rosario Jimenez, Adoracion Resurreccion, and Melissa Anne Fitzgerald
14:35	72	**Cold acclimation in *Arabidopsis thaliana*** Xiaojia Yin, Andrew J. Fleming, and William Paul Quick
14:55	88	**Supporting specificities around improved rice cultivars in a region with diverse biophysical and socioeconomic attributes: lessons from Tanzania, East and Southern Africa** Nhamo Nhamo, Rosemary Murori, and Rakesh K. Singh
15:35	92	**Green Super Rice (GSR) varieties designed for changing climatic conditions** Jauhar Ali, Jianlong Xu, Yongming Gao, Marfel Fontanilla, and Zhikang Li
15:55	96	**Marker-assisted breeding for tolerance to anaerobic conditions during germination** John Carlos I. Ignacio, Tobias Kretzschmar, Abdelbagi M. Ismail, David J. Mackill, and Endang M. Septiningsih
16:15	97	**Heat-tolerant rice for sustainable yield in a warmer climate** Richard Malo, S.V.K. Jagadish, Ludovico Dreni, Zeba I. Seraj, Martin Kater, and Sigrid Heuer

Simultaneous improvement of multiple complex traits of rice by BC breeding method

Ying Wang,[1*] Lubiao Zhang, Kai Chen, Qiang Zhang, Jianlong Xu,[1*] and Zhikang Li[1*]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: xujlcaas@yahoo.com.cn; zhkli1953@126.com

With rapid population growth and the grave threat posed by abiotic stresses, improving rice grain yield is a continuing challenge for rice breeders. Three high yield selective populations (HYSP), three drought tolerance selective populations (DTSP), and three salt tolerance selective populations (STSP) were obtained from three backcross (BC) introgression line (IL) populations derived from HHZ as recurrent parent and three indica cultivars (IR64a, AT354, C418) as donors. First-round selection resulted in 83 high yield (HY), 81 drought tolerance (DT), and 162 salt tolerance (ST) backcross ILs. After repeated selection under normal and drought stress conditions for grain yield (GY) and under salt stress condition for ST, seven superior HHZ ILs from the three HYSP showed significantly higher GY than HHZ under normal conditions across 2 years; one line showed significantly higher GY under both drought stress and normal conditions; seven lines showed significantly higher GY under normal conditions but similar GY under drought stress; and one line showed higher GY under drought stress and unchanged GY under normal conditions. From the three DTSP, 49 superior HHZ ILs had significantly improved DT repeatedly across 2 years and eight lines had significantly higher GY under both drought stress and normal conditions. Furthermore, from the three STSP, 82 superior HHZ ILs consistently showed significantly improved ST across 2 years; one ST line showed higher GY under both normal and drought stress conditions; five ST lines showed significantly higher GY under normal condition and unchanged GY under drought stress condition; and nine ST lines showed significantly higher GY under drought stress condition and unchanged GY under normal condition. This study provided useful materials for QTL mapping of three target traits and confirmed that direct selection against GY is an effective method for obtaining ILs with high GY or DT. Moreover, cross selection is useful for obtaining two or three complex traits. The selected lines with the target traits will become valuable materials for gene mining and molecular breeding for improvement of multiple traits by highly efficient pyramiding of favorable genes.

Keywords: backcross breeding, high yield, drought tolerance, salt tolerance, selection efficiency

Diversity and structure of indica collected from multi-continents for exploitation of potential heterotic groups using 384 single nucleotide polymorphisms

Kai Wang,* D. Madonna, and Fangming Xie*
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: f.xie@irri.org

Characterization of genetic diversity and relationships among varieties and inbreeding lines is vital in assisting breeders to select parental lines in the development of inbred and hybrid varieties and construction of heterosis groups. We genotyped 737 modern varieties or inbreeding lines developed recently and/or widely used by present indica breeding programs using IRRI-developed SNP oligonucleotide pooled assay to provide genetic structure information of mega rice entries for further heterosis group study. Genetic distance for about 93% of the pairs of entries fell above 0.200, and 84% of the pairs of entries also showed relative kinship values ≤ 0.80. This suggests high genetic distance and low kinship coefficients among most pairs of entries. Model-based population structure analysis, neighbor-joining cluster analysis, and principal coordinate analysis revealed the presence of six major groups. More than half of the entries (51.8%) appeared to have less than 0.6 membership in any population, and the SNPs did not show a clear separation of populations associated with breeding programs or geographic origin, indicating the extent of gene flow within indica and the great degree of genetic integration of alleles and shared ancestries among high-yielding modern varieties/lines. This will facilitate the exchange of germplasm among countries, regions, or institutes involved in current rice breeding efforts.

Keywords: genetic diversity, SNP, hybrid rice

Farmers' participatory site-specific nutrient management in the Ganges tidal floodplain for high-yielding boro rice

Fahomida Amin,* Deb Kumar Nath, Dr. Md. Shahidul Islam, and Dr. M. A. Saleque
International Rice Research Institute, South Alekanda, Barisal-8200, Bangladesh.
*Correspondence: f.amin@irri.org

Participatory site-specific nutrient management (SSNM) trials were conducted for irrigated, transplanted high-yielding rice (*Oryza sativa* L.) at Barisal District, Bangladesh, during the 2012 boro season. To observe the response of indigenous nutrient elements on rice yield attributes, four treatments (NPK, PK, NK, and NP) were imposed. The aim is to develop an SSNM approach that farmers in the Ganges tidal floodplain ecosystem can use to increase their fertilizer use efficiency. The highest grain yield (5.7 t ha^{-1}) was observed in the NPK treatment plot, which gave 50.1%, 61.2%, and11.1% higher yield than did the PK, NK, and NP treatments, respectively. The response of indigenous P was very poor and the lowest grain yield (2.2 t ha^{-1}) was found in the P-omission plot. The response of indigenous N was also poor (2.8 t ha^{-1}), but the response of indigenous K was remarkable, giving the second highest grain yield (5.0 t ha^{-1}). These results show that N and P are critical in increasing yield and that they do have a significant impact on yield. To produce high-yielding rice in the boro season, farmers may use N, P, and K at 130, 14.5, and 15.6 kg ha^{-1}, respectively. It can save 5.8% N, 19.7% P, and 70.5% K compared with those of usually applied doses.

Keywords: grain yield, rice, nutrient omission, site-specific nutrient management, NPK treatment

Zinc foliar application improves grain zinc quality of rice

Ranee Christina Mabesa,* Somayanda M. Impa, Grewal Deepinder, and Sarah E.J. Beebout
Crop and Environmental Sciences Division, International Rice Research Institute. DAPO Box 7777, Metro Manila, Philippines
*Correspondence: r.mabesa@irri.org

Zinc (Zn) is an important micronutrient needed in human nutrition. However, various studies reveal that the primary cause of Zn deficiency is poor diversity in diet, together with low Zn content in the food intake of the human population. Likewise, cereals are a popular staple food in most developing countries, but rice is naturally low in Zn. The Zn content of high-Zn genotypes is sometimes limited by the low availability of soil Zn. But Zn biofortification through foliar Zn application can optimize Zn so that the recommended amount required for human diet is reached. Our study provides evidence of Zn remobilization from the leaves to the grains using Zn-biofortified lines of rice. The experiment was conducted during the 2011 dry season at two sites with moderately (IRRI Experiment Station) and severely (Bay, farmer's field) Zn-deficient soil. Foliar Zn was applied at the same rate that was successfully used in wheat biofortification (Cakmak 2010) at different growth stages: control (distilled water), mid-tillering, 50% flowering, and mid-tillering + 50% flowering. All varieties used showed a significant increase when foliar Zn was applied at flowering stage at both sites. In a parallel study in a farmer's field using IR64, only Zn application at the early grain-filling stage significantly increased grain Zn. Some varieties were able to reach the targeted amount of grain Zn without foliar application under moderately Zn soil-deficient condition. This study serves as an initial avenue for investigating Zn effect from foliar application at earlier times compared with basal application to overcome agronomic Zn deficiency. In conclusion, foliar Zn application improves grain Zn quality in rice during the reproductive stage using biofortified lines grown in moderately Zn-deficient soil.

Evaluation of traditional cultivars and wild rice species for reaction to rice ragged stunt virus and rice grassy stunt virus

Minh Tam Dang,[1,2] R.C. Cabunagan,[2] and I.R. Choi[2*]
[1]Cuu Long Delta Rice Research Institute, Thoi Lai, Can Tho, Vietnam
[2]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: i.choi@irri.org

Rice ragged stunt virus (RRSV) and rice grassy stunt virus (RGSV) have caused serious damage to rice production in Southeast Asian countries since 2006. RRSV and RGSV are transmitted by brown planthoppers (BPH). To identify genetic resources with resistance to RGSV and RRSV, we evaluated about 100 traditional rice cultivars and 79 wild rice species for reactions to RGSV and RRSV in Vietnam and IRRI. Among the traditional cultivars examined, two cultivars, Kalu Samba and AC613, seemed promising against RRSV. Among wild rice species evaluated for RGSV and RRSV infection, seven accessions, including *Oryza punctata* and *O. officinalis*, appeared to be resistant to RRSV and RGSV. These promising donors may be used in developing rice varieties resistant to RGSV and RRSV and in mapping loci associated with the resistance traits. We will confirm the reactions to RRSV, RGSV, and BPH using more rigorous evaluation methods.

Keywords: RRSV, RGSV, BPH, rigorous evaluation

Evaluation of biofertilizers in irrigated rice: effects on grain yield at different fertilizer rates

Niño Paul Meynard C. Banayo,[1*] Pompe C. Sta Cruz,[2] Edna A. Aguilar,[2] Rodrigo B. Badayos,[3] and Stephan M. Haefele[1*]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Crop Science Cluster, College of Agriculture (CA), University of the Philippines at Los Baños (UPLB), Laguna 4031, Philippines
[3]Agricultural Systems Cluster, CA, UPLB, Laguna 4031, Philippines
*Correspondence: n.banayo@irri.org, s.haefele@irri.org

Biofertilizers are becoming increasingly popular in many countries and for many crops, but very few studies on their effects on grain yield have been conducted in rice. Therefore, we evaluated three different biofertilizers (based on *Azospirillum*, *Trichoderma*, and unidentified rhizobacteria) in the Philippines during four cropping seasons between 2009 and 2011. Four different fertilizer rates were used: 100% of the recommended rate [RR], 50% of RR, 25% of RR, and no fertilizer (control). The experiments were conducted under fully irrigated conditions in a typical lowland rice environment. Significant yield increases due to biofertilizer use were observed in all experimental seasons with the exception of the 2008/09 dry season. But the effects on rice grain yield varied across biofertilizers, seasons, and fertilizer treatments. In relative terms, the seasonal yield increase across fertilizer treatments was between 5% and 18% for the best biofertilizer (*Azospirillum*-based), but it went up to 24% in the individual treatments. Absolute grain yield increases due to biofertilizer were usually below 0.5 t ha^{-1}, corresponding to an estimated additional N uptake of less than 7.5 kg N ha^{-1}. The biofertilizer effect on yield did not significantly interact with the inorganic fertilizer rate used, but the best effects on grain yield were achieved at low to medium fertilizer rates. Nevertheless, positive effects of the biofertilizers even occurred at grain yields up to 5 t ha^{-1}. However, the trends in our results seem to indicate that biofertilizers might be most helpful in rainfed environments with limited inorganic fertilizer input. For use in these target environments, biofertilizers need to be evaluated under conditions with abiotic stresses typical of such systems such as drought, soil acidity, or low soil fertility.

Keywords: *Azospirillum*, biofertilizer, grain yield, inorganic fertilizer, PGPR, plant growth-promoting rhizobacteria, rice, *Trichoderma*

Screening for C3 and C4 photosynthesis types using low-CO_2 environment

Kelvin Acebron,[1*] Mary Jacqueline Dionora, Julius Rañada, Glenn Dimayuga, Michael Marasigan, Rey Vergara, Michael Orlina, Panopio Isidro, Aris Andaya, Rommel Hibek, Natalia Elayda, Omar Abellera, Govinda Rizal, and William Paul Quick[1*]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: k.acebron@irri.org

Photosynthetic systems of plants have evolved from a primitive C3 type to an efficient C4 type through a changing environment. C4 plants have efficient photosynthesis and reduced photorespiration under high temperature. This also reduced the CO_2 compensation point (Γ) of C4 plants, which is the minimum CO_2 level required to balance the rate of photosynthesis and photorespiration. Scientists now are trying to introduce the C4-type photosynthesis system into C3 plants, particularly in rice, to increase its potential yield. In converting C3 rice into C4, it is necessary to reduce the Γ. To do this, C3 (rice) and C4 (*Setaria* and sorghum) seedlings were grown under varying levels of CO_2 during the early vegetative stage. They were grown for 21 days in CO_2-regulated growth chambers with a capacity of 10,000 seedlings per batch. All representative plants showed a direct relationship between imposed CO_2 level and biomass production. Rice seedlings had a high rate of mortality when grown under 30, 40, and 50 ppm of CO_2 for 21 days. On the other hand, *Setaria* and sorghum seedlings survived under very low CO_2 levels (30–70 ppm of CO_2), but biomass production was limited. This reaction of plants was congruent to a typical CO_2 response curve that can be generated using an infrared gas analyzer. The distinct threshold between mortality and survival for C3 and C4 plants, which is 50–60 ppm of CO_2, is a reliable selection pressure in differentiating plants with C3 and C4 types of photosynthesis. Growth chambers fitted with CO_2-regulation system can be used for high-throughput screening of rice with acquired C4 photosynthesis.

Keywords: CO_2 response curve, CO_2 compensation point (Γ), high-throughput screening, photosynthesis

Light-directed photosynthesis and leaf anatomical plasticity of *Setaria viridis* (L.) Beauv.

Robert A. Nepomuceno,* Anna Mae de los Reyes, Ronilo Bajaro, Ma. April Grace Estonilo, Reychelle Mogul, Glenn Dimayuga, Omar Abellera, Abigail Mabilangan, Mary Jacqueline Dionora, and William Paul Quick
C4 Rice Center, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: r.nepomuceno@irri.org

Green foxtail millet (*Setaria viridis* (L.) Beauv.) is currently getting more and more attention in C4 research because of its relatively short generation time, efficient transformation system, and small plant size. C4 photosynthesis has an efficient mechanism to concentrate CO_2 around Rubisco, preventing the oxygenase activity of this enzyme. Engineering C4 traits in a C3 plant has been a long-standing goal. In this aspect, *Setaria* can serve as a good C4 model, allowing for a multitude of genetic studies. One of the approaches is discovering the C4-related genes through screening large mutant populations of *Setaria*. However, the extent of phenotypic plasticity of some important morphological and photosynthetic characteristics must be determined before standardization of measurements for comparison in the genetic screen. In this experiment, the responses of *Setaria* to various light intensities on morphology and photosynthesis have been observed. The results suggest that light is a potent limiting factor in the development of *Setaria* as the plants, most deprived of light, showed a debilitating photosynthetic inhibition as indicated by gas exchange measurements. As a result, growth was stunted (as indicated by successive height and leaf area measurements). Vein density was likewise affected as it showed a negative correlation to level of light, an indication of compensation for stress. Hence, light levels across an experimental setup must be uniform to minimize, if not eliminate, these effects.

Keywords: photosynthesis, phenotypic plasticity, shade stress, *Setaria viridis*

Connecting the dots from amylose content to cooked rice texture

Jeanaflor Crystal Concepcion,[1] Rosa Paula Cuevas,[1*] Artemio Madrid, Jr.,[1] Teodoro Atienza,[1]
Rosario Jimenez,[1] Adoracion Resurreccion,[1] and Melissa Anne Fitzgerald[1,2]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]University of Queensland, St Lucia, Australia
*Correspondence: r.cuevas@irri.org

Amylose content is one of the most important parameters that predict cooking and eating quality of rice varieties, particularly texture. As such, it is one of the most quantified parameters in breeding programs, especially at the early stages. Because of its importance, amylose content has been studied extensively. Methods to improve the accuracy of measurement have been developed; the structure of amylose has been characterized; and the genetic factors dictating the amount of amylose synthesized by a rice variety have been determined. Through these indirect laboratory methods, rice varieties are classified into different quality classes. At the consumer level, however, the rice eater readily differentiates rice varieties of the same quality class (based on amylose content) because of differences in perceived mouthfeel. Hence, traditional varieties that possess the desired cooked grain sensory properties have remained popular, despite their low yields and the availability of improved varieties of supposedly the same quality class. Evidently, amylose content is not the sole factor affecting the sensory experience of eating rice. How good, then, is amylose content as a predictor of cooked rice eating quality? In this study, a set of diverse rice accessions was characterized for amylose content and for different, more direct indicators of cooked rice texture. Results show that rice samples fell into five known haplotypes of the gene influencing amylose content, the *Waxy* gene. However, the samples only formed three main groups based on apparent amylose content. Instrumental textural parameters also indicated that amylose content may not be predicting texture as reliably as originally thought. The relationships among the different indicators of amylose content and of texture will be further discussed.

Keywords: amylose content, texture, genotyping

Cold acclimation in *Arabidopsis thaliana*

Xiaojia Yin,[1*] Andrew J. Fleming,[2] and W. Paul Quick[1,2]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Department of Animal and Plant Sciences, University of Sheffield, UK
*Correspondence: x.yin@irri.org

Low temperature is one of the most important abiotic stresses that limit growth and distribution of plants. Freezing temperatures are lethal to many plants, but many species are able to increase their cold tolerance through a process termed cold acclimation. Acclimation can be induced by pre-exposure to mild cold temperatures. Increasing the freezing tolerance of plants is controlled by complex and largely unknown gene regulatory networks. A high-throughput screening process was developed to identify mutant *Arabidopsis thaliana* plants with altered responses to a freezing treatment after cold acclimation with the aim of identifying and characterizing new genes underlying adaptation to cold stress. The screen allowed large numbers of *Arabidopsis* seedlings to be subjected to a freezing stress that was lethal to nonacclimated plants, but which cold-acclimated plants survived. The screening was performed on knockout as well as overexpression mutants of *A. thaliana* plants for a spectrum of genes of interest. As a result of this screening process, two independent *A. thaliana* mutants were identified with loss-of-function of the same gene–*LTR1* (Low Temperature Responsive1). These alleles showed more severe injury than wild type Col-0 plants under freezing conditions after cold acclimation but not under optimal growth conditions. These two mutant lines showed some phenotypic differences from Col-0 plants, such as higher photosynthetic pigment content and lower growth rate. These data indicate that the novel gene *LTR1* is required for the process of cold acclimation in *A. thaliana*.

Keywords: *LTR1*, cold acclimation, freezing tolerance, screen, *Arabidopsis*, CBF

Supporting specificities around improved rice cultivars in a region with diverse biophysical and socioeconomic attributes: lessons from Tanzania, East and Southern Africa

Nhamo Nhamo,[1*] Rosemary Murori, and Rakesh K. Singh
[1]International Rice Research Institute, P. O. Box 33581, Mikocheni B-Kawe, Dar es Salaam, Tanzania
*Correspondence: n.nhamo@irri.org

Rice, an important cereal crop second to maize, is used for food and income security of rural farm families in Tanzania. At present, traditional rice production practices dominate where low-to-no inputs are applied to unimproved cultivars. This paper discusses factors that have the potential of driving and supporting a future rice system based on improved rice cultivars. Data from farmer surveys, participatory varietal selection, and multilocation rice yield trials conducted between 2010 and 2012 in Tanzania are presented with the objective of characterizing factors that influence yield gains and their relevance to rice development efforts. Future rice production depends on the successful use of improved rice cultivars and the application of a suite of specific good agricultural practices that answer the biophysical and socioeconomic needs of the east and southern African region. Based on experiences in Tanzania, key research and development areas will be identified in the future.

Keywords: rice system, traditional practices, improved rice varieties, crop combinations, Africa

Green Super Rice (GSR) varieties designed for changing climatic conditions

Jauhar Ali,[1*] Jianlong Xu,[2] Yongming Gao,[2] Marfel Fontanilla,[1] and Zhikang Li[2]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Chinese Academy of Agricultural Sciences, Beijing, China
*Correspondence: J.Ali@irri.org

Fluctuating climatic patterns in recent years have resulted in unprecedented floods, droughts, salinity, and insect and disease outbreaks, making the rice bowls of Asia especially vulnerable. Green Super Rice (GSR) resilience breeding involves developing varieties quickly to cater to the needs of the different regions by incorporating multiple abiotic and biotic stress tolerance without compromising grain yield and quality. The GSR breeding strategy, which involves 16 donors and their introgression into popular adaptive lines (e.g., Huanghuazhan [HHZ]), has allowed us to identify several GSR materials with multiple abiotic and biotic stress-tolerant lines. The BC_1F_2 populations derived from HHZ (recipient parent) and 16 donors at IRRI were screened simultaneously for three rounds for different abiotic stresses (drought, salinity, submergence, low chemical inputs) and under normal irrigated conditions. This resulted in the identification of 845 trait-specific introgression lines (ILs) superior to tolerant checks. Adopting this approach, 37 ILs with multiple abiotic and biotic stresses tolerance were nominated for national cooperative testing in the Philippines and for multienvironment testing at IRRI. Such GSR cultivars can well fit into varied rice ecosystems and under changing climatic conditions. Two promising GSR cultivars bred at IRRI in the last 5 years–GSR IR1-8-S6-S3-Y2 (IRIS179-880151, HHZ8-SAL6-SAL3-Y2) and GSR IR1-12-D10-S1-D1 (IRIS179-880155, HHZ12-DT10-SAL1-DT1)– highlight the strength of this innovative breeding strategy. This success may be attributed to an innovative introgression breeding effort, combined with appropriate cross tolerance screening and selection techniques that tapped the hidden genetic diversity from a large number of donors into an adaptable HHZ varietal background. Designed QTL pyramiding with omic tools may further enhance the grain yield and resilience of GSR.

Keywords: breeding, multiple abiotic stress tolerance, drought, salinity, submergence

Marker-assisted breeding for tolerance to anaerobic conditions during germination

John Carlos I. Ignacio,[1*] Tobias Kretzschmar,[1] Abdelbagi M. Ismail,[1] David J. Mackill,[2] and Endang M. Septiningsih[1]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]MARS Food Global, Department of Plant Science, University of California, Davis, CA 95616 USA
*Correspondence: j.ignacio@irri.org

The direct-seeding (DSR) practice has been increasingly adopted by farmers in both rainfed and irrigated ecosystems as it requires less labor and entails less production cost than does conventional transplanting. However, unleveled fields or heavy rainfall in direct-seeded fields can lead to poor crop establishment because most rice varieties are susceptible to flooding during germination (referred to as anaerobic germination [AG]). Breeding for DSR, which requires tolerance for AG stress, is essential to sustain rice production in these ecosystems. However, this effort had limited success in the past due to lack of donors of the tolerance trait and the complexity of the trait itself. Fortunately, more AG tolerance donors have recently been identified and analysis of mapping populations derived from these donors has led to the identification of several major QTLs. Through marker-assisted breeding, these QTLs are valuable targets for transfer into high-yielding varieties and for pyramiding with other identified QTLs to provide higher AG tolerance. Furthermore, this trait can be combined with other abiotic stress tolerance QTLs to provide more resilient rice varieties for unfavorable environments.

Keywords: direct-seeded rice, flooding, anaerobic germination, quantitative trait loci, marker-assisted breeding

Heat-tolerant rice for sustainable yield in a warmer climate

Richard Malo,[1,2] S.V.K. Jagadish,[1] Ludovico Dreni,[3] Zeba I Seraj,[2] Martin Kater,[3] and Sigrid Heuer[1]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]University of Dhaka, Bangladesh
[3]University of Milano, Italy

High temperature stress on crops results in significant yield reduction. It also affects grain quality, which results in economic loss due to low market price. Rice is known to be sensitive to high temperature stress, particularly at anthesis stage. Temperatures exceeding 38 °C result in a significant decrease in spikelet fertility, anther dehiscence, and pollen germination on stigmas. An aus type variety, Nagina 22 (N22), identified as heat-tolerant, shows a higher rate of spikelet fertility, anther dehiscence, and pollen germination on stigmas under high temperature stress (39 °C), whereas the heat-sensitive variety, Moroberekan, shows high spikelet sterility. To identify the molecular tolerance mechanism, heat-treated anther and spikelet proteome from N22 were analyzed by 2D gel electrophoresis. Differentially expressed proteins were identified from the spots by sequencing using MALDI-TOF. Using BLAST search, these protein sequences were identified; they included heat shock protein, cold shock protein, dirigent-like protein, pollen allergens, and extensin family protein. Genes coding for the identified proteins were cloned and sequenced from N22. However, no sequence polymorphisms were identified compared with Nipponbare alleles. Gene expression analyses by semiquantitative and quantitative PCR using RNA from pollinated stigmas confirmed induction of two heat shock protein-coding genes upon heat stress. These two genes were selected for validating their role in high-temperature stress tolerance by overexpression in the heat-sensitive variety background IR64. These genes were cloned into a binary vector pMDC32 under constitutive CaMV 35S promoter and immature rice embryos from IR64 were transformed-mediated by *Agrobacterium*. Plants were regenerated through tissue culture. Using southern analysis, T0 plants containing a single copy of the transgene were selected. The evaluation of T1 lines overexpressing the heat shock proteins is in progress.

Category 2

Crop Protection

8 November 2012 Category 2: Crop Protection 2012 IRRI Young Scientists Conference

Time	Abstract no.	Abstract title, authors
10:15	10	**Effect of cultivar, tillage system, and herbicide on weed management and grain yield in dry-seeded rice systems** Jhoana L. Opeña and Bhagirath S. Chauhan
10:35	11	**Weed management in zero-till, dry direct-seeded rice systems** Seth Bernard E. Abugho and Bhagirath S. Chauhan
10:55	12	**Influence of rice seeding and nitrogen rates on weed suppression and growth of rice under aerobic conditions** Tahir Hussain Awan and Bhagirath S. Chauhan
11:15	34	**Phenotyping and molecular characterization of rice accessions for resistance to sheath blight** Gil Beligan, Srinivasachary, Serge Savary, Marina Natural, Eula Gems Oreiro, Jelmer Aguire, Ricardo Oliva, and Laetitia Willocquet
11:35	39	**Postharvest resistance of upland NERICA and their parents to *Sitotroga cerealella* Olivier (Lepidoptera: Gelechiidae)** Carline Santos, Francis Nwilene, and Clement Agbangla
11:55	5	**Characterization of resistance to root-knot nematode *Meloidogyne graminicola* in *Oryza glaberrima*** Ma. Teodora Nadong Cabasan, Arvind Kumar, and Dirk De Waele
13:35	45	**Biochemical approach for virulence factor identification in *Xanthomonas oryzae* pv. *oryzae*** Codjo Sylvestre Gerbert Dossa, Petr Karlovsky, and Kerstin Wydra
13:55	64	**Spectrum and stability of hopper resistance in monolocus and pyramided rice lines** Srinivasan Thanga Suja, Ma. Liberty P. Almazan, Daisuke Fujita, and Finbarr G. Horgan
14:15	65	**Interactions between crop management and host-plant resistance to brown planthoppers** Ainara Peñalver Cruz, Ma. Liberty P. Almazan, and Finbarr G. Horgan
14:35	74	**Resistance and tolerance of introgressed and aerobic rice genotypes to root-knot nematode *Meloidogyne graminicola*** Judith Pacya-an Galeng, Mallikarjuna Swamy, Arvind Kumar, and Dirk De Waele
14:55	79	**Field evaluation of certain genotypes against major rice pests in the Karaikal Region** Anil Varma Nalla, D. Adiroubane, K. Kumar, and S. Nadaradjan
15:35	89	**Characterization of injury profiles and production situations in Southeast Asia** Jerico Bigornia, Joselito Villa, Nancy Castilla, Adam Sparks, and Serge Savary
15:55	90	**The snail invasion–an ecological and agricultural disaster** Alexander Stuart, Alvaro Nogues Palenzuela, and Finbarr Horgan
16:15	91	**RICE-PRE, a strategic decision tool for rice farmers** Joselito Villa, Jerico Bigornia, Nancy Castilla, Serge Savary , and Adam Sparks

Effect of cultivar, tillage system, and herbicide on weed management and grain yield in dry-seeded rice systems

Jhoana L. Opeña[1*] and Bhagirath S. Chauhan[1]
[1]Weed Science, Crop and Environmental Sciences Division, International Rice Research Institute, Los Baños, Philippines
*Correspondence: j.opena@irri.org

In Asia, there is a shift from manual transplanting of rice seedlings to direct seeding as a response to increasing cost of labor and decreasing labor and water availability. Weeds, however, are the major constraint to dry-seeded rice production. Field studies were conducted to evaluate the effects on weed growth and rice grain yield of using inbred and hybrid rice cultivars in combination with different herbicides and of using tillage systems and different herbicides under dry-seeded rice systems. Weed density, weed biomass, and rice yield were not influenced by cultivar but were strongly affected by weed control treatments. Nevertheless, the hybrid cultivar (Mestiso 21) had an 11−12% yield advantage over the inbred cultivar (RC222) when seeded at 20 kg seed ha^{-1}. Weed competition in control plots (one handweeding) lowered rice yield by 39–41% compared with weed-free plots. All herbicides significantly reduced weed biomass, providing 75–93% weed control. In another study, with an inbred (50 kg seed ha^{-1}), herbicide efficacy was lower in the zero-till system than in the conventional tillage system. Grain yields in herbicide-treated and weed-free plots were similar between tillage systems. However, grain yield in weedy plots was lower in zero-till than in conventional tillage. The results suggest that hybrid cultivars, using low seed rates, can be grown under dry-seeded conditions and that they have the potential to increase total rice production. The findings also imply that rice can be grown successfully in zero-till, dry-seeded systems if weeds are effectively controlled.

Keywords: zero-till, weed competition, weed biomass, hybrid, inbred

Weed management in zero-till, dry direct-seeded rice systems

Seth Bernard E. Abugho[1*] and Bhagirath S. Chauhan[1]
[1]Weed Science, Crop and Environmental Sciences Division
International Rice Research Institute, Los Baños, Laguna
*Correspondence: s.abugho@irri.org

Appropriate weed management is necessary in dry direct-seeded rice systems to achieve high yields. Screenhouse and field studies were conducted to determine the efficacy of herbicides under zero-till crop establishment methods. In the screenhouse, herbicide (control, oxadiazon at 0.5 and 1 kg ai ha^{-1}, and pendimethalin at 1 and 2 kg ai ha^{-1}) efficacy was determined on four major weeds of rice (barnyardgrass, rice flatsedge, junglerice, and crowfootgrass) when applied with different residue amounts (0, 3, and 6 tons ha^{-1}). Barnyardgrass and rice flatsedge were effectively controlled when herbicides were applied without residue, whereas their emergence was observed when herbicides were applied in the presence of residue cover. These results suggest that residue cover may reduce the efficacy of some pre-emergence herbicides. Junglerice and crowfootgrass were effectively controlled under all residue cover. In the field, a study was conducted during the wet season of 2011 and the dry season of 2012 to evaluate the performance of different herbicides in zero-till dry-seeded rice. Among the treatments evaluated, oxadiazon followed by penoxsulam + cyhalofop followed by one hand-weeding provided 23–35% higher yield than the control treatment. The yield obtained in this herbicide-treated plot was similar to those in the weed-free plots. These results suggest that effective weed control is possible in zero-till systems if appropriate herbicides are used at appropriate times. However, some weed species were not controlled by the evaluated herbicides. Therefore, there is a need to evaluate additional herbicides and integrate these with cultural weed management strategies to manage such problematic weeds.

Keywords: herbicide, efficacy, residue

Influence of rice seeding and nitrogen rates on weed suppression and growth of rice under aerobic conditions

Tahir Hussain Awan* and Bhagirath S. Chauhan
Weed Science, Crop and Environmental Sciences Division
International Rice Research Institute, Los Baños, Philippines
*Correspondence: t.awan@irri.org

Dry-seeded rice is replacing puddled-transplanted rice in many Asian regions because of increased production costs and decreased availability of labor and water. In dry-seeded rice, however, weeds are often the principal biotic constraint to rice production. Herbicides are used to manage weeds but there are concerns over the evolution of resistance in weed population. There is thus a need to develop cultural weed management strategies. Manipulation of crop plant density and fertilization is a promising agronomic practice in reducing weed interference in crops. Increasing seeding rate may suppress weed growth; however, the crop at high plant density may require additional nitrogen. A preliminary study was conducted in a screenhouse to determine the effect of rice plant density and nitrogen rates on the growth of *Cyperus iria, Echinochloa colona, Ischaemum rugosum,* and *Rottboellia cochinchinensis*. The number of leaves, tiller number, leaf area, shoots biomass, and inflorescence number of all the weeds decreased with increasing rice plant density; however, the response was species-specific. At high rice plant density, the growth of rice increased with increasing nitrogen doses. After such responses of weeds and rice to plant density and nitrogen rates, a field study was initiated in the wet season of 2012 to evaluate the effects of seeding rate (50 and 150 kg ha^{-1}), weed control method (partially weedy and weed-free), and nitrogen level (0, 100, 150, and 200 kg ha^{-1}) on the growth of weed and rice and rice yield in a dry-seeded rice system. The results will be discussed in the presentation.

Phenotyping and molecular characterization of rice accessions for resistance to sheath blight

Gil Beligan,[1] Srinivasachary,[1*] Serge Savary,[1,3] Marina Natural,[2] Eula Gems Oreiro,[1] Jelmer Aguire,[1] Ricardo Oliva,[1] and Laetitia Willocquet[1,3]
[1]Plant Breeding, Genetics, and Biotechnology Division, International Rice Research Institute, Los Baños, Laguna, Philippines
[2]Crop Protection Cluster, University of the Philippines, Los Baños, College, Laguna, Philippines
[3]UMR INRA-INP-ENSAT AGIR-Toulouse, Chemin de Borde Rouge, Auzeville, 31320 Castanet Tolosan, France
*Correspondence: charysv@hotmail.com

Sheath blight (ShB), caused by the fungus *Rhizoctonia solani* Kühn, is an important disease of rice (*Oryza sativa* L.) worldwide. To date, no rice accession has been found to be immune to ShB. However, accessions carrying partial resistance have been reported. ShB resistance is mainly a quantitative trait governed by many minor genes. Plant morphological traits, especially plant height and crop duration cycle, have been reported to play an important role in determining disease escape. Breeding for ShB resistance has been slow due to paucity of resistance sources, the complex nature of resistance, and the lack of precise high-throughput phenotyping methods. To identify rice accessions carrying a high level of resistance, 163 cultivated accessions belonging to *O. sativa* were intensively screened using two complementary phenotyping methods. Majority of the accessions (81 indica, 21 intermediate (hybrids), two each from javanica and japonica) used in the study have been reported to carry some level of ShB resistance. Multiple correspondence analyses were employed to identify resistance sources and to test associations between plant morphological traits and ShB resistance. Here, we report 27 cultivated accessions with good agronomic traits carrying high levels of partial resistance and these could be used as sources of resistance. These genotypes have been shared with several NARES partners in South Asia (India, Nepal, Bangladesh), where they are tested. Selected 26 polymorphic SSRs were used to study the genetic diversity of the 163 *O. sativa* genotypes. Using the markers, cultivated accessions were categorized into highly resistant, susceptible, and intermediate groups.

Keywords: partial resistance, sheath blight, QTL, SSRs

Postharvest resistance of upland NERICA and their parents to *Sitotroga cerealella* Olivier (Lepidoptera: Gelechiidae)

Carline Santos,[1,3] Francis Nwilene,[2] and Clement Agbangla[3]
[1]Africa Rice Center (AfricaRice), 01 BP 2031, Cotonou- Benin (carjochrist85@gmail.com)
[2]Africa Rice Center (AfricaRice) Nigeria Station, PMB 5320, Oyo Road, Ibadan, Nigeria (f.nwilene@cgiar.org)
[3]Université D’Abomey Calavi, Faculté des Sciences et Techniques 01 BP 526, Abomey-Calavi, Benin (clementagbangla@gmail.com)

Sitotroga cerealella (Olivier) is a major postharvest pest in rice. In the framework of both conservation and pre-breeding strategies for, respectively, optimization of storage of grain from existing rice varieties and development of new lines tolerant of this pest, a screening of 21 varieties of rice, including the 18 upland NERICAs and their three parents, was conducted. The experiment was performed using the “no choice” (artificial infestation) method. Two hundred grains of paddy of each variety were infested with 20 eggs of *S. cerealella* and stored in controlled conditions of humidity and temperature. Different responses of the rice varieties to *S. cerealella* infestation were observed. Among the NERICAs tested, NERICA 6, 14, 4, 3, 15, and 16 were found to be tolerant, whereas NERICA 9 and 11 were sensitive. The *Oryza glaberrima* parent, CG14, was resistant to the insect, while the *O. sativa* parents WAB 56-50 and WAB 56-104 were sensitive. The resistance to the insect in the progenies may have been provided by the parent GC14. Further studies will determine the genetic basis and mapping of resistance to *S. cereallela* in rice.

Keywords: varietal resistance, tolerance, storage pests, *Sitotroga cereallela*

Characterization of resistance to root-knot nematode *Meloidogyne graminicola* in *Oryza glaberrima*

Ma. Teodora Nadong Cabasan,[1,3,4*] Arvind Kumar,[3] and Dirk De Waele[1,2,3]
[1]Laboratory of Tropical Crop Improvement, University of Leuven, Belgium
[2]Department of Biology, Faculty of Sciences, Ghent University, Belgium
[3]International Rice Research Institute, Philippines
[4]Department of Biological Sciences, University of Southern Mindanao, Philippines
*Correspondence: t.cabasan@irri.org

The root-knot nematode *Meloidogyne graminicola* can cause substantial rice yield losses. Understanding the mechanism(s) of resistance to this nematode species in known resistant rice genotypes may facilitate the improvement of rice varieties resulting in an environment-friendly and cost-efficient nematode management strategy. Using susceptible and resistant rice genotypes, the migration, penetration, development, and reproduction of the rice root-knot nematode in resistant African rice (*Oryza glaberrima*) genotypes TOG5674, TOG5675, CG14, and RAM131, and in susceptible Asian rice (*O. sativa*) genotypes IR64 and UPLRi-5 were studied and compared. The number of second-stage juveniles (J2) that had migrated toward the rhizosphere of the rice plants was comparable with those in both susceptible and resistant rice genotypes. However, penetration of J2 was significantly lower in the resistant rice genotypes than in the susceptible rice genotypes. Nematode development was slower and reproduction was significantly lower in the resistant rice genotypes, which supported fewer eggs per gram of roots and eggs per female. Mature females that had developed in resistant rice genotypes were significantly smaller than their counterparts in susceptible ones. The resistant rice genotypes had significantly fewer galls than the susceptible rice genotypes. A comparative analysis of histological response mechanisms was made during nematode penetration and development. Two types of defense response mechanisms could be distinguished. The early defense response in resistant rice genotypes is manifested by a hypersensitive reaction (HR) in the early stage of infection, characterized by necrosis of cells directly involved in nematode feeding. This HR-like phenotype is observed only in *Meloidogyne*-resistant African rice and not in susceptible Asian rice genotypes. The late defense response in resistant rice genotypes took place after the induction of giant cells by the nematode. Feeding cells degenerated early before the nematode reached maturity.

Keywords: *Meloidogyne graminicola*, mechanism, resistant, susceptible, giant cells

Biochemical approach for virulence factor identification in *Xanthomonas oryzae* pv. *oryzae*

Codjo Sylvestre Gerbert Dossa,[1*] Petr Karlovsky,[1] and Kerstin Wydra[2]
[1]Molecular Phytopathology and Mycotoxin Research, Georg-August University Goettingen, Grisebachstr. 6 37077, Goettiengen, Germany
[2]Centre for Biodiversity and Sustainable Land Use - Tropical and Subtropical Agriculture and Forestry, Georg-August University Goettingen Buesgenweg 1 D-37077, Goettingen, Germany
*Correspondence: d_gerbert@yahoo.com

Bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo) leads to a substantial yield reduction of up to 50% in most rice-growing regions. Host plant resistance is an effective control method against the disease and more than 30 resistance genes have been identified. To understand the interaction of the pathogen leading to a susceptible reaction of the host plant, biochemical analyses for virulence factor identification of *Xoo* were conducted using strains Mai1, PXO88, Dak1, and Dak16 from West Africa (Mai1), Philippines (PXO88), and East Africa (Dand1 and Dak16). These studies revealed that the *Xoo* culture filtrate induced typical bacterial symptoms on susceptible rice genotypes IRBB4 and FKR14. The heated culture filtrate showed phytotoxicity effects on both rice genotypes with 6.9 cm of highest lesion length; 13.4 cm was the maximum length induced by a proteinase K-treated fraction. After ethyl acetate treatment of the culture filtrate, a considerable reduction of phytotoxicity was observed, suggesting that a low molecular-weight toxin, possibly produced by *Xoo*, does not play a major role in virulence. By HPLC-MS, 3-methylthio-acrylic acid and methylthiopropionic acid from the *Xoo* culture filtrate are being identified to further characterize putative virulence factors of *Xoo*.

Keywords: *Xanthomonas oryzae* pv. *oryzae*; culture filtrate, phytotoxicity, rice, virulence

Spectrum and stability of hopper resistance in monolocus and pyramided rice lines

Srinivasan Thanga Suja,[*1,2] Ma. Liberty P. Almazan[1], Daisuke Fujita,[3] and Finbarr G. Horgan[1]
[1]Crop and Environmental Sciences Division, International Rice Research Institute, Philippines
[2]Tamil Nadu Agricultural University, India
[3]Plant Breeding, Genetics, and Biotechnology Division, International Rice Research Institute, Philippines
*Correspondence: s.srinivasan@irri.org

Planthoppers and leafhoppers can damage rice by feeding on the rice phloem sap and/or by acting as vectors of rice viruses. High-yielding, insect-resistant rice varieties can potentially reduce hopper damage in the field. Numerous insect resistance genes have been mapped and successfully introgressed into cultivated rice varieties; however, hoppers have been able to adapt to monogenic resistant varieties within a short period of time. Pyramiding of two or more major resistance genes is suggested to increase the spectrum, stability, and durability of resistance against hoppers. In this study, preliminary near-isogenic lines (NIL) with the BPH25 and BPH26 resistance loci and a pre-pyramided (PYL) line with both loci were examined for their resistance to rice hoppers and compared against recurrent parent T65 and donor line ADR52. The main objective of the study was to compare the spectrum and stability of resistance in the monolocus and pyramided lines. The resistance spectrum was examined using three different hopper species (brown planthopper, *Nilaparvata lugens* (Stål) (BPH); whitebacked planthopper, *Sogatella furcifera* (Horváth) (WBPH); and green leafhopper, *Nephotettix virescens* (Distant) (GLH)) and eight brown planthopper populations. The PYL had generally higher resistance than the monogenic lines. Surprisingly, resistance was more effective against GLH nymphs than BPH nymphs. The PYL reduced egg laying in GLH and BPH but increased the same in WBPH, indicating complex interactions between resistant lines and hopper species. The stability of resistance was studied in the field under different nitrogen levels. The results indicated that the PYLs alone were resistant in the field under low nitrogen, but resistance was lost under high nitrogen levels. Our future work will examine the effects of pyramiding these genes on the durability of resistance against BPH.

Keywords: planthoppers, monolocus, pyramided lines

Interactions between crop management and host-plant resistance to brown planthoppers

Ainara Peñalver Cruz,[*1,2] Ma. Liberty P. Almazan,[1] and Finbarr G. Horgan[1]
[1]Crop and Enviromental Sciences Division, Interantional Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]The Lancaster Environment Center, Lancaster University, Bailrigg, Lancaster, LA1 4YW, United Kingdom
*Correspondence: a.penalvercruz@irri.org

The brown planthopper *Nilaparvata lugens* (Stål) (BPH) has reemerged as a major rice pest in Southeast Asia since the early 2000s. Use of host-plant resistance is regarded as an efficient, pro-poor method of reducing planthopper densities and maintaining rice yield in affected areas. However, the effectiveness of resistant rice varieties in the field can be compromised by incompatible or inadequate crop management. We conducted a series of experiments in the greenhouse, screenhouse, and the field to assess the effects of nitrogen levels and insecticide applications on the resistance of IR62 to BPH. Our results indicate that resistance in IR62 declines under increasing levels of nitrogen fertilizer: BPH laid more eggs under high nitrogen conditions and nymphal development was faster. Shoot tolerance also declined in IR62 under high nitrogen levels, but yield tolerance increased. Insecticide effects on BPH populations varied considerably across seven chemical products; however, single applications were generally insufficient to reduce BPH densities with up to three applications required in most cases. Repeated and late applications will promote insecticide resistance and were shown here to reduce yield in some cases, even in the absence of BPH. Two pyrethroids increased plant susceptibility to BPH, but the outcome differed according to relative levels of BPH insecticide resistance. The results indicate the need for greater attention to crop management for increased efficiency of the host-plant resistance method.

Keywords: host-plant resistance, IR62, *Nilaparvata lugens*, Hemiptera, Delphacidae, fertilizer, nitrogen, pesticide

Resistance and tolerance of introgressed and aerobic rice genotypes to root-knot nematode *Meloidogyne graminicola*

Judith Pacya-an Galeng,[1,3*] Mallikarjuna Swamy,[3] Arvind Kumar,[3] and Dirk De Waele[1,2,3]
[1]Laboratory of Tropical Crop Improvement, University of Leuven, Belgium
[2]Department of Biology, Faculty of Sciences, Ghent University, Belgium
[3]International Rice Research Institute, Philippines

The root-knot nematode *Meloidogyne graminicola* is an obligate biotrophic parasite and one of the most damaging pathogens that cause significant yield losses in upland and rainfed lowland rice in South and Southeast Asia. Resistance to and tolerance for *M. graminicola* hold out the most promising effective and economic approach to control yield losses. One hundred and fifty-five introgressed genotypes derived from IR64 (*Oryza sativa*) and CG14 (*O. glaberrima*) and 26 aerobic genotypes derived from Way Rarem and Vandana were evaluated for their resistance to and tolerance for *M. graminicola* under field conditions at IRRI. In the introgressed genotypes, 26 were resistant and 12 were partially resistant on the basis of the number of infective J2 in the root system. As to yield reduction (YR), 15 lines were tolerant (<10% YR), 11 were less sensitive (10–20% YR), 5 were sensitive (21–30% YR), and 84 were hypersensitive (>30% YR). In aerobic genotypes, 14 genotypes were partially resistant and 13 were susceptible. Only two genotypes were less sensitive with a YR of <20%, three genotypes were sensitive (21–30% YR), and 19 were highly sensitive (>30% YR). The QTLs conferring resistance to and tolerance for *M. graminicola* were mapped in introgressed lines, which were used as mapping population. A QTL for nematode reproduction in the root system was detected in chromosome 7 and it explained 13.4% of the phenotypic variance. One QTL related to dry root weight was detected in chromosome 8, explaining 13.8% of phenotypic variation. In chromosome 2, a QTL for plant yield was detected, which accounted for 13.2% of the phenotypic variance. The QTL for % filled grains mapped in chromosome 12 showed the largest effect, with the LOD value of 5.25, and explained 14.5% of the variation.

Keywords: *Meloidogyne graminicola*, resistant, susceptible, tolerant

Field evaluation of certain genotypes against major rice pests in the Karaikal Region

Anil Varma Nalla,* D. Adiroubane, K. Kumar, and S. Nadaradjan
Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal-3, U.T. of Puducherry, India
*Correspondence: anilvarmanalla@gmail.com

Host plant resistance is a continuing breeding objective. In the Karaikal region, severe damage caused by major rice pests (e.g., yellow stem borers and rice leaffolders) was observed. A field study was conducted by screening 196 rice accessions at the Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal, to identify sources of resistance to major rice pests such as yellow stem borer Scirpophaga incertulas and rice leaffolder complex (*Cnaphalocrocis medinalis*, *Marasmia patnalis*, *M. ruralis,* and *M. exigua*) in 2011. Accessions were screened for stem borer resistance at the vegetative and reproductive stages. At the vegetative stage (deadhearts) during 2011 kharif, five were identified as resistant entries–No. 40 (OR 2324-8), 160 (RTN 62-6-7-1), 140 (CR 2698), 60 (HUR-913), and 150 (CN 1561-70-19-35-9-MLD 1). At the reproductive stage (white ears), four entries were identified as moderately resistant–No. 40 (OR 2324-8), 160 (RTN 62-6-7-1), 70 (R 1138-688-3-533-1), and 140 (CR 2698). Screening for leaffolder resistance carried out at five different growth stages (30, 40, 50, 60, and 70 DAT) resulted in 10 resistant entries identified: No. 30 (ARRH-3626), 40 (OR 2324-8), 140 (CR 2698), 90 (UPR 3506-7-1-1), 120 (HUBR 10-9), 20 (R 1528-1058-1-110-1), 150 (CN 1561-70-19-35-9-MLD 1), 34 (CR 2652-14), 68 (PAU 3371-26-1-3), and 61 (NDR 370135). Results indicated that entries bearing numbers 40 (OR 2324-8) and 140 (CR 2698) showed multiple resistance to stem borers (resistant at the vegetative stage and moderately resistant at the reproductive stage) and leaffolders (resistant). Biochemical factors were analyzed in entries that showed resistance to stem borers and leaffolder complex. Higher total phenol, moderate chlorophyll, and less sugar content were identified as the factors that impart the resistance trait.

Keywords: host plant resistance, stem borers, leaffolder complex, biochemical factors

Characterization of injury profiles and production situations in Southeast Asia

Jerico Bigornia,*[1] Joselito Villa,[1] Nancy Castilla,[1] Adam Sparks,[1] and Serge Savary[1,2]
*Epidemiology and Crop Health Group, PBGB, International Rice Research Institute, Los Baños, Laguna, Philippines
[2]Current address, INRA, Castanet Tolosan, France
*Correspondence: j.bigornia@irri.org

Understanding what groups of pests affect rice and where they occur is critical to developing crop management strategies. Crop health surveys are crucial in collecting these data. A previous survey collected data from 1987 to 1997 in tropical Asia. Since then, production systems have changed and new pests have emerged. New survey data were collected from 400 farmers' fields across Southeast Asia in 2009–10 in collaboration with partners under the Irrigated Rice Research Consortium using IRRI's survey portfolio. Data from eight sites were analyzed using multivariate statistical methods. Results indicated that (i) clusters of production situations and of injuries are strongly associated but are not site-specific; (ii) the mean value of actual yield was 4.8 t ha^{-1}, suggesting that there has been no improvement in actual yield across the region since the previous survey was conducted, in spite of increase in input use (especially mineral fertilizers and pesticides); (iii) high prevalence of diseases, such as bacterial blight, blast, brown spot, bacterial leaf streak, and the emergence of false smut and ragged stunt virus; (iv) increase in the population of several insect pests, especially planthoppers which are vectors of viral diseases; and (v) high weed infestation in Iloilo, Philippines, and Thailand. These data sets require further analysis but, nevertheless, clearly show that crop health problems are not site-specific. The development of management strategies can therefore be recommended on a regional basis.

Keywords: crop health, pest management, production situation, injury profile, multivariate statistical methods

The snail invasion–an ecological and agricultural disaster

Alexander Stuart,[1*] Alvaro Nogues Palenzuela,[1] and Finbarr Horgan[1]
[1]Crop and Environmental Sciences Division, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: a.stuart@irri.org

In tropical and subtropical freshwater aquatic systems, introduced gastropods have had catastrophic impacts in both natural ecosystems and in agriculture. One such example is the introduction of the golden apple snails (GAS), *Pomacea caniculata* and *Pomacea insularum*, from their native range in South America to Asia, North and Central America, and, more recently, to other countries within South America. GAS introductions have been either deliberate, as a potential food resource, or accidental, through the aquarium trade, and as a result of their generalist feeding habits, high fecundity, fast growth, and lack of natural predators, they were able to quickly spread into rice fields, where they subsequently became a serious pest of rice. Over the past year, we have been conducting studies both in the field and in the greenhouse to develop our understanding of GAS ecology and rice vulnerability to GAS under different fertilizer regimes. We will present some of the preliminary results from these studies as well as findings from a visit to Ecuador, where GAS has been recently introduced and is now a major threat to rice farming.

Keywords: golden apple snail, invasive species, rice, pest management

RICE-PRE, a strategic decision tool for rice farmers

Joselito Villa,[1*] Jerico Bigornia,[1] Nancy Castilla,[1] Serge Savary,[1,2] Adam Sparks[1]
[1]Epidemiology and Crop Health Group, PBGB, International Rice Research Institute, Los Baños, Laguna, Philippines
[2]Current address, INRA, Castanet Tolosan, France
*Correspondence: j.villa@irri.org

Yield loss that is often experienced by rice farmers in developing countries can be prevented with proper diagnosis of crop health. However, access to a rice specialist is usually limited or lacking in most areas. To help farmers answer this need, RICE-PRE (Rice Epidemic Prevention) was developed. This is a strategic decision tool that prescribes a set of recommendations that contain the list of strategies for crop production and crop protection aimed at decreasing yield losses. Each prescription was created based on the combination of several elements: 1) rice agroecology, 2) agricultural objectives, 3) major pests, 4) crop management options, and 5) the most appropriate pest management options available. The RICE-PRE prescriptions were derived from survey results in rice fields in Asia that showed very strong statistical links between pest syndromes and production situations in spite of a broad range of environments and highly diverse injuries caused by harmful agents. The prescriptions recommend the use of resistant varieties whenever available against the major pests that are expected to be production constraints. It is only when resistant varieties are not available and the risk of injuries is unacceptably high that judicious pesticide use is recommended. Preliminary results of field experiments in the 2012 dry season showed a 10.5% yield advantage of RICE-PRE treatment over conventional farmers' practice. This indicated the promising potential of the use of RICE-PRE system in farmers' fields.

Keywords: rice, crop health, crop protection, pest injuries, rice production

Category 3

Extension, Marketing, and Policies

8 Nov 2012 Category 3: Extension, Marketing, and Policies 2012 IRRI Young Scientists Conference

Time	Abstract no.	Abstract title, authors
10:15	13	**Ex ante impact assessment of a drought-tolerant rice variety in the presence of climate change** Khondoker A. Mottaleb, Roderick M. Rejesus, Samarendu Mohanty, M.V.R. Murty, Tao Li ,Harold Glenn Valera, and Murali Krishna Gumma
10:35	21	**Assessing women's empowerment among rice farming households in Bangladesh, eastern India, and Nepal** M. L. Malabayabas, T. Paris, and D. Gauchan
10:55	29	**Participatory videos to promote best management practices to rice farmers in Sulawesi, Indonesia** Trina Leah Mendoza, Madonna Casimero, and Rona Niña Mae Rojas
11:15	38	**Asymmetric price transmission on local rice markets in West Africa: the case of two rice sector development hubs in Benin and Mali** Rose Fiamohe, Alia Y. Didier, Papa A. Seck, and Diagne Aliou
11:35	43	**Enhancing capacities of farmers in Lao PDR: a case in Saybouathong District** Pany Vanmanivong
11:55	48	**Economic impact of improved natural resource management on irrigated rice systems in eastern Indonesia** Rowell Dikitanan, Rica Joy Flor, Madonna Casimero, Grant Singleton, and Zainal Abidin
13:35	77	**Total factor productivity (TFP) of northeast Benin rice farmers: a case study of Malanville municipality** Rosaine N. Yegbemey and Jacob A. Yabi
13:55	78	**Farmers' participatory site-specific nutrient management for rainfed transplanted short-duration aman rice in the Ganges tidal floodplain** Deb Kumar Nath, Fahomida Amin, Md. Shahidul Islam, and Md. Abu Saleque
14:15	81	**Rice productivity improvement and contribution to welfare change in the African agricultural sector** Mandiaye Diagne and Aliou Diagne
14:35	85	**Farmers' participatory site-specific nutrient management in the Ganges tidal floodplain soil of Bangladesh for boro rice** M. Sh. Islam, F. Amin, D. K. Nath, and M. A. Saleque
14:55	86	**Competitiveness of the rice sector in Benin** Simon Codjo Ogoudélé, Diagne Aliou, and Kinkingninhoun-Medagbé Florent
15:35	87	**Potential impact of the national rice development strategy in Benin** Allodehou Amos, Diagne Aliou, and Kinkingninhoun-Medagbé Florent
15:55	94	**Does adaptive research help rice farmers integrate and adopt from a range of technology options?** Rica Joy Flor, Madonna Casimero, Grant Singleton, Zainal Abidin, and Nasruddin Razak
16:15	95	**Preliminary results of baseline household surveys in Ayeyarwaddy and East Bago, Myanmar** Arelene Julia Malabayabas, Florencia Palis, and Grant Singleton

Ex ante impact assessment of a drought-tolerant rice variety in the presence of climate change

Khondoker A. Mottaleb,[1,2 *] Roderick M. Rejesus,[2] Samarendu Mohanty,[1] M.V.R. Murty,[1] Tao Li,[1]
Harold Glenn Valera,[1] and Murali Krishna Gumma[1]
[1]International Rice Research Institute, Los Baños, Philippines
[2]North Carolina State University, USA
*Correspondence: k.mottaleb@irri.org

Rice productivity and sustainability are continually threatened by abiotic stresses, particularly in the era of global climate change. In severe cases, 100% yield loss can be experienced due solely to abiotic stresses, such as drought. The situation may become worse due to climate change, which may multiply the frequency and severity of such abiotic stresses. Hence, there is an urgent need to develop improved varieties that are more resilient to abiotic stresses. This article examines the net economic benefit and potential economic impacts of developing and disseminating a drought-tolerant rice variety in South Asia. Drought is one of the most destructive abiotic stresses that cause major rice yield losses not only in South Asia but also in other parts of Asia and Africa. Using the ORYZA2000 crop simulation model, we demonstrate that the new variety can provide yield gains in South Asia both when there is no change in the climate and also under different climate scenarios projected by the CGCM climate model. Moreover, our economic surplus analysis shows that the economic benefits from the successful development and dissemination of a drought-tolerant variety more than outweigh the research investments needed to develop the variety. The partial equilibrium models we used also indicate that rice production is higher and rice prices are lower when a drought-tolerant variety is adopted in South Asia (as compared with the case without this new variety). This, in turn, can lead to more sustainable rice production, improved food security, and better nutritional outcomes for the poor.

Keywords: climate change, drought tolerance, ex ante economic impact, rice varieties, South Asia

Assessing women's empowerment among rice farming households in Bangladesh, eastern India, and Nepal

M. L. Malabayabas,[1*] T. Paris,[1] and D. Gauchan[1]
[1]Social Sciences Division, International Rice Research Institute, Los Baños, Philippines
*Correspondence: m.malabayabas@irri.org

Rice is one of the important crops grown in Bangladesh, India, and Nepal. Covering 59% of the world's total rice area, rice is mostly grown under the rainfed ecosystem (IRRI 2012). However, most of these rainfed rice areas regularly suffer from various abiotic stresses such as drought, flood, and salinity. This leads to low and unstable rice yields and affects the livelihood of farmers. In this stress-prone environment, what are the roles of women in making decisions about farming and household issues? This paper aims to assess women empowerment in making farm-related and family-related decisions among rice farming households in these stress-prone areas. A socioeconomic survey was conducted among 1,908 households in 19 sites in 2008. Gender analysis in terms of labor inputs and decision making related to rice production and overall livelihood activities were carried out. A women empowerment index (WEI) was computed using 16 gender-related indicators to quantify women's empowerment in relation to men's. A censored one-sided Tobit analysis was used to identify the factors that affect women empowerment. Findings revealed that men remain the overall decision-making authority in the household. The proportion of female labor to total labor and the share of modern variety area to total rice area significantly affected WEI. It is thus important to empower women by providing them adequate technical knowledge and skills to enable them to be efficient farmers and, more importantly, better farm managers. Consequently, farming households can better cope with environmental stresses and have greater opportunities to improve their livelihood.

Keywords: women empowerment index (WEI) in rice, censored Tobit analysis, rainfed ecosystem

Participatory videos to promote best management practices to rice farmers in Sulawesi, Indonesia

Trina Leah Mendoza,[1*] Madonna Casimero, and Rona Niña Mae Rojas[1*]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: t.mendoza@irri.org

We tested the Digital Green participatory video approach in July 2011 with rice farmers in South and Southeast Sulawesi, Indonesia. Using this approach, short learning videos that capture new or improved agricultural practices are created by farmers for farmers. Videos on direct seeding and weed management, alternate wetting and drying, and site-specific nutrient management were produced. Farmers developed storyboards guided by staff from the Assessment Institute for Agricultural Technology and the Irrigated Rice Research Consortium. Most farmers confidently shared their experiences and demonstrated their practices in front of the camera. In January 2012, the direct seeding video was shown to farmers to elicit their feedback. Southeast Sulawesi farmers responded positively to the video and remembered key messages. They were delighted to see fellow farmers on screen. To improve the video, they suggested graphics showing economic benefits. The 13-minute video length, arguably long by industry standards, was still short for them. They suggested other video topics leading to postharvest. They are happy for farmers in other areas to see their video. South Sulawesi farmers enjoyed the video; although they do not practice direct seeding, they found other farmers telling their stories convincing. Some scientists wanted more control on video content and topics, while others thought that farmers sharing their success stories is an effective and innovative way to promote best management practices.

Keywords: IRRC, participatory video, Digital Green, rice farmers, Indonesia

Asymmetric price transmission on local rice markets in West Africa: the case of two rice sector development hubs in Benin and Mali

Rose Fiamohe,[1*] Alia Y. Didier,[2], Papa A. Seck,[1] and Diagne Aliou[1]
[1]Africa Rice Center (AfricaRice), 01 BP 2031 Cotonou, Benin
[2]University of Kentucky,400 Charles E. Barnhart Building; Lexington, KY 40546-0276
*Correspondence: e.fiamohe@cgiar.org

Identifying marketing areas with a prevalence of transaction costs is one of the new research approaches for targeting marketing infrastructure that could be introduced to improve market access. In most African countries, spatial dispersion of production and consumption often causes high transaction costs, preventing farmers from having access to markets and causing asymmetry in price transmission. AfricaRice and the NARES have recently established rice sector development hubs in many African countries where modern communication methods will be used to introduce new technologies so that farmers and other stakeholders along the rice value chains can benefit from better information flow and linkages with each other. To achieve this, surveys and studies are ongoing in many hubs to provide baseline information and well-designed impact studies. As a contribution to the baseline information on local rice marketing areas, this paper used the Enders and Siklo threshold models on monthly series of price from 2000 to 2010 to examine asymmetric price transmission between selected markets in the hubs and the nearest important consumption markets in Benin and Mali. The results for Benin indicate that price transmission between market in the hub and the consumption market is asymmetric, probably due to the prevalence of transaction costs. Conversely, the results for Mali indicate a symmetric price transmission between market in the hub and consumer market, suggesting the absence of transaction costs.

Keywords: local rice price transmission, transaction costs, threshold models, asymmetric adjustments

Enhancing the capacities of farmers in Lao PDR: the case in Saybouathong District

Pany Vanmanivong
International Rice Research Institute, IRRI-Lao Office, Vientiane, Lao PDR
Correspondence: P.Vanmanivong@irri.org

Rice is a key staple in Lao PDR, as in most countries of the region and, as such, is an important element of food security. Over the past 20 years (1991-2011), rice production in the country has more than doubled, reaching around 3.3 million tons of paddy in 2011. As Laos has moved from rice deficits to sizable rice surpluses, food security remains a major challenge in many areas. Rice shortage as source of food insecurity is becoming an increasingly localized phenomenon and improving rice production techniques will help farmers become more food-secure. In the past, the government has set up an extension system with district staff of the Agriculture and Forestry Office responsible for training and supporting farmers. However, the number of district staff is limited and not all farmers are served. Saybouathong District is one of poorest districts in Khammouane Province (central part of Lao PDR). Road access in the district is difficult, especially in the rainy season. This limits the visits of extension staff to the villages. A capacity-building project was implemented from 2006 to 2011 to develop local technical knowledge and expertise on rice production in 16 villages of Saybouathong District. This paper presents the outcome of the project after 6 years of implementation. About 26 well-trained farmers in the villages became trainers and subsequently trained fellow farmers on improved rice production techniques. As a result, rice farmers were able to increase rice yields by 0.5 t ha^{-1} after adopting good rice management practices.

Keywords: Lao PDR, capacity building, food security, production techniques, training

Economic impact of improved natural resource management on irrigated rice systems in eastern Indonesia

Rowell Dikitanan,[1*] Rica Joy Flor,[1] Madonna Casimero,[1] Grant Singleton,[1] and Zainal Abidin[2]
[1]International Rice Research Institute. DAPO Box 7777, Metro Manila, Philippines
[2]Balai Pengkajian Teknologi Pertanian, South Sulawesi, Indonesia
*Correspondence: r.dikitanan@irri.org

The economic impact of improved natural resource management (NRM) on irrigated lowland rice systems was examined using propensity score matching. Effects on income, yield, fertilizer, and pesticide costs were determined by calculating average treatment effects on the treated while controlling for selection bias from observable variables. Data were from a cross-section farm-level survey of rice farmers in Sulawesi, Indonesia. Adoption of improved NRM technologies led to a significant increase in income of farmers. The adopters had a mean 53% increase in income compared with non-adopters. The logit regression model indicated that attendance at a farmer field school, which emphasized adaptive management, had a strong positive impact on the likelihood of adoption. Improved NRM reduced the intensity of input use without reducing yield, leading to reduced cost and higher income per household.

Keywords: economic impact assessment, propensity score matching, technology adoption, natural resource management, irrigated rice

Total factor productivity of northeast Benin rice farmers: a case study of Malanville municipality

Rosaine N. Yegbemey[1,2*] and Jacob A. Yabi[1]
[1]Department of Agricultural Economics and Rural Sociology, Faculty of Agronomy, University of Parakou; BP 123 Parakou, Republic of Benin
[2]Faculty of Agricultural Sciences, Nutritional Sciences and Environmental Management; Justus-Liebig University of Giessen, Senckenbergstrasse 3, D-35390; Germany
*Correspondence: rosaine.n.yegbemey@agrar.uni-giessen.de

The economic efficiency of rice farmers used to be assessed using stochastic frontier analysis. But because of gaps between the output implied by the regression line for a given level of inputs and the real output at the same level of inputs, the frontier analysis can provide misleading measures. This article aims to analyze economic efficiency levels using an analytical approach that does not impose any parametric function: the indexes of productivity (TFP). To meet this objective, primary data have been collected from 120 rice farmers in Malanville municipality. Data analysis showed that average TFP was 1.32 (± 0.57) in the wet season, 1.45 (± 0.78) in the dry season, and 1.33 (± 0.55) in both seasons. This assumes that rice producers are economically efficient. Moreover, the farmer's access to credit, his rice production experience, and type of production system were the main determinants of his efficiency level.

Keywords: rice production, indexes of productivity, total factor productivity, economic efficiency, Malanville

Farmers’ participatory site-specific nutrient management for rainfed transplanted short-duration Aman rice in the Ganges tidal floodplain soil

Deb Kumar Nath,[1*] Fahomida Amin,[1] Md. Shahidul Islam,[1] and Md. Abu Saleque[1]
[1]International Rice Research Institute, South Alekanda, Barisal 8200, Bangladesh
*Correspondence: d.nath@irri.org

Farmers’ participatory site-specific nutrient management (SSNM) farm trials were conducted for rainfed, transplanted, and short-duration rice (*Oryza sativa* L.) during the 2011 aman season. Four treatments (NPK, PK, NK, and NP) were used to observe the response of indigenous nutrient elements on rice yield and yield attributes. The aim was to develop a participatory SSNM approach for farmers of the Ganges tidal floodplain ecosystem (AEZ 13) to increase fertilizer use efficiency and compare economic performance. The response of indigenous K was remarkable (3.19 Mg ha^{-1}) and there was no significant yield difference between NPK and NP treatments. The response of indigenous N was very poor and the lowest grain yield was found in the N-omission treatment (1.99 Mg ha^{-1}). The response of indigenous P was also poor (2.76 Mg ha^{-1}). These results show that N and P are most crucial in increasing rice yield and that omission of either N or P or both have a significant impact on yield during the crop season. After harvest, the nutrient omission results and the calculated N, P, and K doses were shared with farmers involved in the trials as well as with nearby farmers through focus group discussions. After the fruitful sharing and group work, N, P, and K doses were set for the locations–56.92, 4.94, and 6.12 kg ha^{-1}, respectively. The doses were 63%, 50%, and 37% that of BRRI-recommended doses for AEZ 13, respectively. Gross return above fertilizer cost (GRF) was calculated as $31.21 ha^{-1} per crop greater with participatory SSNM doses compared with BRRI-recommended doses. This study shows that the use of this sustainable fertilizer management approach will benefit farmers economically as the doses are less, location-specific, and set through participatory decisionmaking.

Keywords: grain yield, aman rice, nutrient omission, participatory SSNM dose, economic benefit

Rice productivity improvement and contribution to welfare change in the African agricultural sector

Mandiaye Diagne[1*] and Aliou Diagne[2]
[1]AfricaRice Center (AfricaRice), BP 96, Regional Station,Saint Louis, Senegal
[2]AfricaRice Center (AfricaRice), BP 2031, Cotonou, Benin.
*Correspondence: m.diagne@cgiar.org

Improving the productivity of staple foods is mainly designed to increase agricultural production and welfare in developing countries. In this paper, we use a partial equilibrium model of trade to compare the contribution of rice and other food staples to welfare change. The model relies on an extension of the standard Ricardian trade model by accounting for geographic barriers and yield variability. The results show that improvement in productivity of rice among other main staple food is associated with higher economic growth and trade flows within Africa. Thus, rice trade strategies need to be implemented to benefit from the comparative advantage of highly competitive rice-producing countries and ensure the supply to rice-deficit countries within Africa.

Keywords: rice, productivity, trade, Africa, welfare change

Farmers' participatory site-specific nutrient management in the Ganges tidal floodplain soil of Bangladesh for boro rice

M. Sh. Islam,[1] F. Amin,[1] D.K. Nath,[1] and M.A. Saleque[2]
[1]CSISA-IRRI, Barisal Hub, Bangladesh
[2]CSISA-IRRI, Bangladesh
*Correspondence: mshahid7862004@yahoo.co.uk

Participatory site-specific nutrient management (SSNM) trials were conducted at Babugonj Upazila in Barisal District, Bangladesh, during the 2012 boro season. Four treatments (NPK, PK (-N), NK (-P), and NP (-K)) were imposed to observe the response of nutrient elements on yield of BRRIdhan 29 in 10 farmers' plots. The experiment used randomized complete block design with disperse replication (each farmer was considered a replication). The initial nutrient content of the soil in all farmers' plots was analyzed. Of 10 farmers' plots, nine were P-deficient. The highest grain yield (6.0 t ha^{-1}) was observed in the NPK treatment and the lowest (3.5 t ha^{-1}) was found in the N-omission plot. Grain yield in the -P plot was 4.3 t ha^{-1} and that in the -K treated plot was 5.5 t ha^{-1}. The NPK-treated plot gave 74.2%, 40.1% and10.1% higher yield than did the -N, -P, and -K plots, respectively. The calculated doses of N, P, and K were 115.2, 7.17, and 13.75 kg ha^{-1}, respectively. Compared with previously recommended dose, savings of 16.5% N, 60.0% P, and 73.8% K were generated. Thus, farmers can save a total of Tk 3,257 per hectare in rice production cost. These results imply that N and P are the most yield-limiting factors and that K has no significant yield impact in that location.

Keywords: grain yield, nutrient omission, NPK, SSNM

Competitiveness of the rice sector in Benin

Simon Codjo Ogoudélé,[1*] Diagne Aliou,[1] and Kinkingninhoun-Medagbé Florent[1]
[1]Africa Rice Center (AfricaRice), BP 2031, Cotonou, Benin
*Correspondence: simcodjo20@yahoo.fr

In spite of favorable ecological conditions to ensure self-sufficiency in rice in Benin, rice consumption is still very dependent on rice import. This paper aims to analyze the competitiveness of the rice sector in Benin. It combines the heterogeneous agent approach and policy analysis matrix to assess the competitiveness of its rice sector. Unlike previous studies, it assesses the competitiveness of producers, processors, and traders using microeconomic data. The results indicate that the net margin of rice production is $150.22 per ton as against $16.62 per ton and $66.86 per ton for milling and marketing, respectively. The average domestic resource cost (DRC) indicates that Benin has a comparative advantage in rice processing and marketing; 96.67% of transformers and 84.72% of traders are competitive. In contrast, Benin does not have a comparative advantage in rice production. This result is explained by the fact that rice production systems in the surveyed regions are upland and rainfed lowland, which are known to be not competitive. Moreover, an analysis of the distribution of CRI shows that only 36.6% of farmers have no comparative advantage in rice production. The use of improved variety, the unit cost of labor, and the price of fertilizer are the main determinants of producers' competitiveness. The homogeneity of the grains and the amount shelled daily determine the transformers' competitiveness. The competitiveness of traders is determined by the selling price of rice and the share of taxes in the total cost.

Keywords: value chain, heterogeneous agent, policy analysis matrix

Potential impact of the national rice development strategy in Benin

Amos Allodehou,[1*] Diagne Aliou,[1] and Kinkingninhoun-Medagbé Florent[1]
[1]Africa Rice Center (AfricaRice), BP 2031, Cotonou, Benin.
*Correspondence: allodehouamos@yahoo.fr

Local rice production in Benin, as in most African countries, fails to meet rice demand. Some of the reasons are low productivity and lack of a good national strategy for rice development. In 2010, Benin's government developed a national rice development strategy (NRDS) to increase production, improve the income of the rice value-chain actors, and generate surpluses for export. This paper aims to assess the potential impact of the NRDS on rice production and household welfare. Following the theoretical framework of agricultural household models, it used the Cobb-Douglas specification and the Almost Ideal Demand System to estimate total rice supply, income, and demand. The data used were collected in 2010 from 342 producers and 377 consumers. The results show that the total supply of rice is inelastic to the selling price of paddy, the price of mineral fertilizers, and the unit cost of hired labor. Rice income is elastic to the selling price of paddy. Rice demand is inelastic to income and relatively inelastic to its price. Moreover, the findings of the simulations show that production targets of the NRDS can be achieved by combining policies of irrigation development and subsidy in rice prices and inputs (fertilizer and improved seeds). The decrease in rice consumer price is more favorable to poor households than to rich households.

Keywords: NRDS, household model, supply, demand

Does adaptive research help rice farmers integrate and adopt from a range of technology options?

Rica Joy Flor,*[1] Madonna Casimero,[1] Grant Singleton,[1] Zainal Abidin,[2] and Nasruddin Razak[3]
[1]Irrigated Rice Research Consortium, International Rice Research Institute, Los Baños, Laguna, Philippines
[2]Balai Pangkajian Teknologi Pertanian, Kendari, Southeast Sulawesi, Indonesia
[3]Balai Pangkajian Teknologi Pertanian, Maros, South Sulawesi, Indonesia
*Correspondence: r.flor@irri.org

Adoption studies mostly examine the uptake of single technologies. Yet, synergies resulting from technological packages are needed to significantly raise yields. For these packages, Byerlee and de Polanco (1989) have theorized a stepwise adoption of technologies. This theory is assumed within the adaptive research approach used in an IRRI-led project in South and Southeast Sulawesi, Indonesia. The question though is: does the process of adaptive research help farmers integrate technologies, facilitating the adoption of a suitable combination of technologies? This study presents results from baseline (n=240) and impact (n=256) socioeconomic surveys done in 2008–09 and in 2010. Documents from need assessments, monitoring interviews, and follow-up visits were used to understand the adoption process. An increase in farmers doing direct seeding in Southeast Sulawesi project villages from 26% to 48% (wet season) and from 1% to 49% (dry season) was seen. While none of the farmers had heard of the technologies before, a range of 10–20% in each project village used site-specific nutrient management (PuPS) in 2010; 19–80% used alternate wetting and drying. There was also evidence of change in knowledge in areas of pest management. A visible but difficult-to-measure outcome of the approach is empowerment of farmers toward innovating. Cases will be shown of farmers tweaking technologies to accommodate changes in knowledge they have gained from the adaptive approach. These results provide evidence that adaptive research helps not only in stepwise adoption toward yield increases but also in building the capacity of farmers to innovate.

Keywords: adoption, adaptive management, innovation, Indonesia, technological learning

Preliminary results of baseline household surveys in Ayeyarwaddy and East Bago, Myanmar

Arelene Julia Malabayabas,[1*] Florencia Palis,[1] and Grant Singleton[1]
[1]International Rice Research Institute. DAPO Box 7777, Metro Manila, Philippines
*Correspondence: amalabayabas@irri.org

A baseline household survey was conducted in Ayeyarwaddy in 2006. This is to ensure that appropriate technologies to rice farmers in the area are identified and technologies from the Productivity and Sustainability Workgroup; Water Saving Workgroup; Labor Productivity Workgroup; and Post-production Workgroup of the Irrigated Rice Research Consortium (IRRC) are integrated to match farmers' needs. A total of 161 farmers were interviewed. This year, a baseline survey in East Bago was also conducted to develop best practices for rice production and innovative approaches to increase the income of farmers in rice-pulse cropping systems. Two hundred farmers were interviewed. The knowledge, attitudes, and practices (KAP) of farmers from production to harvesting and their current farm expenses and income in relation to current practices were collected. These baseline data will be compared with the same set of information after a few years with IRRC activities in place to measure the impact of the technologies and practices introduced by IRRC in the Ayeyarwaddy and East Bago regions. In Ayeyarwaddy, almost 100% of the farmers in both IRRC and non-IRRC villages are dependent on rice farming. Fertilizer input has the largest proportion (46–47%), whereas herbicide has the smallest share (0.2–1.1%) in the expenditure of both IRRC and non-IRRC farmers. In East Bago, most farmers stack their harvested monsoon rice crops in the levee banks for a few weeks as they prepare the land to sow summer pulse, which results in postharvest losses. Appropriate technologies and practices are needed to increase the productivity of rice and pulse crops in lower Myanmar.

Keywords: technologies, best practice, postharvest losses, productivity

Category 4

Environment and Sustainability

8 November 2012 Category 4: Environment and Sustainability 2012 IRRI Young Scientists Conference

Time	Abstract no.	Abstract title, authors
10:15	14	**Optimal irrigation schedule and nitrogen dose for dry-seeded rice in Los Baños, Philippines** Yadav Sudhir, Jaime Faronilo, and Elizabeth Humphreys
10:35	23	**Performance of aerobic rice under drip fertigation in the coastal deltaic region of Karaikal** John Rohit Katuri, R. Mohan, R. Poonguzhalan, and E. Suburayalu
10:55	26	***Rice Crop Manager*: helping farmers increase net income through field-specific integrated crop management** Rowena Castillo, Judith Carla Dela Torre, Ma. Eda Apple Suplido, Marco van den Berg, and Roland Buresh
11:15	30	**Adding value to national rice research–an experience with *Nutrient Manager* in Indonesia** Judith Carla Dela Torre, Zulkilfi Zaini, Mahyuddin Syam, Sunendar Kartaatmadja, Suyamto, Rowena Castillo, Philip Joshua Sinohin, and Roland Buresh
11:35	35	**Feathers−friend or foe: what we know and what we still need to find out** Richard Smedley
11:55	41	**Growth and yield of dry-seeded rice and maize as affected by spatial variation in soil properties** San Hla Htwe, James R. Quilty, Teodoro Correa Jr., Rodrigo B. Badayos, and Roland J. Buresh
13:35	46	**Systems productivity increased through crop diversification and best management practices** Ali M. Akkas, F. Haque, M. M. Rahman, M. A. Saleque, and Portal Christian
13:55	60	**Real-time monitoring of soil water tension and irrigation scheduling for dry-seeded rice and hybrid maize production** Joseph Sandro, Teodoro Correa, Jr., Ma. Carmelita Alberto, Elizabeth Humphreys, and Roland Buresh
14:15	67	**Image quality of digital cameras for nutrient management** Artzai Juaregui Solano and Finbarr G. Horgan
14:35	68	**Solar drying concept for rice in the Philippines** Ana Salvatierra-Rojas, Marcus Nagle, Martin Gummert, Tom De Bruin, and Joachim Mueller
14:55	75	**Soils also need routine checkup and care: how do we do it?** Sheetal Sharma and J.K. Ladha
15:35	76	**Potential effects of global warming on the structure of planthopper assemblages** Ardestani Goli, Arriza Arida, and Finbarr G. Horgan
15:55	84	**Rice genotypic response to high night temperature in situ** Ma. Rebecca C. Laza and Shaobing Peng

Optimal irrigation schedule and nitrogen dose for dry-seeded rice in Los Baños, Philippines

Yadav Sudhir,* Jaime Faronilo, and Elizabeth Humphreys
International Rice Research Institute, Los Baños, Philippines
*Correspondence: s.yadav@irri.org

Dry-seeded rice (DSR) greatly reduces labor costs, facilitates timely establishment, and reduces irrigation requirement if grown without ponding. However, clear, science-based guidelines for irrigation management are lacking. Furthermore, frequent wetting and drying may be conducive to high fertilizer N losses. Therefore, a field experiment was conducted on a clay loam soil at IRRI during the 2012 dry season to investigate the effects of irrigation management and N rate on the performance of DSR. The irrigation schedules were based on soil water tension ranging from ponding/saturation (daily irrigation) to alternate wetting and drying (AWD) with irrigation thresholds of 10, 20, and 40 kPa at 15-cm soil depth. There was also a continuously flooded puddled transplanted rice (PTR) control treatment. Nitrogen was applied at 0, 50, 100, 150, and 200 kg ha^{-1} in four splits 2, 4, 6 and 8 weeks after sowing. There was no significant interaction between irrigation scheduling and N rate on grain yield. Maximum grain yield was achieved with PTR-CF (5.5 t ha^{-1}) which was significantly higher than all DSR treatments. There was a significant effect of N rate, and yield with 200 kg N ha^{-1} (5.5 t ha^{-1}) was significantly higher than yield of all other N rates. The results on this soil in the dry season indicate a yield penalty with DSR, even with daily irrigation and a high N rate, in contrast to previous findings during the rainy season in Punjab.

Keywords: AWD, soil water tension

Performance of aerobic rice under drip fertigation in the coastal deltaic region of Karaikal

John Rohit Katuri,* R. Mohan, R. Poonguzhalan, and E. Suburayalu
Pandit Jawaharlal Nehru College of Agriculture and Research Institute, Karaikal-3,
U.T. of Puducherry, India
*Correspondence: john.katuri@gmail.com

As water becomes a scarce resource and is likely to further decrease in the future, irrigation for the agriculture sector constitutes a pressing concern, more specifically in the coastal deltaic region of Karaikal, U.T. of Puducherry, India. A study was conducted at the Pandit Jawaharlal Nehru College of Agriculture and Research Institute in the 2011 kharif to assess the feasibility of implementing an aerobic rice system under both drip system and flood irrigation. To evaluate productivity and performance, four varieties (TKM9, PMK(R)3, ADT43, and ADT(R) 5) and four irrigation levels (I1 – 0.6 and 0.8 CPE before and after flowering through drip fertigation, I2 – 0.8 and 1.0 CPE before and after flowering through drip fertigation, I3 – 1.0 and 1.2 CPE before and after flowering through drip fertigation, and I4 – flooding through surface irrigation) were taken as treatments and replicated thrice in a factorial randomized block design. The quantity of water used by aerobic rice variety ADT(R)45 was 857.2 mm, whreas the other three varieties consumed 866.0 mm. Similarly, water consumption in the flood irrigation treatment resulted in 1314 mm, equivalent to that used for transplanted rice in the region. In contrast, the drip irrigation treatments (I1, I2, and I3) consumed only 613.3, 712.8, and 815.1 mm, respectively, which was almost 50−75% that of the surface flooding treatment. TKM9, PMK(R)3, ADT43, and ADT(R)45 had grain yields of 2656, 2432, 1354, and 2515 kg ha^{-1}, respectively; under I1, I2, I3 and I4, the yields were 1536, 1447, 1911, and 4062 kg ha^{-1}, respectively. ADT 43 had very low water use efficiency (WUE), 13.77 kg ha cm^{-1}. However, all the other three varieties (TKM9, PMK(R)3 and ADT(R)45) had a WUE of 29.73, 27.05, and 23.71 kg ha cm^{-1}, respectively. The surface flood irrigation treatment had resulted in a WUE of 30.91 kg ha cm $^{-1}$. The treatment that maintained the soil moisture at or above field capacity through drip irrigation (I3) had registered a WUE of 23.45 kg ha cm^{-1}.

Keywords: water, aerobic rice, drip fertigation, water use efficiency

Rice Crop Manager: helping farmers increase net income through field-specific integrated crop management

Rowena Castillo,[1*] Judith Carla Dela Torre,[1] Ma. Eda Apple Suplido,[1] Marco van den Berg,[2] and Roland Buresh[1]
[1]Crop and Environmental Sciences Division, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Information Technology Services, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: r.castillo@irri.org

Research has made much progress in identifying the components of 'better' crop management, which can increase yield when adopted by a rice farmer. These components of 'better' crop management from seed-to-seed have often been incorporated into 'packages' of integrated crop management, but uptake by farmers has often been slow. A new approach to accelerate uptake of 'better' crop management uses a decision support tool to identify—based on information from a farmer—the two to four components of 'better' crop management most likely to provide the largest increase in net income. *Rice Crop Manager* (RCM) recognizes that not all components of 'better' crop management are equally effective in benefiting a farmer, and that most beneficial components vary among farmers because of differences in their management practices and constraints. RCM builds upon *Nutrient Manager for Rice* (NMR) and similarly uses Web or mobile phone application to acquire information—typically through an extension agent—from a farmer, the power of cloud computing to calculate personalized field-specific crop management guidelin, and a suite of media from mobile phones to printouts to provide the guidelines to the farmer. RCM, like NMR, is targeted for use before the start of a crop-growing season to help a farmer invest his resources wisely. It aims to increase the farmer's net income by \$150 ha^{-1} per season with reduced risk. RCM will be interfaced with another decision support tool, the *Rice Crop Doctor,* which provides guidelines to protect the investment of a farmer by appropriately addressing specific problems during the season.

Keywords: better crop management, decision support tools, cloud computing, field-specific guidelines

Adding value to national rice research–an experience with *Nutrient Manager* in Indonesia

Judith Carla Dela Torre,[1*] Zulkilfi Zaini,[2] Mahyuddin Syam,[2] Sunendar Kartaatmadja,[2] Suyamto,[2]
Rowena Castillo,[1] Philip Joshua Sinohin,[1] and Roland Buresh[1]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]IRRI-Indonesia Office, Jalan Merdeka 147, Bogor 16111, Indonesia
*Correspondence: j.delatorre@irri.org

The International Rice Research Institute (IRRI), through scientists based in Indonesia and at its headquarters in the Philippines, has a long history of partnership in research with the Indonesian Agency for Agricultural Research and Development (IAARD). IRRI and IAARD partnered to develop the *Nutrient Manager for Rice*, which provides Indonesian farmers with a fertilizer recommendation matching their specific rice-growing conditions. *Nutrient Manager* or Pemupukan Hara Spesifik Lokasi (PHSL), as it is known in Indonesia, was made available through the Internet in early 2011. There was then an urgent need for field testing to quantify the benefit of PHSL to rice farmers and identify needed improvements before its release as mobile phone applications. IRRI scientists in Indonesia and at headquarters partnered with scientists from Assessment Institutes for Agricultural Technology to evaluate fertilizer recommendations provided by PHSL relative to the farmer's fertilizer practice in 306 farmers' fields across nine provinces during the wet season. Nutrient omission plot trials were also conducted across 65 farmers' fields. Scientists at IRRI headquarters consolidated field results, conducted analyses across locations, and used the results to update PHSL. The use of the PHSL recommendation increased net income for one rice crop by \$123 ha^{-1} in Java and by \$225 ha^{-1} outside Java. PHSL reduced fertilizer N use to about one-half at 75 field sites across Java. Collaboration among staff in Indonesia and at headquarters enabled the rapid release of an updated version of PHSL for use via Internet and mobile phones across Indonesia.

Keywords: *Nutrient Manager for Rice*, PHSL, national partners, field evaluation

Feathers–friend or foe: what we know and what we still need to find out

Richard Smedley
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines and University of Reading, Whiteknights, Reading, United Kingdom
Correspondence: r.smedley@irri.org

A group of scientists in the Crop and Environmental Sciences Division of IRRI is promoting the adoption of natural resource management practices aimed at reducing the ecological footprint of rice production. This initiative was formally launched in November 2011 as the Sustainable Rice Platform (SRP). One area that urgently requires more research effort is the effect of best management practices in intensive rice production systems on animal biodiversity. One group of animals that has been generally overlooked are birds, even though they are one of the most recognized groups in the world. With little work conducted on these mystery feathered beings, do they suffer from being so visual? Is being seen flying in, or out, of a crop, earning them the label ‘pest’? Highlighting work from around the world, combined with data collected since January 2012 within the IRRI farm, this presentation will discuss the positive and negative effects birds have on rice as well as the positive and negative effects that rice may have on them.

Keywords: birds, rice

Growth and yield of dry-seeded rice and maize as affected by spatial variation in soil properties

San Hla Htwe,[1,2,3*] James R. Quilty,[1] Teodoro Correa, Jr.,[1] Rodrigo B. Badayos,[2] and Roland J. Buresh[1]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]University of the Philippines Los Banos, Laguna, Philippines
[3]Department of Agriculture, Myanmar
*Correspondence: s.htwe@irri.org

Soils can vary greatly in properties within short distances as a result of differences in topography, parent material, vegetation, hydrology, and land management. An understanding of how such variations in soil properties affect crop growth and yield can help in developing profitable and sustainable land and crop management practices for high productivity. We measured soil properties, crop growth, and yield within 5-m^2 plots at 27 locations within a 3-ha area uniformly managed with dry-seeded rice (*Oryza sativa* L.) and at 27 locations within another 3-ha area uniformly managed with hybrid maize (*Zea mays* L.). We compared soil physical and chemical properties with leaf area index, crop growth, and yield in each 5-m^2 plot to determine the relationships between soil condition and crop performance and to identify factors that could be managed to efficiently increase yield. Rice yield ranged from 3.6 to 7.0 t ha^{-1}, and maize yield ranged from 5.6 to 9.3 t ha^{-1}. The highest yields of rice were observed with apparent electrical conductivity (ECa) (as measured by EM38 at sowing) at 32 mS m^{-1} at 1 m and 19 mS m^{-1} at 0.5-m depth and high initial water content of the soil. With maize, the highest yields were noted with ECa at 23 mS m^{-1} at 1 m and 15 mS m^{-1} at 0.5 m and relatively low soil initial moisture. Results indicate that performance and yield for both dry-seeded rice and maize varied widely across each field as a result of factors other than soil fertility status.

Keywords: aerobic rice, leaf area index, apparent electrical conductivity (ECa), EM38, soil fertility

Systems productivity increased through crop diversification and best management practices

Ali M. Akkas,* F. Haque, M.M. Rahman, M.A. Saleque, and Portal Christian
Cereal Systems Initiative for South Asia (CSISA), IRRI, IBO, Dhaka, Bangladesh
*Correspondence: akkas.ali@irri.org

Rice-rice is a dominant cropping pattern in the Central East Bangladesh Hub. But a wide yield gap exists between potential and existing crop yield, resulting in low productivity and profitability. There is a wide scope to address this issue by supporting conservation agriculture-based best management practices to minimize the yield gap and cut costs of cultivation of the two existing rice crops and increase cropping intensity by introduction of short-duration high-yielding mustard and rice varieties in the rice-rice pattern. A large number of farmers took part in a participatory demonstration trial on rice-mustard-rice pattern, comparing performance with the rice-rice pattern in farmers' fields. The results indicated that BARI mustard had an average yield of 1.4, 1.2, and 1.2 t ha^{-1} in 2010, 2011, and 2012, respectively. This was an extra crop in the rice-rice pattern. The average yields of boro rice obtained were 6.2, 6.1, and 6.2 t ha^{-1} from intervention plots in 2010, 2011, and 2012, respectively. In T. aman rice, yields averaged 4.3, 4.5, and 4.2 t ha^{-1} in 2009, 2010, and 2011, respectively. In all cases, average yield was 0.5 to 0.88 t ha^{-1} higher in the intervention rice plots than in farmers' fields. Economic analysis showed that the pattern with the intercrop had a net return of $1333, 246% higher than the existing rice-rice pattern ($385). Participatory demonstration trials and capacity-building activities enhance and strengthen farmers' knowledge, adaptive capacity, and farmer-to-farmer experience exchange.

Keywords: systems productivity, management practices, cropping intensity, adaptive capacity, economics

Real-time monitoring of soil water tension and irrigation scheduling for dry-seeded rice and hybrid maize production

Joseph Sandro,* Teodoro Correa, Jr., Ma. Carmelita Alberto, Elizabeth Humphreys, and Roland Buresh
Crop and Environmental Sciences Division, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: j.sandro@irri.org

Rice must be produced in increasing amounts to ensure food security, but this must be done using less water. Research was conducted during the 2012 dry season in the Philippines to monitor water dynamics and use during the production of dry-seeded rice grown without soil submergence and hybrid maize. Both received overhead sprinkler irrigation. At the time of sowing, the soil profile was full of water as a result of the rain. Irrigation scheduling was based on soil water tension and crop evapotranspiration (ETc) estimated from weather data and crop factors. Irrigation was applied when soil tension exceeded 10 kPa at 15-cm depth for rice and 50 kPa at 40-cm depth for maize. For each crop, irrigation was applied such that water input from irrigation slightly exceeded ETc minus rainfall over the previous period. Actual evapotranspiration (ETa) measured using eddy covariance was 475 and 453 mm for rice and maize, compared with in-crop rainfall of 366 and 368 mm, respectively. Irrigation water input from sowing to harvest of rice was 553 mm and 260 mm for maize. Thus, total water input was 919 and 628 mm, respectively, almost double the requirement for rice and 40% more than that needed for maize, largely due to untimely rain after irrigation. Grain yield averaged 5.3 t ha^{-1} for rice and 8.2 t ha^{-1} for maize, given that irrigation water productivity of maize (3.2 kg m^{-3}) was more than triple that of rice (0.95 kg m^{-3}).

Keywords: soil water tension, evapotranspiration, irrigation scheduling, dry-seeded rice, maize

Image quality of digital cameras for nutrient management

Artzai Juaregui Solano* and Finbarr G. Horgan
Crop and Environmental Sciences Division, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: a.solano@irri.org

Image processing and analyses are finding applications in many facets of agriculture. We examined the robustness of photographic imagery for remote diagnostic applications. We determined the suitability of images from different cameras under different conditions of exposure for rice-nutrient management applications. We examined the effects of scope, camera angle, and ambient daylight conditions on image-resolution quality. We also examined the quality of images from a range of digital cameras, cell phones, and smart phones for their potential application in remote diagnostics. Relative fertilizer inputs in replicated fields at IRRI could be distinguished by RGB-analyses of images taken with high-quality cameras. We found 50 mm as the optimal lens for quality images with sufficient resolution for diagnostics. There were minimal effects of camera angle, and images were best on cloudless days. Cell phones and smart phones varied considerably in image quality and failed to detect nitrogen effects in our fields. Further analyses are required to determine minimum camera requirements for successful color-based diagnostics.

Keywords: digital camera, image, nitrogen, rice

Solar drying concept for rice in the Philippines

Ana Salvatierra-Rojas,[1] Marcus Nagle,[1*] Martin Gummert,[2] Tom De Bruin,[3] and Joachim Mueller[1]
[1]University of Hohenheim, Department of Agricultural Engineering, Tropics and Subtropics Group, Germany
[2]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[3]GrainPro Philippines, Inc., Subic Bay Freeport Zone, Philippines
*Correspondence: naglem@uni-hohenheim.de

Drying of rice is especially problematic in monsoon-climate areas such as the Philippines where there is much precipitation during the harvesting period. In the Philippines, “highway dryers” are used─here, wet paddy is spread out in sufficiently thick layers to dry alongside rural roads, raking the grain while drying to continuously mix it, preventing the grain from being exposed to the strongest rays of the sun (which could cause lower head rice values). This traditional practice can allow grain germination when done during the wet season and can lead to undesirable microbiological development and reduced product quality. Rice millers in the Philippines claim that, despite the greater expense of drying rice using air dryers, they cannot afford to sun-dry anymore because damage to grain quality costs too much to control. As a response, the present study proposes a low-cost solution to reduce drying time during the rainy season and ensure complete drying by testing different prototypes based on the greenhouse concept. We aim to demonstrate a new, low-cost approach toward solar drying of rice using new, locally available materials that would keep investment at an acceptable level.

Keywords: greenhouse dryer, sun-drying, grain quality

Soils also need routine checkup and care: how do we do it?

Sheetal Sharma* and J.K. Ladha
International Rice Research Institute. DAPO Box 7777, Metro Manila, Philippines
*Correspondence: sheetal.sharma@irri.org

Current agricultural practices of tillage and poor resource management have resulted in the deterioration of soils, thereby restricting yield, profitability, and sustainability of agricultural land use. With the increased demand for food, the intensification of common systems of agriculture will continue to result in a decline in the soil's inherent productive capacity. Regular monitoring of soil health helps to identify management practices and alternative systems that are productive and equally sustainable. The process of quantitative assessment of sustainability, as defined by soil health, is not only complicated but needs to be studied comprehensively and assessed systematically. In this process, we identify certain stages using soil health indicators as a quantitative measure of agricultural sustainability. The first stage is to conduct a detailed resource survey for sources of data (primary and secondary) and to develop an inventory of soil health indicators relevant to diverse cereal-based management systems. The second stage involves an evaluation of the effects of soil-modifying management that induces changes in the soil health indicators. In the third stage, potential soil health indicators are identified (general and site-specific). Scoring of indicators and indexing follow in the fourth stage. The fifth stage comprises testing and using the indices for assessing current management systems and evaluating future systems. The challenge for the future is to develop sustainable management systems that maintain soil health; soil health indicators are merely a means to this end.

Keywords: soil health indicators, sustainability, cereal-based systems

Potential effects of global warming on the structure of planthopper assemblages

Ardestani Goli,* Arriza Arida,* and Finbarr G. Horgan
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: a.goli@irri.org, a.arida@irri.org

The brown planthopper *Nilaparvata lugens* (Stål) (BPH) and the whitebacked planthopper *Sogatella furcifera* (Horváth) (WBPH) are two of the most damaging rice herbivores in South and East Asia. While BPH was once the dominant species in Asian rice paddies, there was a notable shift toward WBPH-dominated assemblages in recent decades. We examined the possibility that climate anomalies (in particular, higher temperatures) might have altered the dynamics of interspecific planthopper interactions in favor of WBPH. We hypothesized that WBPH would outcompete BPH during egg laying under higher temperature conditions. Using climate chambers at a range of temperatures, we determined optimal temperatures for egg laying in both species. The optimal temperature for oviposition by BPH on T65 (japonica) and IR22 (indica) was 30 ºC, whereas, for WBPH, it was 25 ºC. As a prerequisite to assessing temperature effects on interspecific competition, we examined patterns in intraspecific competition under the temperature optima for each species. At 30 ºC, the densities at which intraspecific competition occurred in WBPH were higher than those at 25 ºC, whereas intraspecific competition for egg laying was intense for BPH at both temperature regimes. Having identified the densities at which intraspecific competition occurs in our system, we will complete this study by assessing the outcome of interspecific competition for egg laying under 25 ºC and 30 ºC.

Keywords: planthoppers, inter- and intraspecific competition, global warming

Rice genotypic response to high night temperature in situ

Ma. Rebecca C. Laza[1*] and Shaobing Peng[2]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Crop Physiology and Production Center, College of Plant Science and Technology, Huazhong Agricultural University,Wuhan, Hubei, China
*Correspondence: m.r.laza@irri.org

Predicted increases in night temperature will have negative impacts on rice production as has been reported using historical data sets from field experiments. Recent studies on the effect of night temperature on rice growth and yield were done under temperature-controlled chambers using pot-grown plants and a limited number of genotypes. Low-cost, temperature-controlled field chambers were developed and used to study a larger population of rice plants under different night temperature treatments in situ. Experiments were conducted in the 2007 and 2008 wet (WS) and dry seasons (DS) to confirm the effects of night warming on the yield of three rice varieties (IR8, IR72, and PSBRc 82) and to determine genotypic variation in sensitivity to higher night temperature (HNT). Temperature treatments of 23 °C (low) and 25 °C (high) in 2007, and 22 °C and 25 °C in 2008 were imposed starting at panicle initiation until maturity. An HNT of 2−3 °C decreased yields in both years ranging from 7% to 35%. The decline in yield was greater in the WS (9−35%) than in the DS (4.0−19.5%). Among the varieties, IR8 had the highest significant decrease in yield (11−35%) than IR72 (-4−12%) and PSBRc 82 (8−10%). Total dry weight and spikelet fertility were also reduced by HNT, but magnitude was lesser compared with yield. The results confirmed previous findings of yield reduction at HNT. Varieties differed in their response: the older bred varieties such as IR8 were more sensitive to increases in night temperature than recently developed ones.

Keywords: field chambers, temperature control, varieties, yield

Category 5

Genetics and Genomics

8 November 2012 Category 5: Genetics and Genomics 2012 IRRI Young Scientists Conference

Time	Abstract no.	Abstract title, authors
10:15	6	**Genetic analysis of salinity tolerance at the reproductive stage in rice (*Oryza sativa* L.)** Mohammadi Reza, Merlyn S. Mendioro, Genaleen Q. Diaz, Glenn B. Gregorio, and Rakesh K. Singh
10:35	7	**Identification of quantitative trait loci (QTLs) for salinity tolerance in rice (*Oryza sativa* L.) using IR29/Hasawi mapping population** Bizimana, Ashura Luzi-Kihupi, and Rakesh K. Singh
10:55	15	**Identification of major QTLs for salinity tolerance at the reproductive stage in rice (*Oryza sativa* L.)** Cecilia Diana C. Palao, Celia B. dela Vina, Glenn B. Gregorio, MichaelJ. Thomson, and Rakesh K. Singh
11:15	16	**Rice heat tolerance at booting and flowering stages** Fatima Amor Tenorio, Changrong Ye, Edilberto Redoña, and S.V. Krishna Jagadish
11:35	18	**Phenotypic characterization and genetic mapping of an open-hull sterile mutant in rice** Yoye Yu, Rihua Piao, Wenzhu Jiang, and Hee-Jong Koh
11:55	20	**Genetic study on blast disease resistance of African rice germplasm** T. Odjo, Y. Fukuta, Y. Koide, A. Tanaka-Kawasaki, and S. Yanagihara
13:35	32	**EcoTILLING as a SNP discovery tool for drought candidate genes in *Oryza* germplasm** Ma. Elizabeth Naredo, Jill Cairns, Rolando Torres, and Kenneth L. McNally
13:55	36	**Heterosis QTLs for grain yield and yield-related traits in indica-japonica crosses of rice** Chu Sang-Ho, Wenzhu Jiang, Joong Hyoun Chin, and Hee-Jong Koh
14:15	37	**Optimization of de novo-based genome assembly of the *Oryza sativa* indica type IR 64-21 genome from paired-end short sequence reads** Victor Jun Ulat, Jeffrey Detras, Ramil P. Mauleon, and Kenneth L. McNally
14:35	42	**Genetic diversity for root morphology and molecular profile in aerobic/lowland indica rice genotypes** Nitika Sandhu, Sunita Jain, and Rajinder Kumar
14:55	52	**Allele-specific expression imbalance in rice (*Oryza sativa* L.) under normal and drought conditions assayed by single-base extension and RNA sequencing** Nelzo Ereful, Katrina Malabanan, Antonio Laurena, David Lee, Ian Mackay, and Hei Leung
15:35	66	**Distribution of InDel markers of indica-japonica differentiation in wild rice relatives of rice (*Oryza sativa* L.)** YooJin Lee, Joong Hyoun Chin, Michael J. Thomson, and Hee-Jong Koh
15:55	71	**SNP marker technology for various breeding applications** Christine Jade Dilla-Ermita, Ma.Ymber Reveche, Dennis Nicuh Lozada, Erwin Tandayu, Socorro Carandang, Marjorie De Ocampo, Ramil Mauleon, Kenneth McNally, Hei Leung, Susan McCouch, and Michael Thomson
16:15	73	**qDTY3.1, a large-effect and consistent QTL for grain yield under drought in rice** Noraziyah Abd Aziz Shamsudin, B.P. Mallikarjuna Swamy, Joahna Ruth Ramirez, John Christian Ontoy, Jennylyn Trinidad, Margaret Catalos, and Arvind Kumar

Genetic analysis of salinity tolerance at the reproductive stage in rice (*Oryza sativa* L.)

Mohammadi Reza,[1] Merlyn S. Mendioro,[2] Genaleen Q. Diaz,[2] Glenn B. Gregorio,[1] and Rakesh K. Singh[1]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]University of the Philippines Los Baños, Laguna, Philippines
Correspondence: rmohammadi@irrialumni.org

Genetic components and combining ability estimates of rice (*Oryza sativa* L.) at the seedling and reproductive stages under salinity stress were investigated using a seven-parent full-diallel cross analysis. The parental lines were IR4630-22-2-5-1-3, FL 478 (IR66946-3R-178-1-1), Pusa Basmati 1, CSR28, IR64, IR70023-4B-R-12-3-1, and Sadri. The resultant 42 F_1s and the seven parents were evaluated under salinity stress at the seedling and reproductive stages. The general combining ability estimates at the seedling stage revealed that, among the parents, FL 478 was the best general combiner for salinity score, shoot dry weight, and K^+ uptake and a good combiner for Na^+ exclusion and K-Na ratio. Estimates of genetic parameters revealed that both additive and dominance effects were significant for salinity score, shoot height, root dry weight, Na^+, K^+, and K-Na ratio. For root length and shoot dry weight, only dominance effects were significant. The general combining ability estimates at the reproductive stage showed Sadri as the best general combiner for grain yield and a good to average combiner for most of the yield components. In the F_1 hybrids, Sadri/CSR28 and Sadri/FL 478 had the highest grain yield with 55.68 and 54.29 g per plant, respectively. Estimates of genetic parameters of 14 characters at the reproductive stage indicated that both additive and dominance effects were significant for days to flowering, plant height, panicle length, number of sterile spikelets, spikelet fertility, 1000-grain weight, Na^+, K^+, and K-Na ratio. For number of panicles, straw dry weight, number of fertile spikelets, number of total spikelets, and grain yield, only dominance effects were significant. The 232 F_2 progenies produced from the cross between Sadri and FL 478 were used for phenotyping under salinity stress at the reproductive stage and identification of associated QTL regions. Phenotyping was conducted at IRRI in the artificially salinized field condition using salt stress of 6-8 dS m^{-1}. The performance of the F_2 population showed transgressive segregation in the yield components under salinity stress. A genetic linkage map was constructed using 123 microsatellite markers on 232 F_2 progenies. The total size of the linkage map was 1855 cM and the distance between markers ranged from 0.9 to 60.6, with an average of 15 cM. QTL identification was done through composite interval mapping using QGENE software. In total, 36 QTLs were detected, 35 QTLs for yield components under salinity stress and one major QTL for pericarp color. The QTLs detected in this study may be useful for molecular breeding and for identifying useful genes for salinity tolerance.

Identification of quantitative trait loci (QTLs) for salinity tolerance in rice (*Oryza sativa* L.) using IR29/Hasawi mapping population

Bizimana,[1*] Ashura Luzi-Kihupi,[1] and Rakesh K. Singh [2]
[1]Department of Crop Science and Production, Plant Breeding, Sokoine University of Agriculture, P.O. Box 3005, Morogoro, Tanzania
[2]Plant Breeding, Genetics, and Biotechnology Division, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: berchbiz@hotmail.com

Thirty-day-old rice seedlings of 300 $F_{5:6}$ recombinant inbred lines (RILs) derived from a cross between salt-sensitive IR29 (indica) and salt-tolerant Hasawi (indica) were evaluated for salinity tolerance. Thereafter, QTLs linked to salinity tolerance were identified. Final salinity injury scores categorized the RILs from highly tolerant to highly sensitive with a transgressive segregation toward the susceptible parent. However, for the other parameters studied, the RILs showed transgressive segregation on both parental sides. One hundred and ninety-four SNP markers were used to construct a genetic linkage map involving 142 selected RILs (extremes and intermediate) based on final salt injury scores. SNPs covered 1441.96 cM genome with an average distance of 7.88 cM between loci. Twenty QTLs (LOD–3) were identified on chromosomes 1, 2, 4, 6, 8, 9, and 12 using composite interval mapping for eight studied traits in salinized (EC 12 dS m^{-1}) Yoshida nutrient culture solution following IRRI standard protocol. Located on chromosomes 1, 2, 4, 6, 8, 9, and 12 were 2, 3, 3, 3, 1, 2, and 6 QTLs, respectively. The QTLs identified on chromosome 1 (qSL1.1) were located on the long arm of chromosome 1, which is a position very different from the SALTOL locus. This was the major QTL explaining 20.6% of the total phenotypic variation for shoot length. Fine-mapping of these novel QTLs in a very different genetic background is suggested. Novel QTLs could be useful in enhancing the level of tolerance through marker-assisted selection for the pyramiding of different QTLs in one background.

Keywords: seedling stage, single nucleotide polymorphism (SNP) markers, recombinant inbred line (RIL)

Identification of major QTLs for salinity tolerance at the reproductive stage in rice (*Oryza sativa* L.)

Cecilia Diana C. Palao,[1,2], Celia B. dela Vina[2], Glenn B. Gregorio[1], Michael J. Thomson[1], and Rakesh K. Singh[*1]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]University of the Philippines Los Baños, Laguna, Philippines
*Correspondence: r.k.singh@irri.org

The two most vulnerable stages for salt stress in rice are the seedling and reproductive stages. Salt tolerance in these two stages has poor or no correlation. While the importance of seedling-stage tolerance cannot be ignored, the reproductive stage is regarded more crucial as it ultimately determines grain yield. To identify the major QTLs for reproductive-stage salinity tolerance, 201 plants from the F_2 generation of the IR64 (sensitive)/IR4630-22-2-5-1-3 (tolerant) cross were grown to maturity in the screenhouse. Salt stress was imposed at the time of boot leaf emergence. A 1282-cM linkage map was constructed using 104 SSR markers distributed over the 12 chromosomes of rice at an average interval of 15.62 cM. Comparative QTL analysis using QTL cartographer v2.5 and Qgene 4.3.10 revealed 17 unique QTLs tagged in nine of the 12 chromosomes and three common QTLs in chromosomes 3, 4, and 7 associated with reproductive-stage salinity tolerance by IM and CIM. Of these, two major QTLs for K^+ concentration were mapped in chromosomes 4 and 7, explaining more than 10% of phenotypic variation. Other characters associated with reproductive-stage salinity tolerance are plant height, panicle length, shoot and root dry weights, Na^+ ion concentration, and Na-K ratio. The alleles of QTLs identified were not necessarily always contributed by the salt-tolerant parent but those for K^+ concentration was from IR4630-22-2-5-1-3. Fine-mapping using a permanent mapping population derived from this cross is suggested in order to confirm and refine results.

Keywords: indica rice, QTL, salinity, potassium concentration, reproductive stage

Rice heat tolerance at booting and flowering stages

Fatima Amor Tenorio, Changrong Ye,* Edilberto Redoña, and S.V. Krishna Jagadish
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: c.ye@irri.org

It is well known that the rice plant is very sensitive to high temperature at the booting and flowering stages. However, previous studies focused on only the flowering stage or booting stage, and a standard phenotyping method was not established. This study aimed to seek a good method for evaluating heat tolerance of rice genetic resources and breeding lines at the booting and flowering stages and to screen rice varieties with heat tolerance at different growth stages for future breeding programs. Sixteen and twenty-five rice varieties from Egypt, India, IRRI, Japan, Korea, Pakistan, and Italy were planted in a net house for wet- and dry-season experiments, respectively. Three treatments were used: 1) Control: no high temperature; 2) booting stage: treatment at 39/38 ^{o}C from booting stage (auricle distance,-2 to +2 cm) to heading; and 3) flowering stage: treatment at 38 ^{o}C for 2 weeks from heading to end of flowering. The results showed that, during the wet season, Dular and Todorokiwase were tolerant at the booting stage, whereas Milyang 23 and TR22183 were tolerant at the flowering stage. Giza 178 tolerated the two high temperature treatments. From the dry-season experiment, IR2006-p-12-12-2 and TR22183 were found to be most tolerant at flowering. For screening heat tolerance at the booting stage, 39 ^{o}C was identified as the proper temperature treatment. Varieties with heat tolerance at different growth stages constitute a very important resource for future breeding programs. The methods described in this study could be used for precise screening of heat tolerance of rice varieties and breeding lines.

Keywords: rice, genetic resources, reproductive stage, heat tolerance, spikelet fertility

Phenotypic characterization and genetic mapping of an open-hull sterile mutant in rice

Yoye Yu, Rihua Piao, Wenzhu Jiang, and Hee-Jong Koh*
Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 151-742, Korea
*Correspondence: heejkoh@snu.ac.kr

Rice hulls remain closed throughout the ripening period to maintain the internal humidity of the grains. An open-hull sterile mutant was induced by N-methyl-N-nitrosourea (MNU) treatment on Sinsunchalbyeo, a japonica rice variety. This mutant showed open hulls, even in the ripening stages, and fully mature grains. In addition, several altered characteristics were observed, including a narrowed palea, decreased grain size, partial pollen sterility, and erect panicles. Microscopic analysis showed that the palea was positioned slightly inside the lemma and that the size of the palea decreased in the mutant. Genetic analysis of F_2 and F_3 segregation populations derived from the cross between Sinsunchalbyeo open-hull sterile mutant (japonica) and Milyang 23 (indica) indicated that the open-hull trait was controlled by a single recessive allele. Fine-mapping was conducted with sequence-tagged site markers and it revealed that the open-hull sterile mutant was located on the short arm of chromosome 3. We were able to narrow it down to 30.6 Kb and three candidate genes were found.

Keywords: rice, mutant, open-hull sterile, gene mapping

Genetic studies on blast disease resistance in African rice germplasm

T. Odjo,[1] Y. Fukuta,[2] Y. Koide,[2] A. Tanaka-Kawasaki,[2] and S. Yanagihara[2]
[1]Faculty of Agricultural Sciences of University of Abomey-Calavi, Cotonou 01BP526 Benin
[2]Japan International Research Center for Agricultural Sciences, Tsukuba, Japan

Rice blast caused by *Magnaporthe oryzae* (Couch and Kohn) is an important fungal disease of rice (*Oryza sativa* L.), causing significant yield losses in most rice-producing areas of the world. In West Africa, it is a major constraint to rice production. Information on genetic variability in West African germplasm in relation to diversity of resistance to rice blast is essential in understanding and controlling the disease. To investigate the genetic variability and relationship among rice accessions from West Africa, genotyping by microsatellite (SSR) markers and phenotyping by blast isolates were carried out. For the classification and diversity study of resistance, 20 standard differential blast isolates from Japan and 12 blast isolates from West Africa were used. A total of 196 rice varieties, which included 165 accessions (55 *O. sativa*, 45 *O. glaberrima*, 60 NERICAs, and five *O. barthii*), 27 monogenic lines targeting for 23 resistance genes, and four control varieties (US-2, LTH, Nipponbare, and Kasalath) were used. Sixty-seven simple sequence repeat (SSR) markers distributed on 12 rice chromosomes were used to classify the genetic variability of rice in West Africa. Cluster analysis was carried out using Ward's hierarchical clustering method, and these results showed significant genetic variation among West African rice varieties as revealed by genetic distance, which ranged from 0 to 26.7. With a genetic distance of 13.6, the clusters were classified into three major groups: A, B, and C. Groups A and B were mainly *O. sativa* varieties, NERICAs, and monogenic lines, whereas group C was composed of *O. glaberrima* varieties. *O. barthii* varieties were distributed in the three groups. A total of 133 alleles were detected by 61 SSR markers in the 196 rice varieties with an average of 2.2 alleles per locus. The mean allele number per locus on each chromosome was lower in the O. glaberrima varieties (1.3) than in the *O. sativa* varieties (2.1). The genetic diversity in the upland and rainfed lowland NERICAs was similar. The characterization of West African rice varieties against blast isolates revealed four classifications–groups a, b, c, and d. Each group showed unique reactions and was differentiated from the other groups. The 165 West African germplasm was classified into groups b, c, and d, which showed resistant, specific resistant, and strongly resistant reactions against blast isolates, respectively. Group a included monogenic lines, except IRBLsh-B and IRBLzt-T (clustered to group d) and control varieties US-2, LTH, and Nipponbare. Almost all *O. glaberrima* varieties were classified in groups b and c, while in group d were the *O. sativa* varieties and NERICAs. The data have provided very useful information for developing strategies to deploy resistance genes in rice breeding programs to improve varieties in West Africa. However, further studies are needed to clarify the classification of *O. glaberrima* varieties and their progenitor *O. barthii* using more accessions and DNA markers.

Keywords: germplasm, genetic diversity, SSR markers, *Oryza sativa* L., *Oryza glaberrima* Steud, *Oryza barthii*, NERICA, differential system, West Africa

EcoTILLING as a SNP discovery tool for drought candidate genes in *Oryza* germplasm

Ma. Elizabeth Naredo,* Jill Cairns, Rolando Torres, and Kenneth L. McNally
International Rice Research Institute. DAPO Box 7777, Metro Manila, Philippines
*Correspondence: e.naredo@irri.org

Rice genetic resources form an important source of genes that are potentially useful in crop improvement. EcoTILLING, a tool that detects polymorphism in the form of SNPs or indels in natural populations, was employed to survey the variation in a panel of varieties representing the range of diversity in cultivated rice. Candidate genes for drought tolerance were selected based on a holistic approach that linked information on gene function and expression, co-localization with drought QTLs, shifts in allelic frequency under selection, and existing literature incorporating results obtained from other species and studies. Primers were designed based on the Nipponbare sequence. Each sample DNA was independently pooled against IR64 (indica) and Nipponbare (japonica) contrasts. Digestion products generated from the cleavage of mismatch sites by the endonuclease action of the CEL 1 enzyme appeared as distinct bands representing complementary fragments from putative SNPs. Sequencing of representative samples confirmed the SNP position observed on agarose. Population structure in the panel consisting of indica, japonica, and a group composed of aus and indica varieties was detected by model-based and distance-based clustering. Significant associations between sequence variation notably in the *ERF3*, *DREB*, and *MAPk* genes and phenotypic performance to drought stress, specifically grain yield and biomass, were detected by both general linear model and mixed linear model approaches used in association analysis. To address the possible confounding effects of population differentiation, association analysis was conditioned on a population structure determined from existing SSR data on the diverse panel subjected to principal component analysis.

Keywords: EcoTILLING, allele mining, association analysis, genetic diversity

Heterosis QTLs for grain yield and yield-related traits in indica-japonica crosses of rice

Chu Sang-Ho,[1, 2] Wenzhu Jiang,[1] Joong Hyoun Chin,[2] and Hee-Jong Koh[1*]
[1]Department of Plant Science, Seoul National University, Seoul 151-921, Korea
[2]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: heejkoh@snu.ac.kr

Heterosis describes the increased performance of F_1 hybrid plants in terms of increased biomass, yield, vegetative growth rate, and tolerance for biotic and abiotic stresses as compared with their genetically different inbred parents. Two sets of rice materials, 166 RILs derived from a cross between Milyang 23 (a Korean tongil-type rice) and Tong 88-7 (a temperate japonica variety), and BC_1F_1 hybrids derived from crosses between the RILs and the female parent, Milyang 23, were produced to identify heterosis QTLs for yield and yield-related traits in indica-japonica crosses. The QTLs were detected from three different phenotype data sets that include RILs, BC_1F_1 hybrids, and mid-parental heterosis data set. A total of 57 QTLs were detected for nine traits. Out of eight QTLs identified for yield heterosis, five overlapped with other heterosis QTLs for yield-related traits such as spikelet number per panicle, days to heading, and spikelet fertility. Four heterosis QTLs for yield (gy1.1, py6, gy10, and py11) were newly identified in this study. We identified a total of 17 epistatic QTLs for yield heterosis.

Keywords: hererosis, QTL, yield, RILs

Optimization of de novo-based genome assembly of the *Oryza sativa* indica type IR 64-21 genome from paired-end short-sequence reads

Victor Jun Ulat,* Jeffrey Detras, Ramil P. Mauleon, and Kenneth L. McNally
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: v.ulat@irri.org

As a consequence of its wide adaptability and large number of valuable agronomic characteristics, IR64 has been the most widely grown indica rice cultivar in Southeast Asia. However, its yield is affected by drought stress. Efforts to improve the variety through the integration of genomics and biotechnology would be enhanced by having a reference genome sequence. Using an optimized de novo genome assembly approach, the IR 64-21 genome was assembled from paired-end short-read sequences. Although long-sequence reads are not available, more than 80% of the genome was assembled containing more than 80% of the predicted genes for both japonica Nipponbare and indica 93-11 rice varieties. The assembly also contains 14,938 rice microsatellite markers, of which 1,991 are unique to IR 64-21.

Keywords: next-generation sequencing, comparative genomics, genome sequence

Genetic diversity for root morphology and molecular profile in aerobic/lowland indica rice genotypes

Nitika Sandhu,[1] Sunita Jain,[2] and Rajinder Kumar[1*]
[1]Department of Molecular Biology and Biotechnology, CCS Haryana Agricultural University, Hisar, India
[2]Bioinformatic Section, CCS Haryana Agricultural University, Hisar, India
*Correspondence: rajinder.jain@gmail.com

The development of ‘aerobic rice,’ which combines the drought-resistance characteristics of upland varieties with the high-yield traits of lowland varieties, is one of the most promising approaches to address the problem of increasing water scarcity. A total of 22 crosses were made between aerobic (MAS25, MAS26, MAS109) and indica (HKR47, PAU201, Taraori Basmati, Pusa1121) rice varieties. Molecular analysis using 50 SSR and BAD2-specific markers led to the identification of a number of SSRs, which displayed polymorphism among aerobic and lowland indica rice varieties. Two of these SSRs (RM212 and RM302) amplified a specific allele in all the aerobic rice genotypes, which were absent in the lowland indica rice genotypes. Two-dimensional PCA (NTSYS-pc) scaling placed aerobic rice genotypes in the indica rice cluster, which was quite distinct from the Basmati cluster. Polymorphic markers were used for the identification of F_1 plants on 2.5% agarose as well as denatured polyacrylamide gels. Of the 60 Pusa 1121/MAS25 F_2 plants, 20, 18, and 22 plants, respectively, had Pusa1121, MAS25, and Pusa1121 + MAS25-specific alleles at the BAD2 locus. The F_2 population also showed a wide variation in various traits, including root length and/or dry biomass, yield per plant, and length-breadth ratio. Yield per plant showed a significant positive correlation with fresh root weight (0.370; p=0.01) and dry root weight (0.328; p=0.01). A number of F_2 plants were identified with higher root length and/or dry biomass, yield per plant, length-breadth ratio, and with Pusa1121-specific alleles in homozygous or heterozygous condition at the BAD2 locus; these lines shall serve as novel materials for the selection of stable aerobic Basmati rice varieties. Experiments were also conducted for linkage mapping of QTLs for aerobic root traits using HKR47 x MAS26 and MASARB25 x Pusa Basmati 1460 F_2 populations under field and screenhouse conditions. Of the 95 HKR47/MAS26 F_2 plants, 16 plants, and of 73 MASARB25/Pusa Basmati 1460 F_2 plants, 32 plants showed better performance than the tolerant parent. Phenotypic correlation coefficient analysis of HKR47 x MAS26 F_2 population under pot house conditions showed that fresh root weight, root length, root volume, and root number were positively and significantly correlated with yield/plant (0.346, p=0.01), (0.317, p=0.05), (0.455, p=0.01) and (0.386, p=0.05), respectively. Phenotypic correlation coefficient analysis of MASARB25 x Pusa Basmati 1460 F_2 population under pot house

conditions showed that dry root weight, root thickness, and root number were positively and significantly correlated with yield/plant (0.330, p=0.01), (0.278, p=0.05) and (0.285, p=0.05), respectively. A total of 184 and 226 alleles were identified in the HKR47 × MAS26 and MASARB25 × Pusa Basmati 1460 F_2 populations, respectively. NTSYS-pc-based two-dimensional PCA analysis showed a scattering of the F_2 population between the two distinct parental genotypes. Composite interval mapping analysis by WinQTL cartographer 2.5 revealed a total of 26 QTLs associated with 13 traits on chromosomes 2, 5, 6, 8, and 11 in MASARB25 x Pusa Basmati 1460 population under pot house conditions and nine QTLs associated with five traits on chromosomes 1, 2, 8, 9, and 11 under field conditions. Nine QTLs were associated with eight traits on chromosomes 1, 8, 9, 11, and 12 in MASARB25 x Pusa Basmati 1460 populations under pot house conditions and five QTLs were associated with five traits on chromosomes 2, 8, and 10 under field conditions. Several workers have mapped QTLs for root traits but which QTLs to target in these particular sets of crosses are not yet confirmed.

Allele-specific expression imbalance in rice (*Oryza sativa* L.) under normal and drought conditions assayed by single-base extension and RNA sequencing

Nelzo Ereful,[1*] Katrina Malabanan,[1] Antonio Laurena,[2] David Lee,[3] Ian Mackay,[3] and Hei Leung[1]
[1]Plant Breeding, Genetics, and Biotechnology Division, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Institute of Plant Breeding, University of the Philippines Los Banos, Laguna, Philippines
[3]John Bingham Laboratory, National Institute of Agricultural Botany, Cambridge, UK
*Correspondence: n.ereful@irri.org

To understand the possible roles of allelic imbalance in genetic regulation of drought response in rice, we identified a set of differentially expressed genes from previous microarray transcript-profiling experiments in Apo, a drought-tolerant indica, and IR64, a drought-sensitive indica. After validating these genes by co-localizing QTL and the differentially expressed genes and bidirectional selective genotyping, they were assayed for allele-specific expression (ASE) by SNaPshot™ single-base extension assay in the F_1 hybrid using cSNPs. Results of the assay showed allele-specific copy number variation between the two alleles in the F_1 hybrid. This phenomenon occurs when, in a bi-allelic organism such as rice, one of the parental alleles was replicated several times relative to the other allele. In this study, allelic ratios of 1:3 and 2:1 between Apo- and IR64-specific alleles in the F_1 hybrid were observed. To further investigate ASE imbalance in a genomewide scale, RNA sequencing was performed using the same parental genotypes (IR64 and Apo) and their F_1 hybrid under normal and drought stress conditions (two treatments, three genotypes each). Results showed that ASE imbalance was found to occur in both control and stress conditions, indicating that such behavior is a phenomenon inherent to the organism. The imbalance was originally thought to be attributed to cis-acting polymorphism because, in an F_1 nuclear environment, both alleles are exposed to the same pool of trans-acting factors. However, by comparing F_1 hybrids in two different conditions, the degree of imbalance is higher during drought condition, which could be attributed to the condition-dependent trans-acting factors. This study shows that ASE imbalance is common in rice and reveals potentially new regulatory mechanisms that have a bearing on drought response, phenotypic variation, and heterosis in rice.

Keywords: allelic imbalance, copy number variation, NGS RNA-Seq, rice

Distribution of InDel markers of indica-japonica differentiation in wild rice relatives of rice (*Oryza sativa* L.)

YooJin Lee,[1] Joong Hyoun Chin,[1] Michael J. Thomson,[1*] and Hee-Jong Koh[2*]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Seoul National University, 151-921,Seoul, South Korea
*Correspondence: m.thomson@irri.org, heejkoh@snu.ac.kr

Subspecies-specific (SS) InDel markers were designed from indica-japonica polymorphic insertion/deletion variations based on Nipponbare and 93-11 DNA sequences throughout the whole genome. Of 765 polymorphic markers, only 67 STS markers showed clear indica-japonica specific polymorphisms. The selected markers may be linked to conserved genomic regions related to insertion/deletion mutations in *Oryza sativa* due to domestication. The distribution of InDel SS regions among *Oryza* species was investigated by PCR across 290 accessions, including 61 Asian cultivated rice cultivars, 27 African cultivated rice accessions, and 202 accessions of wild relatives of *Oryza* species, using 67 InDel SS-STS primers. Average SS allele frequency of AA genome species, BB~EE, and FF~HHKK showed an increased proportion of non-*O. sativa* and null alleles in the more distant wild species. Most of the wild species, except EE GG, HHJJ, and HHKK genome accessions, consisted of relatively more indica-type alleles of SS markers. Interestingly, some SS alleles were present throughout all *Oryza* species, while others were only in AA genome species. PCR products of 24 to 33 accessions from various species using nine markers were sequenced to confirm the polymorphisms. Sequencing results showed that *Oryza* species largely share SS regions across the different genomes, although with some small variations. This study showed InDel polymorphisms as another reliable criterion to trace back how alleles determining indica or japonica have been distributed after domestication. The evolutionary pathway in the genus *Oryza* and the differentiation process of indica and japonica can thus be further investigated.

Keywords: subspecies-specific, evolution, domestication, InDel

SNP marker technology for various breeding applications

Christine Jade Dilla-Ermita,*[1] Ma.Ymber Reveche,[1] Dennis Nicuh Lozada,[1] Erwin Tandayu,[1] Socorro Carandang,[1] Marjorie De Ocampo,[1] Ramil Mauleon,[1] Kenneth McNally,[1] Hei Leung,[1] Susan McCouch,[2] and Michael Thomson[1]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Cornell University, Ithaca, New York, USA
*Correspondence: c.dilla@irri.org

The evolution of genomic tools has given rise to molecular marker platforms that are high-throughput and cost-effective. Single nucleotide polymorphism (SNP) markers are now gaining acceptance and have established their unique importance in molecular breeding. The abundance of SNPs across the rice genome has been instrumental in revealing genetic variations that could not be elucidated by other molecular markers. This study showcases the molecular breeding applications of Illumina BeadXpress and Fluidigm EP1 system. High-throughput SNP genotyping in 384-plex Illumina BeadXpress platform is cost-effective and less laborious than the gel-based markers. The Illumina platform has an automated allele-calling system that makes data analysis more accurate, easier, and less time-consuming. A total of seven customized marker sets based on informative SNPs for different rice variety groups were chosen from the 1,536 Illumina and 44k Affymetrix SNP chips developed at Cornell University. These marker sets are very useful for various molecular breeding applications such as DNA fingerprinting, genetic diversity, QTL mapping, and marker-aided selection. Using this system, each data point costs only $0.10. Furthermore, a flexible SNP set is currently being developed using the Fluidigm EP1 system, which exists in three formats for trait-specific SNP genotyping. The three formats–48.48, 96.96 and 192.24–will enable more flexible SNP genotyping for foreground selection using functional markers, background selection, and QTL analysis for specific genotypes and breeding objectives. Thus, these SNP marker platforms are cost-effective and can expedite routine molecular breeding work.

Keywords: single nucleotide polymorphism, molecular markers, molecular breeding, genetic variation

qDTY3.1, a large-effect and consistent QTL for grain yield under drought in rice

Noraziyah Abd Aziz Shamsudin,[1,2] B.P. Mallikarjuna Swamy,[1] Joahna Ruth Ramirez,[1] John Christian Ontoy,[1] Jennylyn Trinidad,[1] Margaret Catalos,[1] and Arvind Kumar[1*]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]National University of Malaysia, Bangi, Selangor, Malaysia
*Correspondence: a.kumar@irri.org

Rice (*Oryza sativa* L.) is highly susceptible to drought stress throughout its life cycle, but huge economic losses or even complete crop failure is observed if stress occurs during flowering. The identification and introgression of major-effect QTLs for grain yield under reproductive-stage drought stress in drought-susceptible rice varieties have been suggested as an appropriate marker-assisted breeding (MAB) strategy. We developed a back-derived mapping population using Apo, an aerobic adapted rice variety from the Philippines as a donor parent and BR11, an elite but drought-susceptible rice variety from Bangladesh as a recipient parent. The population was phenotyped for yield and yield-related traits under drought stress and nonstress during the 2011 and 2012 dry seasons (DS). Bulk segregant analysis (BSA) using polymorphic SSR markers was followed to genotype the population. A large-effect QTL, qDTY3.1 was detected for grain yield under drought QTL on chromosome 3. The QTL was flanked by markers RM15935 and RM520, with a peak at RM520. In combined analysis over 2 years, this QTL explained an additive effect of 22% of the trial mean yield. This QTL was also reported earlier in an Apo/Swarna-derived population, thus confirming its consistency across genetic backgrounds and environments. This QTL can be exploited in MAB to improve the drought tolerance of rice varieties. The results also indicate that BSA is an effective method to identify large-effect QTLs for grain yield under drought stress.

Keywords: marker-assisted breeding, bulk segregant analysis, drought tolerance

Category 6

Innovations and
Novel Approaches

8 November 2012 Category 6: Innovations and Novel Approaches 2012 IRRI Young Scientist Conference

Time	Abstract no.	Abstract title, authors
10:15	9	**Building a dynamic architectural and biochemical plant model for *Oryza sativa*** Katherine Meacham, Robert Furbank, Paul Quick, Susanne von Caemmerer, and Xavier Sirault
10:35	17	**Function of plasma membrane aquaporins in stomatal movements in *Arabidopsis thaliana*** Alexandre Grondin, Lionel Verdoucq, and Christophe Maurel
10:55	24	**Mobile phones as a tool for reaching farmers with personalized information** Maria Eda Apple Suplido, Rowena Castillo, Michaela Glaiza Milagrosa, Jo Anne Holly Torres, Marlon Guerra, Philip Joshua Sinohin, Jemima Manansala, Marco van den Berg, and Roland J. Buresh
11:15	33	**MAGIC Indica: a new genetic resource for multiple-trait improvement and QTL discovery in the indica rice subspecies** Nonoy Bandillo, Edilberto Redoña, Jose Hernandez, Pompe Sta. Cruz, Gregorio Gregorio, Chitra Raghavan, Irish Lobina, Michael Thomson, Rakesh Kumar Singh, and Hei Leung
11:35	47	**Physiological and molecular responses of rice to heat and drought stress** Reneeliza Jean Melgar and S.V. Krishna Jagadish
11:55	50	**Developing an approach for recombination breakpoint analysis on the short arm of chromosome 1 from patterns of single nucleotide polymorphisms in 20 varieties of rice (*Oryza sativa* L.)** Jeffrey Detras,, Merlyn Mendioro, Evelyn Mae Tecson-Mendoza, and Kenneth McNally
13:35	51	**Evaluation of ORYZA2000 under nitrogen-limited conditions: updates and improvements** Manuel Marcaida III and Tao Li
13:55	57	**Using simple and quick PCR to determine transgene copy number in rice** Christian F. Cantos, I. Slamet-Loedin I, N. Oliva N, and P. Chadha-Mohanty
14:15	61	**Leaf anatomy screening: production line toward the identification of C3, C3-C4 intermediate, and C4 traits** Abigail Mabilangan, Anna Mae de los Reyes, Maricar Mercado, Leanilyn Castanar, Elmer Duque, Robert Coe, Reychelle Mogul, Jacqueline Dionora, and William Paul Quick
14:35	63	**Evidence on the impacts of training and technology interventions: capacity building of rural women in some villages in Central Luzon, Philippines** Joyce Luis and Thelma Paris
14:55	80	**Integrating best management practices into the portfolio of farmers' own technology following the principles of integrated crop and resource management–a potential option for minimizing the yield gap in rice** M. Murshedul Alam, Md. Rezaul Karim, and J. K. Ladha
15:35	83	**Microclimatic modifications in controlled growth facilities and their implications on climate change research** A.A. Boling, R.J. Cabangon, T.P. Tuong, A.V. Madrid, Jr., F.Javier, M.A.E. Burac, L.P. Llorca, C. Balingbing, and K. Hayashi
15:55	93	**ORYZA2000 ability in salinity stress modeling: limits and opportunities** Ando Mariot Radanielson and Tao Li
16:15	98	**Molecular characterization of *OsPupk20-2* (dirigent-like) gene** Krystal Phillip, Rico Gamuyao, and Sigrid Heuer

Building a dynamic architectural and biochemical plant model for *Oryza sativa*

Katherine Meacham,[1,2] Robert Furbank,[1] Paul Quick,[3] Susanne von Caemmerer,[2] and Xavier Sirault[1]
[1]High Resolution Plant Phenomics Centre, CSIRO Plant Industry, Canberra, ACT 2601, Australia
[2]Plant Science Division, Research School of Biology, Australian National University, Canberra, ACT, Australia
[3]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: Katherine.Meacham@csiro.au

It is widely recognized that the yield increases required to meet global demand for rice must be achieved through increases in radiation and light use efficiency (RUE and LUE). Traditional breeding techniques have hit a recognized plateau and potential yield in breeder trials at IRRI have not increased in 30 years. Defining LUE as kg biomass/PAR intercepted and assuming that RUE is a product of LUE and light interception, improving RUE becomes a matter of understanding the relationship between plant and canopy architecture, and plant and canopy biochemistry. With a subset of sequenced rice lines from IRRI, we are working toward creating a dynamic biochemical and architectural plant model. Weekly 3-D imaging with a novel digitization platform is used to characterize plant architecture and phenology, while photosynthesis is characterized with gas exchange measurements of CO_2 response and measurements of chlorophyll fluorescence. Nitrogen partitioning and distribution throughout the plant are derived from SPAD and chlorophyll extraction. We are presenting early results from the 3-D imaging platform and the underlying models into which it will be incorporated.

Keywords: phenomics, RUE, LUE, modeing, 3-D imaging

Function of plasma membrane aquaporins in stomatal movements in *Arabidopsis thaliana*

Alexandre Grondin,[2*] Lionel Verdoucq,[1] and Christophe Maurel[1]
[1]Biochimie et Physiologie Moléculaire des Plantes, CNRS/INRA/SupAgro/UM2, Montpellier, France
[2]International Rice Research Institute, Los Banos, Philippines
*Correspondence: a.grondin@irri.org

Stomatal movements are mediated by drastic changes in guard cell volume. A role in these processes for water channel proteins named aquaporins has been proposed but not demonstrated. Transcriptome analyses have indicated that several plasma membrane aquaporins (PIPs), including AtPIP1;2 and AtPIP2;1, are expressed in *Arabidopsis thaliana* guard cells. In the present work, we investigated the function of these two aquaporins in stomatal movements. The stomata of pip1;2 and pip2;1 knock-out mutants showed a normal opening response to light and low CO_2, a normal closing response to darkness and high CO_2, but almost insensitive response to abscisic acid (ABA)-induced stomatal closure. A direct role of AtPIP1;2 and AtPIP2;1 in water transport was investigated by measurement of guard cell protoplast water permeability (Pf) under darkness, light, and light with ABA. The Pf of pip2;1 guard cell protoplasts was significantly reduced, specifically in the presence of ABA. As extracellular hydrogen peroxide (H_2O_2) production is essential for intracellular ABA signaling, we also investigated the possibility that AtPIP1;2 and AtPIP2;1 facilitate the diffusion of H_2O_2 through the guard cell plasma membrane. Time-dependent accumulation of reactive oxygen species in response to ABA was abolished in pip2;1 but not in pip1;2 guard cells. Altogether, our results suggest that AtPIP2;1 and, to a lesser extent, AtPIP1;2 play important and distinct roles in water and H_2O_2 fluxes during ABA-induced stomatal closure in *A. thaliana*.

Keywords: *Arabidopsis thaliana*, guard cell, abscisic acid, aquaporin, water, hydrogen peroxide

Mobile phones as a tool for reaching farmers with personalized information

Maria Eda Apple Suplido,[1] Rowena Castillo,[1] Michaela Glaiza Milagrosa, Jo Anne Holly Torres,[1] Marlon Guerra,[1] Philip Joshua Sinohin,[1] Jemima Manansala,[1] Marco van den Berg,[2] and Roland J. Buresh[1]
[1]Crop and Environmental Sciences Division, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Information Technology Services, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: m.suplido@irri.org

The production of food across Asia relies heavily on farmers with small landholdings. Access of these farmers to guidelines on ‘actionable’ management practices specific to their small landholding could be valuable for increasing productivity and profit. The rapid physical transfer of information from research and extension services to farmers has been challenging and costly. Thanks to recent advances in information and communication technology (ICT), new tools and approaches for rapid transfer of information are emerging. The development of *Nutrient Manager for Rice* (NMRice), which is a country-specific decision support tool targeting rice farmers and extension agents, addresses the need for precision management of fertilizers in small rice fields. It can be accessed through the Internet and mobile phones. The availability of inexpensive smart phones can provide a new pathway for extension agents to reach farmers with NMRice. We partnered with the Agricultural Training Institute and local government units in the Philippines to monitor and evaluate the use of smart phones in reaching farmers in eight municipalities across seven provinces. Information on the use of NMRice by extension agents was captured and used to analyze the extent and effectiveness of the ‘reach’ to farmers by extension agents provided with smart phones. This information was cross-referenced with results of field trials comparing the NMRice recommendation with farmer’s fertilizer practice. Results from this project will guide the development of more user-friendly mobile phone applications and more effective techniques for reaching farmers through smart phones in the hands of extension agents.

Keywords: information and communication technology, *Nutrient Manager for Rice*, phone application

MAGIC Indica: a new genetic resource for multiple-trait improvement and QTL discovery in the indica rice subspecies

Nonoy Bandillo,[1*] Edilberto Redoña,[1] Jose Hernandez,[2] Pompe Sta. Cruz,[2] Glenn Gregorio,[1] Chitra Raghavan,[1] Irish Lobina,[1] Michael Thomson,[1] Rakesh Kumar Singh,[1] and Hei Leung[1]
[1]Plant Breeding, Genetics, and Biotechnology Division, International Rice Research Institute, Los Baños, Philippines
[2]Crop Science Cluster, University of the Philippines Los Baños, Los Baños, Philippines
*Correspondence: n.bandillo@irri.org

Indica rice is one of two major subspecies of the cultivated Asian rice species *Oryza sativa* L., which is the staple food of more than half of the world's population. Key economic traits in indica rice, such as tolerance for biotic and abiotic stresses, are quantitatively inherited and influenced by large GxE interactions. Their complex inheritance and oftentimes narrow genetic resource base for mining favorable alleles make trait improvement through breeding inherently difficult. To harness natural allelic variation comprehensively in breeding while allowing the genetic dissection of complex traits individually, we generated a multiparent advanced generation intercross (MAGIC) population using, as founder parents, eight elite indica cultivars with desirable traits such as high yield, good grain quality, and tolerance for a suite of stresses. Genomewide association (GWA) mapping using genotyping-by-sequencing on a subset of MAGIC indica lines was able to tag known genes/QTLs such as the *Sub1* for submergence tolerance, the *qBR9.1* for blast disease resistance, and the *Saltol* for salinity tolerance, with SNP markers within or very close to the gene/QTL itself. Moreover, several novel QTLs for these same traits were also identified. The new and diverse genetic resource, which we now refer to as 'MAGIC Indica,' promises to be a valuable source of breeding-ready materials for the extraction of new commercial varieties with multiple economically important traits as well as a rich resource for fine-mapping known QTLs and/or precisely identifying multiple QTLs for multiple traits in indica rice.

Keywords: multiparent advanced generation intercross, genotyping-by-sequencing, genomewide association mapping, allelic variation, genetic dissection

Physiological and molecular responses of rice to heat and drought stress

Reneeliza Jean Melgar and S.V. Krishna Jagadish*
1International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: k.jagadish@irri.org

Under actual field conditions, multiple abiotic stresses occur, among which the combined heat and water-deficit stress is most common. Global climate models predict an increase of up to 4 oC by the end of the century. This can potentially reduce water availability and can, in turn, double the water deficit-stressed area under rice cultivation. Plant responses are different when exposed to a combination of stresses as compared with either heat or drought applied individually. Exposure to the combined heat and drought stress during sensitive developmental stages such as flowering leads to increased spikelet sterility and yield losses in rice. Water-deficit stress, in combination with heat stress, significantly reduced peduncle length ($P < 0.05$), panicle exsertion ($P < 0.05$), and anther dehiscence ($P < 0.01$). The number of pollens germinating on the stigma and anther dehiscence showed moderate association. Reduced spikelet fertility was observed in heat, water-deficit, and combined heat and water-deficit stress treatments, with heat stress recording the lowest fertility. Molecular analyses showed that heat shock transcripts and proteins were strongly upregulated under combined stress compared with either heat or water-deficit stress. Proteins favoring pollen germination were highly upregulated under water-deficit stress but are within normal levels of expression under combined stress. This interesting phenomenon has been observed in Arabidopsis, cotton, and rice (after rewatering drought-stressed seedlings). Physiological and molecular responses under combined heat and drought stress in rice will be discussed and compared with those of other crops.

Keywords: flowering, heat stress, rice, spikelet fertility, water-deficit stress

Developing an approach for recombination breakpoint analysis on the short arm of chromosome 1 from patterns of single nucleotide polymorphisms in 20 varieties of rice (*Oryza sativa* L.)

Jeffrey Detras,[1*] Merlyn Mendioro,[2] Evelyn Mae Tecson-Mendoza,[3] and Kenneth McNally[1]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Genetics and Molecular Biology Division, Institute of Biological Sciences, University of the Philippines Los Banos (UPLB), Los Banos, Laguna, Philippines
[3]Institute of Plant Breeding, Crop Science Cluster, College of Agriculture, UPLB, Los Banos, Laguna, Philippines
*Correspondence: jdetras@irri.org

A methodology for recombination breakpoint analysis was developed and tested on the short arm of chromosome 1. The pipeline for analysis used customized PERL scripts. It included (1) imputation of missing data points in OryzaSNP data (http://www.oryzasnp.org), (2) creation of genome blocks, (3) phylogenetic analysis in each block by parsimony with bootstrapping using PHYLIP software, (4) distance value calculation using the Bio::TreeIO Perl module, (5) distance matrix analysis for clustering using k-means (R-statistics software) with k = 3. Then, block-by-block comparison of clustering results was done to examine the introgression patterns. As for the biological significance, the introgression pattern shows that recombination breakpoints spread out across the chromosome and reveal relationships among the varieties at specific regions in the chromosome. The approach can be used for whole-genome analysis of the OryzaSNP data.

Keywords: SNP, phylogenetic analysis, introgression

Evaluation of ORYZA2000 under nitrogen-limited conditions: updates and improvements

Manuel Marcaida III* and Tao Li
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: m.marcaida@irri.org

The rice growth and development model ORYZA2000 is extensively used in simulating potential, water stress, and nitrogen stress conditions. A new version of this model is being released to improve its precision and suitability for various simulation purposes. In the new version, a new routine in soil carbon and nitrogen dynamics was developed and the nitrogen uptake and nitrogen stress quantification routine was modified. Using goodness-of-fit parameters suggested by Bouman and van Laar (2006) in evaluating the model under nitrogen-limited conditions, a comparison of the same study will be made using recent updates in the model. A comparison of simulated and measured leaf, stem, panicle, and total aboveground biomass and leaf area index will be carried out using slope, intercept, and adjusted correlation coefficients; Student's t test of means; absolute and normalized root mean square errors; and a graphical method. These updates will increase the model's accuracy in supporting experiments that involve nitrogen management practices and other potential and yield-forecasting studies.

Keywords: ORYZA2000, model validation, crop simulation, rice, nitrogen

Using simple and quick PCR to determine transgene copy number in rice

Christian F. Cantos,* I. Slamet-Loedin, N. Oliva, and P. Chadha-Mohanty
Genetic Transformation Laboratory, Plant Breeding, Genetics, and Biotechnology Division,
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: c.cantos@irri.org

Functional genomic study in rice requires the establishment of an efficient transformation systems platform. For various transgenic events and data interpretation, copy number of the target gene (transgene) is an important component of product development. The existing DNA gene copy analyses, based on Southern blot technique, are time-consuming, tedious, and expensive. Therefore, developing cost-effective high-throughput protocols to screen for single-copy insertions using simple and rapid methods is very important for the transformation platform. We present a simple, rapid, and low-cost polymerase chain reaction (PCR)-based method for copy number analysis in transgenic rice. Clear distinctions can be observed in band densities between the single copy and the multiple copies of the transgenic rice in comparison with the standards. In future research, this method can be used as preliminary screening for thousand of transgenic events before performing the more intricate copy number analysis methods.

Keywords: quick PCR, transgene copy number

Leaf anatomy screening: production line toward the identification of C3, C3-C4 intermediate, and C4 traits

Abigail Mabilangan, Anna Mae de los Reyes,* Maricar Mercado, Leanilyn Castanar, Elmer Duque, Robert Coe, Reychelle Mogul, Jacqueline Dionora, and William Paul Quick
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: a.delosreyes@irri.org

Rice plays a major part in the nutritional diet of the world's population. Accordingly, there is a desire and a need to increase production amidst population growth, resource limitations, and environmental changes. A potential yield increase of 50% may be achieved by enhancing the C3-type of photosynthesis of rice to the more efficient C4-type. The C4 Rice Project aims to identify genes controlling the C4 properties and to test the feasibility of introducing these into rice. Complementary to the other approaches of the project, leaf anatomy screening is conducted to find interesting phenotypes from thousands of activation-tagged rice lines, sorghum, and *Setaria* plants being generated. The study involves a series of laboratory activities that facilitates identification of altered or interesting phenotypes. Primarily, fresh leaf samples pass through vein counting using portable microscopes, followed by confirmation where altered vein density was observed. Subsequently, samples go through fixation, hand-sectioning, and different staining and processing techniques. Sections are then forwarded to imaging using either light or fluorescence microscope. The digital images produced were used in the measurements of different cell and tissue types such as mesophyll, bundle sheath, and vein parameters that may be associated with alterations in vein density. Thus far, in 2011, a total of 14,462 activation-tagged rice lines and 33,840 sorghum mutants were screened. Employment of the screening techniques contributes to identification of lines with phenotype changes to advance to gene sequencing and, ultimately, to the identification of potential C4 genes for use in rice engineering.

Keywords: C4 photosynthesis, vein density, microscope, image analysis

Evidence on the impacts of training and technology interventions: capacity building of rural women in some villages in Central Luzon, Philippines

Joyce Luis* and Thelma Paris
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: j.luis@irri.org

In 1991, research on gender issues was initiated by the International Rice Research Institute to quantify the labor and income contributions of men and women. Gender disparities in terms of access to resources and participation in decisionmaking were determined. Several training courses were conducted and appropriate technologies were tested, evaluated, and managed by women's groups. In 2011, a resurvey was conducted in the same villages and the same families interviewed in 1991. The specific objectives of the resurvey were to 1) identify the major changes in the villages; 2) assess the effects of these changes on the community, farming systems, livelihood, and gender roles; 3) determine the drivers of these changes; and 4) recommend strategies to improve the socioeconomic conditions of the households, of women in particular. Qualitative and quantitative methods were used to gather information and to analyze data. One distinct change was the availability of irrigation, which also led to double rice cropping and adoption of new rice varieties. In the villages without change, women continued to work as unpaid family workers and felt more pressured to obtain additional income. In the villages with irrigation, the women's socioeconomic status has improved. They have assumed managerial roles and spent more time earning money from non-farm activities. Thus, technologies have led to sustainable crop productivity as well as improved family welfare. To evaluate the impact of the training and technologies on building the capacity of rural women, a regression analysis using the difference-in-difference approach will be used. This analysis will show trends in membership in informal women's group, empowerment index, and yield using 2-year panel data that allow control of non-random selection.

Keywords: gender analysis, difference-in-difference, panel data

Integrating best management practices into the portfolio of farmers' own technology following the principles of integrated crop and resource management–a potential option for minimizing the yield gap in rice

M. Murshedul Alam,[1*] Md. Rezaul Karim,[1] and J. K. Ladha[2]
[1]International Rice Research Institute (IRRI)-Bangladesh Office, Dhaka, Bangladesh
[2]IRRI-India Office, New Delhi, India
*Correspondence: m.alam@irri.org; j.k.ladha@irri.org

The major cereal cropping system in Bangladesh is dry-season (boro) rice − wet-season (aman) rice. The average productivity (7 t ha^{-1}) of this system is far below the attainable yields in farmers' fields (14 t ha^{-1}), resulting in a large yield gap. This is mainly attributed to poor management practices adapted by farmers. Since the possibility of expanding the rice area is limited, the major challenge is how to minimize this yield gap with less water, less agrochemicals, and less labor to make rice farming more profitable and sustainable. We evaluated a set of selected best management practices (BMP) in the farmers' portfolio in farmers' fields over five consecutive seasons during 2006–08. In the wet seasons, compared with farmers' practice (FP), BMP increased grain yield by as much as 0.5–0.9 t ha^{-1} when N was given as urea supergranule and by 0.6–1.1 t ha^{-1} when N was applied using a leaf color chart. In the dry seasons, grain yields were 6.4–8.4 t ha^{-1} in BMP, irrespective of N management (these were higher that FP yields by 0.2–1.2 t ha^{-1}). The average added net returns with BMP were US$22−120 ha^{-1} in the wet season and US$93−115 ha^{-1} in the dry season. Our study shows that the integration of BMP in the farmers' own portfolio of practices has the potential to boost rice productivity and profit from rice farming in Bangladesh.

Keywords: rice-rice cropping system, productivity increase, net profit

Microclimatic modifications in controlled growth facilities and their implications on climate change research

A.A. Boling,* R.J. Cabangon, T.P. Tuong, A.V. Madrid, Jr., F. Javier, M.A.E. Burac, L.P. Llorca, C. Balingbing, and K. Hayashi
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: a.boling@irri.org

Greenhouses and screenhouses (controlled growth facilities) protect plants from biotic stresses and adverse weather conditions. In these facilities, however, changes in solar radiation, air temperature, humidity, and wind speed (microclimate) may occur. This study aimed to determine the differences in microclimate between that obtaining in controlled growth facilities and ambient condition. In 1999−2008, solar radiation, air temperature, relative humidity, and wind speed were measured in IRRI's controlled growth facilities using an Eijkelkamp 16.98 automatic agro-meteo station. These weather data were compared with those measured at the IRRI wetland site using Student's t-test. In the controlled growth facilities, solar radiation was 6−14 MJ m^{-2} d^{-1} lower than in the wetland site. Similarly, wind speed in these facilities was more than 90% lower than ambient condition. On the other hand, air temperature in the greenhouses was 4−7 °C higher than ambient. These changes in solar radiation, air temperature, and wind speed affect the consumptive water use, phenological development, and growth of the rice crop. Microclimatic changes in controlled growth facilities should be taken into account in the experimental design and analysis as well as in the design of facilities for climate change research.

Keywords: glasshouse, screenhouse, solar radiation, temperature, wind speed

ORYZA2000 ability in salinity stress modeling: limits and opportunities

Ando Mariot Radanielson* and Tao Li
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines.
*Correspondence: a.radanielson@irri.org

Sustaining and improving crop production under limiting environments is a crucial issue for our generation. For rice, considerable progress has been done in improving the genetic potential of the last-released varieties and highly conservative technology has been developed by agronomists to meet this objective. A crop model, as a tool, can bring efficiency into the delivery of these achievements. It has always tried to integrate available knowledge in the soil-plant-atmosphere system by a series of mathematical functions. With these functions, an integrative trait such as yield is decomposed into different key traits expressing the plant system's responses to its environment. Crop model development and contribution has been pushed at its high point this time in predicting crop production, scheduling crop establishment and irrigation, and assessing varieties in both conventional and molecular breeding. In the context of all the challenges that rice production is facing, this tool has advantages and limitations. The case of the rice model ORYZA2000 in predicting rice response to salinity stress illustrates this aspect and from this, interesting science making and critical concepts have risen.

Keywords: abiotic stress, breeding, crop modeling, environment, genotype

Molecular characterization of *OsPupk20-2* (*dirigent-like*) gene

Krystal Phillip, Rico Gamuyao, and Sigrid Heuer*
International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
*Correspondence: s.heuer@cgiar.org

The Phosphorus uptake 1 (Pup 1) locus was identified as a major quantitative trait locus for tolerance to phosphorus deficiency in rice. One of the genes located within the Pup1 locus, *OsPupk20-2*, codes for a dirigent-like protein that is said to bind and orient lignin monomer radicals during lignin biosynthesis. *OsPupk20-2* has been shown to be downstream of the recently identified major determinant of tolerance, the Pup1 protein kinase gene *OsPSTOL1*. To study the effect of *OsPupk20-2*, overexpression plants (35S::*OsPupK20-2*) were grown in both P-deficient and P-containing soil, and in hydroponics. Phenotypic analyses revealed greater shoot length in transgenic plants at 13 days after germination (DAG) in both P-deficient and P-containing soil. However, at 16 DAG, transgenics showed longer shoots only in P-deficient, slightly arid soil conditions. Root scan analyses revealed that transgenics had more total root length and greater surface area than nontransgenics in hydroponics. Lignin analysis using phloroglucinol stain further indicated the occurrence of more lignins in roots grown in P-deficient soil and hydroponic conditions in both transgenics and nulls. Therefore, the increase in lignification is a clear effect of P deficiency. Analyses of *OsPupk20-2* promoter::GUS transgenics further showed gene expression in anthers undergoing microsporogenesis. Transgenic plants grown to maturity in soil containing P showed higher shoot length, higher root length, higher tiller number, and higher panicle length. Future studies will determine the exact function of *OsPupK20-2* and its interaction with *OsPSTOL1*.

Keywords: dirigent-like protein, phosphorus, root, lignin

Abstracts

Best Paper Competition

9 November 2012

IRRI Havener Auditorium

9 November 2012 Best Paper Competition 2012 IRRI Young Scientists Conference

Time	Abstract no.	Abstract title, authors
8:30	19	**Gene validation of a major QTL for tolerance to anaerobic conditions during germination** Tobias Kretzschmar, Rudi K. Trijatmiko, Margaret A. Pelayo, Lourd F. Gabunada, John C. Ignacio, Pamella M. D. Sendon, Inez H. Slamet-Loedin, David J. Mackill, Adelbagi M. Ismail, and Endang M. Septiningsih
8:50	28	**Ubiquitous resistance to rice tungro spherical virus is mediated by a gene for translation initiation factor 4G** Genelou A. Atienza, Jong-Hee Lee, Muhammad Muhsin, Jaymee R. Encabo, Suk-Man Kim, Edgardo Coloquio, Norman P. Oliva, Kurniawan Rudi Trijatmiko, Editha M. Abrigo, Rogelio C. Cabunagan, Pepito Q. Cabauatan, Daisuke Fujita, Inez H. Slamet-Loedin, Hei Leung, and Il-Ryong Choi
9:10	54	**Impact of rice price hike on poverty in Bangladesh** Taznoore Samina Khanam and Humnath Bhandari
9:30	58	**Methane emission and rice yield as affected by elevated temperature, rice straw incorporation, and soil properties in lowland rice paddy soils** Yam Kanta Gaihre, Reiner Wassmann, Gina Villegas-Pangga, and Eugenio Aquino
9:50	62	**Transformation of rice with C4 genes and characterization of transgenic plants** Kamal Swati, Shanta Karki, Sarah Covshoff, Helen Woodfield, Juvy Reyes, Florencia A. Montecillo, Robert Coe, Czarina Mae Realubit, Gemma Lorenzana, Menard Dela Rosa, Michelle Grace Acoba, Albert Chris de Luna, Florence Danila, Inez Slamet-Loedin, Julian Hibberd, and Paul Quick
10:10	69	**Introduction of transport proteins into *Oryza sativa* L. to facilitate installation of the C4 pathway** Ronald Tapia, Shanta Karki, Sarah Covshoff, Florencia A. Montecillo, Robert Coe, Juvy Reyes, Czarina Mae Realubit, Gemma Lorenzana, Menard Dela Rosa, Michelle Grace Acoba, Albert Chris de Luna, Inez Slamet- Loedin, Julian Hibberd, and Paul Quick

Gene validation of a major QTL for tolerance to anaerobic conditions during germination

Tobias Kretzschmar,[1*] Rudi K. Trijatmiko,[1] Margaret A. Pelayo,[1] Lourd F. Gabunada,[1] John C. Ignacio,[1] Pamella M.D. Sendon,[1] Inez Slamet-Loedin,[1] David J. Mackill,[2] Adelbagi M. Ismail,[1] and Endang M. Septiningsih[1]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]MARS Food Global, Department. of Plant Science, University of California, Davis, CA 95616 USA
*Correspondence: t.kretzschmar@irri.org

Most rice varieties cannot survive prolonged submergence during germination and early seedling establishment. However, several landraces were identified that display a pronounced tolerance for flooding during germination. This unique ability is associated with efficient starch mobilization and active fermentative pathways that provide energy for extensive coleoptile elongation under complete submergence. This trait, referred to as anaerobic germination (AG), is of particular importance for direct-seeded systems, which, due to escalating labor costs for transplanting, are becoming increasingly attractive for farmers in both rainfed and irrigated ecosystems. Other than providing a safety net for smallholder farmers, having varieties that are tolerant of AG conditions will help suppress weed infestation, a major challenge in direct seeding practices. A major QTL for AG derived from Khao Hlan On, qAG9-2, was previously identified and fine-mapped to a ~58-kb region on chromosome 9. A near-isogenic line (NIL) of qAG9-2 in the background of susceptible variety IR64 shows enhanced AG tolerance as validated by the increased seedling establishment and coleoptile elongation under submergence. Fine-mapping of qAG9-2 resulted in the identification of five putative candidate genes, *qAG9-2-a* to *qAG9-2-e*. Expression studies and sequencing analysis point to *qAG9-2-d* as the responsible gene underlying qAG9-2. This hypothesis is currently being confirmed by an evaluation of *qAG9-2-d* overexpression in IR64 and *qAG9-2-d* T-DNA insertion in the semi-tolerant background Dongjin. As susceptibility in IR64 can be rescued by exogenous sucrose application, we speculate on an implication of *qAG9-2-d* in starvation responses that are associated with anaerobic metabolism.

Keywords: anaerobic germination, direct-seeded rice, starch mobilization, coleoptile elongation

Ubiquitous resistance to rice tungro spherical virus is mediated by a gene for translation initiation factor 4G

Genelou A. Atienza,[1] Jong-Hee Lee,[2] Muhammad Muhsin,[1] Jaymee R. Encabo,[1] Suk-Man Kim,[1] Edgardo Coloquio,[1] Norman P. Oliva,[1] Kurniawan Rudi Trijatmiko,[1] Editha M. Abrigo,[1] Rogelio C. Cabunagan,[1] Pepito Q. Cabauatan,[1] Daisuke Fujita,[1] Inez H. Slamet-Loedin,[1] Hei Leung,[1] and Il-Ryong Choi[1*]
[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]National Institute of Crop Sciences, Rural Development Administration, Milyang, Korea
*Correspondence: i.choi@irri.org

Tungro virus disease is one of the most serious diseases of rice in Southeast and South Asia. Tungro disease is caused by rice tungro bacilliform virus (RTBV) and rice tungro spherical virus (RTSV). Cultivar Utri Merah was found to be resistant to both RTBV and RTSV. To identify gene(s) linked to RTSV resistance in Utri Merah, genetic and molecular analyses for RTSV resistance were conducted. Inheritance patterns of resistance to RTSV and to RTBV, both originating from Utri Merah, indicated that resistance to RTSV and RTBV is governed by different mechanisms. Genetic analysis of RTSV resistance in Utri Merah revealed that RTSV resistance is controlled by a single recessive locus (tsv1) mapped around 22.1 Mb of chromosome 7. A survey of more than 50 RTSV-resistant rice genotypes for the allele types of a gene for translation initiation factor 4G (*eIF4Gtsv1*) located within tsv1 indicated a strong association of RTSV resistance with single nucleotide polymorphisms in *eIF4Gtsv1*. To verify the involvement of *eIF4Gtsv1* in RTSV resistance, transgenic plants in which the expression of *eIF4Gtsv1*was suppressed were produced and evaluated for reaction to RTSV. Examination of T1 and T2 plants showed that suppression of *eIF4Gtsv1* correlated well with resistance to RTSV, confirming the association of RTSV resistance with *eIF4Gtsv1*. Collectively, these results demonstrate that RTSV resistance, which is widely distributed among rice genotypes, is mediated by *eIF4Gtsv1*.

Keywords: virus resistance, rice tungro spherical virus, eukaryotic translation initiation factor 4-gamma, artificial microRNA

Impact of rice price hike on poverty in Bangladesh

Taznoore Samina Khanam* and Humnath Bhandari
International Rice Research Institute, Dhaka, Bangladesh
*Correspondence: t.khanam@irri.org

Rice, the staple food of Bangladesh, is both an economic and a political commodity. It contributes to 62% of total calories, 30% of total protein intake, and 15% of total income of a household. A typical Bangladeshi household consumes 2.5 kg of rice everyday and spends about one-third of total income on rice. The poorest households spend as high as 50% of their total income on rice. This indicates that an increase in rice price is equivalent to a decrease in real income of the household. Rice price increase, thus, has a direct impact on the food security and poverty of millions of households in Bangladesh. The retail nominal price of medium-coarse rice declined from US$380 per ton in 1980 to US$310 per ton in 2000. The green revolution-led high rice productivity lowered the price of rice and thereby increased food security and decreased poverty. The luxury of low rice prices ended by the late 1990s. Rice price started to rise from the early 2000s, reaching its peak at US$525 in 2008. The price has been highly volatile from 2008 to 2012. In this paper, we analyze the short- and long-term factors that have contributed to the rapid rise in rice prices in Bangladesh. We also examine the impact of rice price upsurge on poverty and household income and consumption-smoothing strategies during a food crisis arising from the price hike. Finally, we discuss technological and policy solutions to keep rice prices low, tackle the upcoming price spike, and make rice affordable to millions of the poor in Bangladesh.

Keywords: rice price, factors, poverty, food security, Bangladesh

Methane emission and rice yield as affected by elevated temperature, rice straw incorporation, and soil properties in lowland rice paddy soils

Yam Kanta Gaihre,[1,2,3*] Reiner Wassmann[1], Gina Villegas-Pangga,[2] and Eugenio Aquino[1]
[1]Crop and Environmetnal Sciences Division, International Rice Research Institute, Los Baños, Laguna, Philippines
[2]Farming Systems and Soil Resources Institute, Agricultural Systems Cluster, University of Philippines Los Baños, Los Baños, Laguna, Philippines
[3]Soil Science Division, Nepal Agricultural Research Council, Nepal
Correspondence: y.gaihre@cgiar.org; gaihreyam@gmail.com

Irrigated lowland rice fields are considered major sources of methane (CH_4). The source strength of CH_4 from rice fields may further increase under changing climatic conditions–i.e., increasing global temperature. A pot experiment in a walk-in growth chamber with controlled day and night temperatures was conducted in the International Rice Research Institute, Philippines, to determine the influence of elevated temperature, rice straw, and soil properties on the source strength of CH_4 and rice grain yield. Three levels of temperature (29/22, 32/25, and 35/28 ^{o}C representing daily maxima/minima) and two levels of rice straw (0 and 6 t ha^{-1}) were arranged in complete randomized design with four replications in two different soils (low and high organic carbon) consecutively. Soil redox potential and CH_4 emission were monitored weekly throughout the rice-growing period. Elevated temperatures increased CH_4 emission rates throughout the growth period of rice. The increment in CH_4 emission triggered by the higher temperature was especially prominent after the incorporation of rice straw. A decrease in soil redox potential to < -100 mV and CH_4 emission was observed earlier in pots with rice straw as compared with that in pots without rice straw. Moreover, the decrease in soil redox potential and CH_4 emission was earlier and the magnitude of emission was higher in soil with high organic carbon. On the other hand, the high temperature significantly increased spikelet sterility and reduced grain yield ($p<0.05$) of rice. Increasing global temperatures with rice straw incorporation could increase CH_4 emission and reduce rice grain yield.

Keywords: elevated temperature, rice straw, lowland rice, organic carbon, methane emission

Transformation of rice with C4 genes and characterization of transgenic plants

Kamal Swati,[1] Shanta Karki,[1] Sarah Covshoff,[2] Helen Woodfield,[2] Juvy Reyes,[1] Florencia A. Montecillo,[1] Robert Coe,[1] Czarina Mae Realubit,[1] Gemma Lorenzana,[1] Menard Dela Rosa,[1] Michelle Grace Acoba,[1] Albert Chris de Luna,[1] Florence Danila,[1] Inez Slamet- Loedin,[1] Julian Hibberd,[2] and Paul Quick[1]
[1]C4 Rice Center, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Department of Plant Sciences, The University of Cambridge, UK

Everyday, almost one billion people suffer from chronic hunger and the situation is expected to deteriorate with a projected population growth to 9 billion worldwide by 2050. To provide adequate nutrition to this booming population, rice yields need to increase by 60%. This drastic improvement may be achieved by converting the existing photosynthetic pathway of rice (C3) to the more efficient C4-type. This would increase rice yields while using resources (sunlight, water, and fertilizer, specifically nitrogen) more effectively. In an attempt to introduce C4 photosynthetic pathway into rice, C4-specific genes encoding enzymes, transporters, and regulators need to be introduced. Due to the limitations of conventional techniques, the transgenic approach seems to be the only available solution. In the initial stage, we have introduced the genes encoding C4 enzymes individually into IR64, an indica mega variety of rice by *Agrobacterium*-mediated transformation. Through different screening methods, we found that these genes are stably integrated in the desired number of copies and also show appropriate levels of expression. Transgenic rice plants in which we have successfully expressed C4 phosphoenolpyruvate carboxylase (*PEPC*), pyruvate, orthophosphate dikinase (*PPDK*), and NADP-malate dehydrogenase (*MDH*) genes from *Zea mays* are currently being further analyzed for appropriate traits. The selected transgenic plants with individual genes are being crossed in order to start the stacking of C4 transgenes to develop a prototype of a rice plant that will be optimized to achieve a fully functional C4 pathway.

Keywords: C4 genes, genetic transformation, rice, yield potential

Introduction of transport proteins into *Oryza sativa* L. to facilitate installation of the C4 pathway

Ronald Tapia,[1] Shanta Karki,[1] Sarah Covshoff,[2] Florencia A. Montecillo,[1] Robert Coe,[1] Juvy Reyes,[1] Czarina Mae Realubit,[1] Gemma Lorenzana,[1] Menard Dela Rosa,[1] Michelle Grace Acoba,[1] Albert Chris de Luna,[1] Inez Slamet-Loedin,[1] Julian Hibberd,[2] and Paul Quick[1]
[1]C4 Rice Center, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Department of Plant Sciences, The University of Cambridge, UK

Because of the C4 crop plants' (maize and sorghum) increased photosynthetic efficiency, they yield much more than C3 crops (rice and wheat). The photosynthetic activities in C4 plants are partitioned between two morphologically and physiologically distinct cell types, the mesophyll (M) and the bundle sheath (BS). Distinct sets of transcripts and proteins accumulate in each cell type and enable the cooperative fixation of carbon. The C4 pathway has greater efficiency of carbon assimilation than C3 because it maintains higher CO_2 concentration in chlorophyll-containing BSC where carboxylation by Rubisco takes place. This prevents the oxygenase action of Rubisco. Introducing an efficient carbon assimilation mechanism into the C4 pathway is expected to increase rice yield by 50% of its maximum current yield. In earlier efforts of C4 rice engineering, the core C4 photosynthetic enzymes had been inserted into rice and had been evaluated for transcript and protein abundance, but expressions of the transporters necessary for organelle metabolite exchange have not been modified. To introduce an efficient C4 photosynthetic pathway into rice, these enzymes and other intermediates have to be facilitated by specific C4 transporters from one cell to another. Therefore, genes that code for C4 transporters such as *OMT1* (2-oxoglutarate/malate transporter), *DiT1* (dicarboxylate transporter 1), *DiT2* (dicarboxylate transporter 2), and *PPT* (phosphoenolpyruvate phosphate translocator) have been cloned from *Zea mays* and introduced into rice. These transgenic plants are being evaluated at the molecular level. Transcript abundance is being analyzed by RNA blot and semi-quantitative PCR. The plants with stable C4 transport protein expression will be intercrossed with the plants expressing the core C4 genes and will be analyzed further at the biochemical and physiological levels.

Keywords: carbon assimilation, photosynthesis, C4 transporters, Rubisco

Govinda Rizal
Postdoctoral fellow
IRRI

Shanta Karki
Postdoctoral fellow
IRRI

Changrong Ye
Postdoctoral fellow
IRRI

Teodora Cabasan
Affiliate PhD scholar, IRRI
PhD student, KU Leuven,
Belgium

Jedeliza Ferrater
PhD scholar, IRRI
PhD student, Wageningen
University, Netherlands

Rico Gamuyao
Postdoctoral fellow
IRRI


IRRI YOUNG SCIENTISTS CONFERENCE
2012