

CURRICULUM VITAE

Benildo G. de los Reyes, Ph.D.

Professor of Genetics and Bayer CropScience Chair in Plant Genomics
Department of Plant and Soil Science, Texas Tech University
215 Experimental Sciences Building; Box 42122, Lubbock, TX USA 79409-2122
(Ph) 806-834-5073, (Fx) 806-742-0775, benildo.reyes@ttu.edu
ORCID-0000-0002-5557-7398

EDUCATION AND TRAINING:

Post-doctorate (Plant Genomics), 1999 to 2001, Michigan State University, East Lansing, Michigan, USA

Ph.D. (Plant Science, Cell and Molecular Biology), 1999, Oklahoma State University, Stillwater, Oklahoma, USA

M.S. (Genetics and Biochemistry), 1993, University of the Philippines and International Rice Research Institute, Los Banos, Philippines

B.S. (Biology/Genetics), 1986, University of the Philippines, Los Banos, Philippines

PROFESSIONAL APPOINTMENTS:

Professor and Bayer CropScience Endowed Chair, 2016 to present, Department of Plant and Soil Science, Texas Tech University, Lubbock, TX

Associate Department Chair for Research and Graduate Programs, 2017 to present, Department of Plant and Soil Science, Texas Tech University, Lubbock, TX

Director of Graduate Programs, 2017 to 2020, Department of Plant and Soil Science, Texas Tech University, Lubbock, TX

Associate Director, 2014-2015, School of Biology and Ecology, University of Maine, Orono, ME

Graduate Programs Director for Botany and Plant Pathology, Biological Sciences, and Interdepartmental Plant Science Programs, 2009-2010, 2014-2015, School of Biology and Ecology, University of Maine, Orono, ME

Professor (2012 – 2015), Associate Professor (2008 – 2012), and Assistant Professor (2004 – 2007) of Molecular Genetics, School of Biology and Ecology; Adjunct Professor of Molecular Genetics, Department of Biochemistry and Molecular Biology, University of Maine, Orono, ME

Assistant Professor of Plant Molecular Genetics and Genomics, 2001 to 2003, Department of Crop, Soil and Environmental Sciences, University of Arkansas, Fayetteville, AR

Postdoctoral Research Associate in Molecular Genetics and Genomics, 1999 to 2001, Department of Crop and Soil Sciences, Michigan State University, East Lansing, MI

Graduate Research Associate in Plant Molecular Biology, Department of Plant and Soil Sciences, 1995 to 1999, Oklahoma State University, Stillwater, OK

Graduate Research Assistant in Plant Genetics, 1994, Department of Horticulture, Pennsylvania State University, State College, PA

Research Assistant in the Rice Genome Program, 1986 to 1993, Plant Breeding, Genetics and Biochemistry Division, International Rice Research Institute, Los Banos, Philippines

RESEARCH TOPICS, TEACHING, AND GRADUATE MENTORING:

Research keywords: Molecular Genetics, Genomics, Epigenetics, Systems Biology, Gene Regulation, Chromatin-Level Regulation, DNA Methylation, Genetic Networks, Plant Growth and Adaptation, Stress Physiology, Crop Breeding and Evolution, Rice Biology; **Teaching:** PSS3421 (Fundamental Principles of Genetics; *Undergraduate*); PSS5301 (Advanced Genetics; *Graduate*), PSS6325 (Epigenetic Mechanisms; *Graduate*), PSS6001 (Plant Responses to the Environment; *Graduate*); **Mentoring:** Graduated eighteen (18) Master's students, fifteen (15) PhD students, and eight (8) Postdoctoral scientists from across 20 countries since 2004.

HIGHLIGHTS OF LEADERSHIP ACCOMPLISHMENTS:

Texas Tech University: Since joining the faculty of Plant and Soil Science as Professor of Genetics and Bayer CropScience Endowed Chair in Plant Genomics in 2016, I have acted in various high profile leadership roles at both departmental and college levels. In my capacity as Associate Department Chair, I have established a strong reputation in the college through my successes in a number of major initiatives that created positive transformations and strengthened the position of the department as a leader in externally funded research and graduate education across the College of Agricultural Sciences and Natural Resources and wider Texas Tech campus. Some of the most notable examples of my recent successes and accomplishments are as follows:

1) I joined Texas Tech around the time (2016) when the university was acquiring a status among the highest level of research activities across the country. Along with the newly acquired tier-1 status was the pressure from upper administration to boost even further our research activities through federally funded faculty and graduate student research, enhancement of research capacity, and establishment of the critical mass of expertise in certain disciplines that are considered to be emerging areas of excellence across campus. The university also seeks to enhance its global reputation through excellence in basic research particularly in some of its flagship research programs. The recently named Davis College of Agricultural Sciences and Natural Resources is considered among the flagship colleges of Texas Tech, and plant sciences are among the rapidly emerging areas of excellence in research and graduate studies. With my strong appreciation of the unique ecology of West Texas and its large footprint in semi-arid agriculture (specifically applied research), I played a key leadership role in envisioning and creating a new initiative that acquired the seed funding of \$5-million from the highly competitive Governor's University Research Initiative (GURI) of the State of Texas. As Principal Investigator of this effort, I develop the overall scientific vision that distinguished Texas Tech and West Texas from the programs at TAMU and UT-Austin, and I wrote the proposal for such initiative. Our success at GURI jump-started the enhancement of research infrastructure and critical mass of faculty expertise

(basic and translational scientists) in plant genomics and biotechnology. The seed money from GURI subsequently expanded with additional matching funds from various intramural sources, which allowed us to successfully address the overarching goals of the GURI program through: a) Strategic hiring of a plant biologist to the Plant and Soil Science faculty who is a member of the National Academy of Sciences (NAS) USA; b) Establishment of a new research institute led by the strategically hired NAS faculty focused on the applications of genomics-centered research paradigm to semi-arid agriculture (IGCAST = Institute for Genomics of Crop Abiotic Stress Tolerance); c) Cluster hiring of three pre-tenure and one tenured new faculty for IGCAST; d) Establishment of a state-of-the-art phytotron and controlled environment plant growth research facility to support the research efforts of the new IGCAST and other faculty in plant sciences; and e) Successful placement and integration of IGCAST faculty into the undergraduate and graduate teaching and graduate mentoring structure of the Department of Plant and Soil Science. The last item was a major accomplishment given that Plant and Soil Science programs have been traditionally focused on applied sciences. The GURI-hired faculty were mostly basic and translational scientists.

2) I led the revitalization, modernization, and internationalization of the Plant and Soil Science graduate programs through major curricular adjustments, streamlining and expansion of course offering, programmatic enhancements, creation of formal disciplinary clusters across the diverse composition of the department (*i.e.*, plant breeding, genetics and biotechnology, agronomy and crop physiology, crop protection, soil science, horticulture, plant conservation, and fiber and biopolymer), enhancement of faculty and graduate student research networking across disciplinary clusters, and promotion of intellectual vibrancy across the department through seminars and colloquia. Establishment of a reenergized seminars and colloquia brought high-profile agricultural scientists and plant biologists like World Food Prize Laureates and NAS fellows to inspire and network with our graduate students. These transformational changes helped position the Department of Plant and Soil Science as the leader in grant-funded research and doctoral programs across the Davis College.

3) I have been the biggest advocate and leader of formal mentoring programs for pre-tenure faculty in the Department of Plant and Soil Science. Since joining the department, I have led efforts to formalize these programs, which have now expanded to also include formal mentoring for junior faculty members who are on non-tenure track appointments. Since joining the department, I have successfully mentored six junior faculty from the clusters of Plant Breeding, Genetics and Biotechnology (three), Horticulture (two), and Soil Science (one) through their successful mid-tenure and tenure evaluation processes.

4) I have played important roles in promoting diversity and inclusivity in the Plant and Soil Science faculty through my leadership efforts in recruiting and mentoring new faculty from diverse academic, racial, and ethnic backgrounds from within and outside the U.S.

5) I have successfully led the strategic recruitment and hiring of an Endowed Chair in Soil Science/Pedology (B.L. Allen Endowed Chair), despite the fact that the sub-discipline of Pedology is comprised of only a handful of active scientists across the country.

6) The College of Agricultural Sciences and Natural Resources has recently been named the 'Davis College' after a transformational gift of \$44-million from a family of alumni. With this naming comes a renewed vision of enhancing the global reputation of the college through excellence in teaching and research. I have served an important role to represent the perspective of a basic plant scientists in the strategic hiring of a transformational leader as the new Dean of the Davis College of Agricultural Sciences and Natural Resources.

7) I have successfully led the Department of Plant and Soil Science through its ten-year external graduate program reviews. In this review, our graduate programs received excellent feedbacks for strong links to the strategic plan of the university as well as with the future research direction of a rapidly expanding department with research strengths in both applied and now fundamental plant and soil sciences. A major highlight of this successful external program review was the recognition by the panel of the high level of success of Plant and Soil Science PhD students in peer-reviewed publishing, a component of our graduate program requirements that was implemented when I became Associate Chair of the department for research and graduate programs. The Department of Plant and Soil Science stands-out in research productivity and success across the Davis College because of the effects of these positive changes in our programs.

An offshoot of the success of the ten-year external program review is the concerted efforts across the department, which I also led, to review the structure of the graduate programs in terms of: a) Disciplinary concentrations or tracks that align with the disciplinary clusters across the department and the newly established IGCAS; b) Streamlining of graduate course offering across the disciplinary clusters to reduce duplications and major overlaps, to ensure that our program is at par with the programs of the leading universities across the country; c) Addressing major gaps in graduate curricular offering and balancing faculty efforts for research and scholarship with graduate and undergraduate teaching; and d) Adjusting the required course works in the PhD program to ensure that the foundational knowledge required in each concentration/track are being achieved and that graduate students (especially PhD) are getting the appropriate credits for their research and publication efforts.

8) I have been directly involved in the management of college and university funding for graduate student fellowship and scholarship, when I was both the Associate Department Chair for Research and Graduate Programs and Director of Graduate Programs.

9) I was part of the Texas Tech delegation comprised of six faculty and two administrators that established formal cooperation in plant science and agricultural research as well as pedagogy in humanities and languages with several universities and research institutes in China, led by the Vice President for Research and Innovation.

University of Maine: I have led the graduate programs in plant sciences (Inter-departmental Doctoral Program in Plant Sciences and Master's Program in Botany and Plant Pathology) for a number of years until I left the university to join Texas Tech. I have also served as Associate Director of the School of Biology and Ecology, where I successfully led the revitalization of Plant Sciences Program through new faculty hiring.

I have also played an important role in the establishment of formal procedures for the assessment of learning outcomes across the different graduate programs of the school. During my term at UMaine, I have also completed a crash course on '*Leadership in Science and Academia*' at Cornell University sponsored by UMaine's Office of the Dean of the College of Natural Sciences, Forestry, and Agriculture.

INTERNATIONAL ACTIVITIES:

International Research Partnership – International Rice Research Institute, Los Banos, Philippines; National Institute of Genetics, Mishima, Japan; Meiji University, Chiyoda, Japan; National University of Singapore, Singapore; Chonbuk National University, Jeonju, South Korea; International Center for Biosaline Agriculture, Dubai, United Arab Emirates; Ateneo de Manila University, Quezon City, Philippines; Punjab Agricultural University, Ludhiana, India; International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, India; National Agriculture and Food Research Organization, Tsukuba, Japan

D.S. Brar Memorial Lecture in Plant Epigenetics – '*Genetic and Epigenetic Novelty for Adaptive Traits in Rice*', through the invitation of the G.S. Khush Foundation, 2022, Punjab Agricultural University, Ludhiana, India

Distinguished Lecture in Plant Genetics and Epigenetics, Indian Council for Agricultural Research (NAHEP-CAAST), 2020, Punjab Agricultural University, Ludhiana, India

Distinguished Panelist on New Frontiers and Impacts of Genomic Innovations in the 21st Century: Is genomics a sign of the apocalypse or the answer? Global Forum on Innovations for Marginal Environment (GFIME), 2019, Dubai, United Arab Emirates

Mentor's Distinguished Lecture in Rice Genetics, Monsanto's Beachell-Borlaug International Scholars Program, 2016, Punjab Agricultural University, Ludhiana, India

Visiting International Research Scientist, 2011, National Institute of Genetics of Japan, NIG-JOINT International Collaborative Research Award; Epigenetic mechanisms and stress tolerance phenotypes in *Oryza*, Mishima, Shizuoka, Japan

Visiting Scientist on Academic Sabbatical, 2011, 2012, Wild *Oryza* as a tractable evolutionary system for comparative functional genomics and network biology; International Rice Research Institute, Los Banos, Philippines

Balik Scientist for Plant Genetics and Genomics, Official Guest Expert of the Government of the Republic of the Philippines, Department of Science and Technology, to advance the state of Philippine Science and Technology for Crop Breeding; Hosted by the Department of Biology, Ateneo de Manila University, Philippines

Distinguished Lecture in Rice Genetics and Breeding, 2009, *Celebration of Rice and Human History and Civilization Month*, Chonbuk National University, Jeonju, Korea

Visiting Research Fellow in Rice Genomics, 1993, Japan Rice Genome Program, Society for Techno-Innovation on Agriculture, Forestry and Fisheries, Tsukuba, Japan

Visiting Scholar in Cereal Genomics, 1989, Cambridge Laboratory, John Innes Centre, Norwich, United Kingdom

PROFESSIONAL AND HONOR SOCIETIES:

American Society of Plant Biologists (ASPB), 2006 to present
American Association for the Advancement of Science (AAAS), 2002 to present
Gamma Sigma Delta Honor Society, 1999 to present
Crop Science Society of America (CSSA), 1998 to present
University of the Philippines Genetics Society, Charter Member, 1983 present

AWARDS AND RECOGNITIONS:

Faculty Medal of Excellence in Research, 2021, Office of Vice President for Research and Innovation, Texas Tech University, Lubbock, TX, USA
International Collaborative Research Award, 2011, National Institute of Genetics of Japan, Mishima, Shizuoka, Japan
Balik Scientist Award, 2008, Department of Science and Technology, Republic of the Philippines
University Research Excellence Award in Biological Sciences, 1999, Oklahoma State University, Stillwater, OK, USA
Gerard O. Mott Outstanding Graduate Student, 1998, Crop Science Society of America, Madison, Wisconsin, USA
Outstanding Researcher in Plant Genetics, 1994, The International Rice Research Institute, Los Banos, Philippines

REPRESENTATIVE RESEARCH PUBLICATIONS: (JIF = Five-year Journal Impact Factor)

Note: Papers published starting from 2016 are all parts of the overall productivity in research at Texas Tech

Kitazumi A, Pabuayon ICM, Cushman KR, Yano K, de los Reyes BG (2022) Plant Transcriptomics: Data-driven Global Approach to Understand Cellular Processes and their Regulation in Model and Non-model Plants. ***In Plant OMICS: Advances in Big Data Biology***, Ohyanagi H, Yamamoto E, Kitazumi A, and Yano K (Eds.), CAB International, Wallingford, UK, DOI: 10.1079/9781789247534.0002.

Asari M, Kitazumi A, Nambara E, de los Reyes BG, Yano K (2022) Plant Gene Expression Network (2022) ***In Plant OMICS: Advances in Big Data Biology***, Ohyanagi H, Yamamoto E, Kitazumi A, and Yano K (Eds.), CAB International, Wallingford, UK, DOI: 10.1079/9781789247534.0010.

Mandal SN, Sanchez J, Bhowmick R, Bello OR, Van-Beek CR, de los Reyes BG (2022) BTB/POZ proteins and their gene family in *Oryza rufipogon*: Novel genes and alleles from the progenitor of the domesticated japonica rice (*O. sativa* L.). ***Scientific Reports, In Review, Research Square***, DOI: <https://doi.org/10.21203/rs.3.rs-1918471/v1>. [JIF = 4.996]

Kumar K, Mandal SN, Neelam K, de los Reyes BG (2022) MicroRNA-mediated host defense mechanisms against pathogens and herbivores in rice: Balancing gains from genetic resistance with trade-offs to crop productivity potential. ***BMC Plant Biology*** 22:e35, <https://doi.org/1.1186/s12870-022-03723-5>. [JIF = 5.26]

Pabuayon ICM, Pabuayon ILB, Singh RK, Ritchie GL, de los Reyes BG (2022) Applicability of hyperspectral imaging during salinity stress in rice for tracking Na⁺ and K⁺ levels in planta. **PLoS ONE** 17(7): e0270931, <https://doi.org/10.1371/journal.pone.0270931>. [JIF = 3.752]

Sanchez J, Pal Kaur P, Pabuayon ICM, Karampudi NBR, Kitazumi A, Sandhu N, Catolos M, Kumar A, De los Reyes BG (2021) *DECUSSATE* network with flowering genes explains the variable effects of *qDTY12.1* to rice yield under drought across genetic backgrounds. **The Plant Genome** 2021:e20168, <https://doi.org/10.1002/tpg2.20168>. [JIF = 5.826]

Shu X, Singh M, Karampudi NBR, Bridges D, Kitazumi A, Wu VCH, De los Reyes BG (2021) Responses of *Escherichia coli* and *Listeria monocytogenes* to ozone on non-host tomato: Efficacy of intervention and evidence of induced acclimation. **PLoS ONE** 16(10):e0256324, <https://doi.org/10.1371/journal.pone.0256324>. [JIF = 3.752]

Shu X, Singh M, Karampudi NBRK, Bridges D, Kitazumi A, Wu VCH, De los Reyes BG (2021) Responses of *Escherichia coli* and *Listeria monocytogenes* to ozone treatment on non-host tomato: Efficacy of intervention and evidence of induced acclimation. **Cold Spring Harbor Laboratory Press bioRxiv** doi: <https://doi.org/10.1101/2021.08.13.456288>.

De los Reyes BG, Sanchez J, Pal Kaur P, Pabuayon ICM, Karampudi NBR, Kitazumi A, Sandhu N, Catolos M, Kumar A (2021) Yield maintenance under drought is orchestrated by the *qDTY12.1*-encoded *DECUSSATE* gene of rice through a network with other flowering-associated genes across the genetic background. **Cold Spring Harbor Laboratory Press bioRxiv** doi: <https://doi.org/10.1101/2021.02.09.430414>.

Pabuayon ICM, Kitazumi A, Cushman KR, Singh RK, Gregorio GB, Dhatt BK, Zabet-Moghaddam M, Walia H, De Los Reyes BG (2021) Novel and transgressive salinity tolerance in recombinant inbred lines of rice created by physiological coupling-uncoupling and network rewiring effects. **Frontiers in Plant Science (Section Systematics and Evolution)** 12:615277, doi:10.3389/fpls.2021.61527; *Special Issue on Cereal Genome Evolution*. [JIF = 6.627]

Cushman KR, Pabuayon ICM, Hinze LL, Sweeney ME, De Los Reyes BG (2020) Networks of physiological adjustments and defenses, and their synergy with sodium (Na⁺) homeostasis explain the hidden variation for salinity tolerance across the cultivated *Gossypium hirsutum* germplasm. **Frontiers in Plant Science (Section Plant Physiology)** 11:588854, doi:10.3389/fpls.2020.588854. [JIF = 6.627]

Pabuayon ICM, Kitazumi A, Gregorio GB, Singh RK, De Los Reyes BG (2020) Contributions of adaptive plant architecture to transgressive salinity tolerance in recombinant inbred lines of rice: Molecular mechanisms based on transcriptional networks. **Frontiers in Genetics (Section Systems Biology)** 11:594569, doi:10.3389/fgene.2020.594569. [JIF = 4.772]

Shu X, Singh M, Karampudi NBR, Kitazumi A, Bridges D, Wu VCH, De los Reyes BG (2020) Xenobiotic effects of chlorine dioxide to *Escherichia coli* O157:H7 on non-host tomato environment revealed by transcriptional network modeling: Implications to adaptation and selection. **Frontiers in Microbiology (Section Food Microbiology)** 11:1122, doi:10.3389/fmicb.2020.01122. [JIF = 5.640]

Kaur A, Neelam K, Kaur K, Kitazumi A, De los Reyes BG, Singh K (2020) Novel allelic variation in the Phospholipase-D-alpha1 gene (*OsPLD α 1*) of wild *Oryza* species implies to its low expression in rice bran. **Scientific Reports – Nature** **10:6571**, doi.org/10.1038/s41598-020-62649-w. [JIF = 4.996]

Pabuayon ICM, Kitazumi A, Cushman KR, Singh RK, Gregorio GB, Dhatt BK, Zabet-Moghaddam M, Walia H, De Los Reyes BG (2020) Transgressive segregation for salt tolerance in rice due to physiological coupling and uncoupling and genetic network rewiring. **Cold Spring Harbor Laboratory Press bioRxiv** 2020.06.25.171603, <https://doi.org/10.1101/2020.06.25.171603>. [Open-access Repository; Reviewed]

Cushman KR, Pabuayon ICM, Hinze LL, Sweeney ME, De los Reyes BG (2019) Physiological networks governing salinity tolerance potentials in *Gossypium hirsutum* germplasm. **Cold Spring Harbor Laboratory Press bioRxiv** 2019.12.16.877787, <https://doi.org/10.1101/2019.12.16.877787>. [Open-access Repository; Reviewed]

De los Reyes BG (2019) Genomic and epigenomic bases of transgressive segregation – New breeding paradigm for novel plant phenotypes. **Plant Science** **288:110213**, doi.org/10.1016/j.plantsci.2019.110213. [COMMISSIONED] [JIF = 5.363]

Kaur A, Neelam K, Kitazumi A, Kaur K, Sharma P, Mangat GS, De los Reyes BG, Brar DS, Singh K (2019) Novel cis-acting regulatory elements in wild *Oryza* species impart improved rice bran quality by lowering the expression of phospholipase-D-alpha1 enzyme (*OsPLD α 1*). **Molecular Biology Reports**, [doi:10.1007/s11033-019-05144-4](https://doi.org/10.1007/s11033-019-05144-4). [JIF = 2.316]

Shim JH, Gannaban RB, De los Reyes BG, Angeles-Shim RB (2019) Identification of novel sources of genetic variation for the improvement of cold germination ability in upland cotton (*Gossypium hirsutum*). **Euphytica** **215:190**, doi.org/10.1007/s10681-019-2510-6. [JIF = 2.13]

Quintela IA, de los Reyes BG, Lin CS, Wu VCH (2019) Simultaneous colorimetric detection of a variety of *Salmonella* spp. in food and environmental samples by optical biosensing using oligonucleotide-gold nanoparticles. **Frontiers in Microbiology (Section Food Microbiology)**, **10:1138**, [doi10.3389/fmicb.2019.01138](https://doi.org/10.3389/fmicb.2019.01138). [JIF = 5.640]

Kitazumi A, Pabuayon ICM, Ohyanagi H, Fujita M, Osti B, Shenton M, Kakei Y, Nakamura Y, Brar DS, Kurata N, De los Reyes BG (2018) Potential of *Oryza officinalis* to augment the cold tolerance genetic mechanisms of *Oryza sativa* by network complementation. **Scientific Reports - Nature** **8:16346**, [doi:10.1038/s41598-018-34608-z](https://doi.org/10.1038/s41598-018-34608-z). [JIF = 4.996]

De los Reyes BG, Kim YS, Mohanty B, Kumar A, Kitazumi A, Pabuayon ICM, Sandhu N, Lee DY (2017) Cold and water deficit regulatory mechanisms in rice – Optimizing stress tolerance potential by pathway integration and network engineering. In '**Rice Genomics, Genetics, and Breeding**', T. Sasaki and M. Ashikari (Eds.), **Springer-Nature Publishing**, [doi:978-981-10-7460-8](https://doi.org/10.1007/978-981-10-7460-8).

Alpuerto JB, Mukherjee A, Kitazumi A, Alyokhin A, De Koeyer D, De los Reyes BG (2017) Impaired expressions of the beta and delta isoforms of vacuolar processing enzymes compromise the basal defenses of *Arabidopsis thaliana* against the phloem-feeding insect *Myzus persicae*. **Acta Physiologia Plantarum** **39:e233**. [JIF = 2.354]

- Panes VA, Kitazumi A, Butler M, Baoas A, De los Reyes BG (2017) Analysis of the oil biosynthesis transcripts of the *Moringa oleifera* Lam. mature seed embryos using RNA sequencing. **Acta Horticulturae 1158: 55-62**, doi:10.17660/ActaHortic.2017.1158.7. [JIF = 0.530]
- Mohanty B, Takahashi H, De los Reyes BG, Wijaya E, Nakazono M, Lee DY (2016) Transcriptional regulatory mechanism of alcohol dehydrogenase 1-deficient mutant of rice for cell survival under complete submergence. **RICE 9:e51**. [JIF = 6.097]
- Mohanty B, Lakshmanan M, Kitazumi A, Cheung C, De los Reyes BG, Jang IC, Lee DY (2016) Validation of critical network hubs involved in drought response mechanisms by integrating transcriptome data and genome-scale metabolic model: Potential applications for drought tolerance breeding in rice. **Plant Science 242:224-239**. [JIF = 5.363]
- Kitazumi A, Kawahara Y, Onda TS, De Koeyer D, De los Reyes BG (2015) Implications of miR166 and miR159 induction to the basal response mechanisms of andigena potato (*Solanum tuberosum* ssp. andigena) to salinity stress predicted from gene network models in Arabidopsis. **Genome 58:13-24**. [HIGHLY ACCESSED] [JIF = 2.351]
- De los Reyes BG, Mohanty B, Yun SJ, Park MR, Lee DY (2015) Upstream regulatory architecture of rice genes: Establishing the baseline for genus-wide comparative analysis of regulatory networks and allele mining. **RICE 8:e14**. [COMMISSIONED] [JIF = 6.097]
- Chen J, Kitazumi A, Alpuerto JB, Alyokhin A, De los Reyes BG (2015) Heat-induced mortality and expression of heat shock proteins in Colorado potato beetles treated with imidacloprid. **Insect Science**, doi:10.1111/1744-7917.12194. [JIF = 1.325]
- Quintela I, Lin CS, De los Reyes BG, Wu VCH (2014) Simultaneous direct detection of various Shiga-toxin producing *E. coli* (STEC) by optical biosensing with oligonucleotide-functionalized gold nanoparticles. **Nanoscale**, doi:10.1039/cn4nr05869k. [JIF = 6.895]
- Xu F, Park MR, Mohanty B, Herath V, Kitazumi A, Yun SJ, De los Reyes BG (2012) Cis-regulatory signatures among orthologous groups of stress-associated bZIP transcription factors from rice, sorghum and Arabidopsis based on phylogenetic footprints. **BMC Genomics 13:e497**. [JIF = 4.478]
- Mohanty B, Yeo HC, Wijaya E, De los Reyes BG, Lee D-Y (2012) Patterns of cis-element enrichment revealed potential regulatory modules involved in the regulation of low-oxygen response transcriptome of rice. **Gene 511:235-242**. [JIF = 3.688]
- De los Reyes BG, Yun SJ, Herath V, Xu F, Park MR, Lee JI, Kim KY (2012) Phenotypic, physiological and molecular evaluation of chilling stress response of rice at the vegetative stage. **In: Methods in Molecular Biology: Rice Protocol Series**, Volume 956, Y. Yang (Ed.), Humana Press-Springer Science, ISBN:978-1-62703-193-6.
- Park MR, Baek S-H, De los Reyes BG, Yun SJ, Hasenstein KH (2012) Transcriptome profiling characterizes phosphate deficiency effects on carbohydrate metabolism in rice leaves. **Journal of Plant Physiology 169:193-205**. [JIF = 3.549]

- Rioux R, Manmathan H, Jia Y, De los Reyes BG, Tavantzis S (2011). Comparative analysis of putative pathogenesis-related gene expression in two *Rhizoctonia solani* pathosystems. **Current Genetics** 57:391-408. [JIF = 3.697]
- Park MR, Yun KY, Herath V, Mohanty B, Xu F, Bajic VB, Yun SJ, De los Reyes BG (2010) Supra-optimal expression of the cold-regulated *OsMyb4* transcription factor in transgenic rice changes the complexity of transcriptional network with major effects on stress tolerance and panicle development. **Plant Cell and Environment** 33:2209-2230. [JIF = 7.947]
- Yun KY, Park MR, Mohanty B, Herath V, Xu F, Mauleon R, Wijaya E, Bajic VB, Bruskiwich R, De los Reyes BG (2010) Transcriptional regulatory network triggered by oxidative signals configures the early response mechanisms of japonica rice to chilling stress. **BMC Plant Biology** 10:e16. [HIGHLY ACCESSED] [JIF = 4.215]
- Zhang Y, Xuan J, De los Reyes BG, Clarke R, Ressom HW (2010) Reconstruction of gene regulatory modules in cancer cell cycle by multi-source data integration. **PLoSOne** 5:4-e10268. [JIF = 3.752]
- Ressom HW, Lakshman D, Yun SJ, Pramanik SK, De los Reyes BG (2009) Microarray data analysis using machine learning methods. In: **Biosystems Engineering, A. Nag (editor), McGraw Hill Pub., pp. 1-32.**
- Zhang Y, Xuan J, De los Reyes BG, Clarke R, Ressom HW (2009) Reverse engineering module networks by PSO-RNN hybrid modeling. **BMC Genomics** 10:S15e. [JIF = 4.561]
- Antoine W, de los Reyes BG, Miernyk JA, Stewart JM (2009) Molecular evolution of the plant SLT protein family. **Icfai University Journal of Genetics and Evolution** 2:56-73.
- Wu VCH, Qiu X, De los Reyes BG, Lin CS, Pan Y (2009) Application of cranberry concentrate (*V. macrocarpon*) to control *Escherichia coli* O157:H7 in ground beef and its anti-microbial mechanism related to the downregulated *slp*, *hdeA* and *cfa*. **Food Microbiology** 26:32-38. [JIF = 3.451]
- Zhang Y, Xuan J, De los Reyes BG, Clarke R, Ressom HW (2008) Identification of network motifs for transcription factors by integrating multi-source biological data. **BMC Bioinformatics** 9:e203. [HIGHLY ACCESSED] [JIF = 3.242]
- De los Reyes BG, Lakshman D, Yun SJ, Ressom H (2008) Agricultural genomics. In: **Agricultural Biotechnology, A. Nag (editor), PHI Learning Private Ltd., pp. 55-88.**
- McGrath JM, Elawady A, El-Khishin D, Naegele RP, Carr KM, De los Reyes BG (2008) Sugar beet germination: Phenotypic selection and molecular profiling to identify genes involved in abiotic stress response. **Acta Horticulturae** 782: 35-48. [JIF = 0.523]
- Irish BM, Corell JM, Feng C, Bentley T, De los Reyes BG (2007) Characterization of a resistance locus (*Pfs-1*) to the spinach downy mildew pathogen (*Peronospora farinosa* f. sp. *spinaciae*) and development and evaluation of a co-dominant molecular marker linked to *Pfs1*. **Phytopathology** 98:894-900. [JIF = 3.234]
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peroxide in seedlings of chilling-tolerant japonica rice. **BMC Genomics 8:e175. [JIF = 4.561]**

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Glaszmann JC, De los Reyes BG, Khush GS (1988) Electrophoretic variation of isozymes in plumules of rice (*O. sativa* L.) – A key to the identification of 76 alleles at 24 loci. ***International Rice Research Paper Series, No.134***.

PRESENTATIONS AND INVITED LECTURES:

Invited Conference Workshop Lecture: *Genomic and epigenomic bases of transgressive segregation.* Abiotic Stress Workshop, Plant and Animal Genome XXX Conference, January 13 – 18, 2023, San Diego, CA

Symposium Lecture: *Adaptive phenotypic novelties in plants: Does the epigenome matter?* 1st Research Symposium of the Institute of Genomics for Abiotic Stress Tolerance (IGCAST), Texas Tech University, December 7, 2022, Lubbock, TX

Conference Lecture: *Genetic and epigenetic novelties for adaptive traits in rice.* 19th International Symposium on Rice Functional Genomics (ISRFG), Driving the Next Green Revolution, November 4 – 7, 2022, Phuket, Thailand

Invited Seminar: *Transgressive segregation in rice – A non-reductionist approach for re-exploiting an old science for novel adaptive traits.* Plant Biology Graduate Group (PBGG) Seminar Series, University of California-Davis, December 3, 2021, Davis, CA

Invited Conference Lecture: *Genomic and epigenomic bases of transgressive segregation – Using an old science to create novel adaptive phenotypes in rice.* Abiotic Stress Workshop, Plant and Animal Genome XXVIII Conference, January 11 – 15, 2020, San Diego, CA

Invited Lecture: *New paradigms for an old science – Exploring the epigenome to breed the new generation of ecologically resilient crops; Climate-Smart Agriculture for Food Security, Global Forum on Innovations for Marginal Environments (GFIME),* International Center for Biosaline Agriculture and Ministry of Food Security of the United Arab Emirates and Islamic Development Bank, November 20 – 21, 2019, Dubai, United Arab Emirates

Invited Lecture: *Genomic and epigenomic bases of transgressive segregation in rice: New breeding paradigm for novel adaptive phenotypes. Invited Lecture on Epigenetic Mechanisms, 17th International Symposium on Rice Functional Genomics,* November 4 – 6, 2019, Academia Sinica, Taipei, Taiwan

Special Seminar: *Genomic and epigenomic bases of transgressive segregation: Using an old science to create novel adaptive phenotypes. USDA-ARS AgSciences Seminar Series,* October 18, 2019, USDA-ARS Cropping Systems Research Laboratory, Lubbock, TX

Lecture: *Genetic mechanisms associated with xenobiotic potency, bacterial defenses, and acclimation: What do they tell us about how we should fine-tune chemical intervention approaches? USDA-NIFA-AFRI-CAP Annual Symposium on Enhancing*

Food Safety through Improved Processing Technologies, July 20, 2019, Kentucky International Convention Center, Louisville, KY

Keynote Lecture: *Genomic shock, transgressive segregation and salinity tolerance in rice: Genetics or epigenetics? Keynote address at the International Conference of the Korean Society for Breeding Science and Society for the Advancement of Breeding Research in Asia and Oceania*, July 10, 2019, Gwangju, Korea

Invited Lecture: *Mechanistic basis of transgressive segregation: Genetics or epigenetics? Lecture Series on Adaptation to Marginal Environments Using Novel Biotechnological Approaches*, August 14, 2019, International Center for Biosaline Agriculture, Dubai, United Arab Emirates

Invited Lecture: *DNA methylation, network rewiring, and transgressive salinity tolerance in rice. 16th International Symposium on Rice Functional Genomics*, Tokyo University, September 2018, Tokyo, Japan,
<http://nodaiweb.university.jp/isrfg2018/eng/index.html>

Invited Lecture: *Network rewiring in transgressive segregants for stress tolerance in rice: Epistasis, complementation, regulatory RNA, and DNA methylation. Abiotic Stress Workshop, W005 - Plant and Animal Genome XXV*, January 2018, San Diego, CA,
<https://pag.confex.com/pag/xxvi/meetingapp.cgi/Session/4733>

Keynote Lecture: *Molecular basis of transgressive stress tolerance phenotypes in rice: Complementation, epistasis, and network rewiring by regulatory RNA. International Symposium on Rice Functional Genomics*, October 2017, Suwon, Republic of Korea,
<http://isrfg2017.kspb.kr/isrfg2017/>

Special Seminar: *Network rewiring and transgressive stress tolerance phenotypes in rice: Genetic and epigenetic mechanisms. Genetics Seminar Series*, School of Agriculture, Meiji University, August 2017, Hosted by Professor Kentaro Yano and Dr. Matthew Shenton, <http://www.meiji.ac.jp/>

Keynote Lecture: *Genetic and epigenetic basis of transgressive stress tolerance phenotypes in rice. Genomics Seminar Series*, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju, Republic of Korea, October 2017, Hosted by Dr. Sangho Kang, http://www.rda.go.kr/foreign/eng/rda_his.jsp

Special Seminar: *Molecular basis of transgressive stress tolerance phenotypes in rice. Genetics and Biotechnology Seminar Series*, Department of Biotechnology, Chonbuk National University, Jeonju, Republic of Korea, October 2017, Hosted by Prof. S.J. Yun

Special Seminar: *Epigenetics and stress tolerance phenotypes in rice. Molecular Biology Seminar Series*, Institute of Biology, University of the Philippines-Diliman, May 2017, Hosted by Dr. Jessica Rey

Plant stress genomics and epigenomics research: 11 months after relocating from the far northeast to the deep southwest. Plant and Soil Science Fall Seminar Series, Texas Tech University, November 29, 2016

Plenary Lecture: *Network rewiring and transgressive stress tolerance phenotypes in rice: Genetic and epigenetic mechanisms. Department of Plant Breeding and Genetics*

Seminar Series, Punjab Agricultural University, Ludhiana, Punjab, India, November 15, 2016. Lecture sponsored by the Office of the Chancellor

Epigenetics and transgressive segregation for stress tolerance in rice. National Bureau of Plant Genetic Resources Seminar Series, New Delhi, India, November 18, 2016.

Keynote Lecture: *Network rewiring and transgressive stress tolerance phenotypes: New paradigms for a classical concept in rice breeding.* 14th International Symposium on Rice Functional Genomics (ISRFG 2016), September 26 to 28, 2016, Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), Le Corum, Montpellier, France

Special Seminar: *Transgressive stress tolerance in rice: Genomic complementation, epistasis, epialleles, and network rewiring.* Department of Biochemistry and Molecular Biology Seminar Series, Oklahoma State University, Stillwater, OK USA, April 8, 2016

Cold stress response genetic networks in rice: Complementation, epistasis, epialleles, and transgressive phenotypes. 36th Rice Technical Working Group Meeting, March 1 to 4, 2016, Galveston, Texas, USA

Stress response genetic networks in rice: Hierarchy, epistasis, epialleles, and transgressive phenotypes, School of Biology and Ecology Fall 2015 Seminar Series, University of Maine, Orono, Maine, December 4, 2015

Keynote Lecture: *Stress response regulatory networks in rice: Hierarchy, epistasis, epialleles, and transgressive variation,* International Rice Research Seminar Series, International Rice Research Institute, Philippines, June 12, 2015

Special Seminar: *Stress response regulatory networks in rice: Hierarchy, epistasis, epialleles, and transgressive variation,* USDA-ARS-Cereal Crops Research Unit, University of Wisconsin, Madison, Wisconsin, February 10, 2015

Invited Lecture: *Low temperature stress regulatory networks in rice: Hierarchy, epistasis, and transgressive variation,* Molecular Biology Graduate Program Seminar Series, Purdue University, Lafayette, Indiana, April 15, 2014

Keynote Lecture: *Evolution of stress tolerance mechanisms in plants by network rewiring,* Colby College, Waterville, Maine, April 10, 2013

Plenary Lecture: *Genetically modified crops: Importance for the security of the world's food, feeds and fiber supply,* Kiwanis International, Orono, Maine, November 3, 2012

Testimonial Lecture at State Legislature: *Transgenic versus cisgenic crops: Friends or Foe,* Agricultural Commission of Maine, Augusta, Maine, September 24, 2012

Lecture: *Interspecific introgression of disease and insect resistance in Solanum,* 20th Annual Northeast Potato Technology Forum, University of Maine, Orono, ME, March 5, 2012

Lecture: *Stress tolerance engineering in rice by transcriptional switches,* Lecture sponsored by the USDA-Foreign Agricultural Service and Norman Borlaug International Scholars Program, Visayas State University, Philippines, June 5, 2012

Keynote Lecture: *Implications of transcriptional regulatory networks to stress tolerance engineering in rice*, Molecular Plant Sciences Graduate Program Seminar Series, Washington State University, Pullman, Washington, November 18, 2012

Seminar: *Implications of transcriptional regulatory networks to stress tolerance engineering in rice*, School of Biology and Ecology Fall Seminar Series, University of Maine, Orono, Maine, December 1, 2011

Seminar: *Implications of transcriptional regulatory networks to stress tolerance engineering in rice*, National Institute of Agrobiological Sciences, Tsukuba, Japan, August 16, 2011

Seminar: *Implications of transcriptional regulatory networks to stress tolerance engineering in rice*, Genetic Stock Center and Plant Genetics Laboratory, National Institute of Genetics, Mishima, Japan, July 12, 2011

Seminar: *Implications of transcriptional regulatory networks to stress tolerance engineering in rice*, Institute of Biological Sciences, University of the Philippines, Los Banos, Philippines, February 20, 2011

Seminar: *Implications of transcriptional regulatory networks to stress tolerance engineering in rice*, Plant Breeding, Genetics and Biotechnology Division Seminar Series, International Rice Research Institute, Philippines, February 15, 2011

Special Seminar: *Stress response regulatory networks in rice*. National University of Singapore, Singapore, October 8, 2010

Seminar: *Evolution of stress response gene networks in plants: Learning from comparative analysis of Arabidopsis and rice transcriptomes*, Potato Research Center, Agriculture and Agri-Food Canada, Fredericton, New Brunswick, Canada, August 19, 2010

Keynote Lecture: *Phylogenetic footprinting and transcription factor shuffling: Fine-tuning the abiotic stress transcriptomes of rice*, Chonbuk National University, *Rice and Civilization Month*, Departments of Crop Sciences and Anthropology, Chonbuk National University, Jeonju, Korea, September 15, 2009

Plenary Lecture: *Analysis of stress response regulome of flowering plants: Comparison of genetic models*, Philippine Society for Biochemistry and Molecular Biology Annual Conference, Nueva Ecija, Philippines, November 15, 2008

Seminar: *Organization of the low temperature regulome of japonica rice*, Plant Science Research Horizon Seminar Series, Dept. of Plant Sciences, McGill University, Montreal, Canada, September 20, 2008

Seminar: *Genetic regulatory networks in plants*, Distinguished lecture, University of the Philippines Los Banos, University of the Philippines Diliman, University of the Philippines Mindanao, Ateneo de Manila University, Central Mindanao University, and Department of Trade and Industry, Balik Scientist Award, Dept. of Science and Technology, Republic of the Philippines, February 10, 2008

Lecture: *Cold stress response gene regulon in rice*, Project update presented at the USDA-NRI-Plant Genome Research Program Annual Project Director's Workshop at the Plant and Animal Genome Conference XVI, San Diego, California, January 12, 2008

Seminar: *Chilling stress transcriptional regulatory networks of japonica rice*, 5th International Rice Functional Genomics Symposium, Tsukuba, Japan, October 15, 2007

Seminar: *Low temperature stress early response regulatory modules of japonica rice*, Plant Breeding, Genetics and Biotechnology Division Seminar, The International Rice Research Institute, Los Banos, Philippines, May 16, 2007

Plenary Lecture: *Assembling the cold stress transcriptional regulatory network of rice*, Mid-Atlantic Plant Molecular Biology Society, Beltsville, Maryland, August 18, 2006

Seminar: *Potato genomics research at the University of Maine*, Northeast Potato Technology Forum, Bangor, Maine, February 15, 2006

Special Seminar: *Stress response signaling pathway of rice*, Plant Breeding, Genetics and Biotechnology Division Seminar, The International Rice Research Institute, Los Banos, Philippines, April 27, 2005

Keynote Lecture: *Stress response pathway of japonica rice: Insights on transcriptional and translational regulatory mechanisms*, Korean Rice Genome Sequencing Program, National Institute of Agricultural Biotechnology, Suwon, Republic of Korea, April 9, 2005

Keynote Lecture: *Stress response genetic networks of rice: Transcriptional and translational regulatory mechanisms*, Faculty of Biological Resources Science, Chonbuk National University, Chonju, Republic of Korea, April 7, 2005

Seminar: *Cold stress response gene regulon in rice: A genome-wide functional genomics approach*, USDA-NRI-Functional Genomics Program and Coordinated Agricultural Research Program on Translational Genomics Joint Project Director's Conference, Houston, Texas, February 15, 2005

Invited Conference Lecture: *Low temperature stress-induced gene expression in rice seedlings: Tools for transcriptome analysis*, Third International Temperate Rice Conference, Punta del Este, Uruguay, March 12, 2003

PUBLISHED ABSTRACTS:

Mandal SN, Sanchez J, Bhowmick R, Bello OR, Van-Beek CR, de los Reyes BG (2023) BTB/POZ proteins and their gene family in *Oryza rufipogon*: Novel genes and alleles from the progenitor of the domesticated japonica rice (*O. sativa* L.). *Poster P49839*: Plant and Animal Genome XXX Conference, San Diego, CA.

Mandal SN, Kitazumi A, Pabuayon ICM, de los Reyes BG (2023) Variation in transcriptomic fluxes across rice genotypes representing a spectrum of variation for salinity tolerance and susceptibility. *Poster P49833*: Plant and Animal Genome XXX Conference, San Diego, CA.

De los Reyes BG (2022) Genetic and epigenetic novelties for adaptive traits in rice. Proceedings of the 19th International Symposium on Rice Functional Genomics – Driving the Next Green Revolution, Phuket, Thailand.

Mandal SN, Bello OCM, Sanchez J, Cushman KR, Van-Beek CR, Pabuayon ICM, De los Reyes BG (2021) Transgressive salinity tolerance phenotypes configured by chromosome segment substitution of *Oryza rufipogon* in *Oryza sativa* ssp. *japonica*. *Poster P1291*: Annual International Conference of the American Society of Agronomy (ASA), Crop Science Society of America (CSSA), and Soil Science Society of America (SSA): A creative economy for sustainable development, Salt Lake City, UT.

Naidenov B, Chen C, Cushman KR, Lim A, Gupta A, Hinze LL, Shim J, Sweeney ME, Chomet P, De los Reyes BG (2020) Transposable element dynamics in the subgenomes of allotetraploid cultivated cotton (*G. hirsutum* L.). *Poster PE0602*: Plant and Animal Genome XXVIII Conference, San Diego, CA.

Cushman KR, Pabuayon ICM, Hinze LL, Sweeney ME, De los Reyes BG (2020) Physiological networks rather than cellular Na⁺ transport and sequestration explain phenotypic variation for salt tolerance potential across the cultivated *Gossypium* germplasm. *Poster PE0614*: Plant and Animal Genome Conference, San Diego, CA.

Pabuayon ICM, Pabuayon IL, Walia H, Ritchie G, Singh RK, De los Reyes BG (2020) Profiling Na⁺ and K⁺ accumulation across biparental recombinant inbreds of rice by hyperspectral imaging. *Poster PE0840*: Plant and Animal Genome XXVIII Conference, San Diego, CA.

Sanchez J, Pal Kaur P, Karampudi NBR, Kitazumi A, Pabuayon ICM, Sandhu N, Catolos M, Kumar A, De los Reyes BG (2020) Rice *Decussate* gene mediates yield retention under drought and provides evidence of functional interactions between qDTY12.1 and the resident genomic background. *Poster PO0853*: Plant and Animal Genome XXVIII Conference, San Diego, CA. **[Award Winner]**

Pabuayon ICM, Kitazumi A, Walia H, Singh RK, Gregorio GB, De los Reyes BG (2020) Positive and negative complementation effects determine transgressive salt stress tolerance in recombinant inbreds of rice. *Poster PO0857*: Plant and Animal Genome XXVIII Conference, San Diego, CA.

Cushman K, Hinze L, Pabuayon ICM, Sweeney M, De los Reyes BG (2019) Contributions of Na⁺ sequestration and mobilization mechanisms to observed variation for salinity tolerance across the *Gossypium* Germplasm Diversity Panel. *Poster 616*: *Plant and Animal Genome XXVII*, San Diego, CA.

Karampudi NGR, Kitazumi A, Gendron JM, De los Reyes BG (2019) RNA-Seq dataset comparability and discovery of low-abundance but differentially expressed transcripts across diverse samples. *Poster 097*: *Plant and Animal Genome XXVII*, San Diego, CA.

Kitazumi A, Pabuayon ICM, Singh RK, Gregorio GB, De los Reyes BG (2019) DNA methylation and network rewiring in salt-tolerant transgressive segregants from biparental recombinant inbred population of rice. *Poster 688*: *Plant and Animal Genome XXVII*, San Diego, CA.

Pabuayon ICM, Kitazumi A, Cushman K, Walia H, Singh RK, Gregorio GB, De los Reyes BG (2019) Coupling of growth and defense potentials from genetically diverse parents potentially lead to salt tolerance in rice: Genomic and biochemical evidences. *Poster 911*: *Plant and Animal Genome XXVII*, San Diego, CA.

Sanchez J, De los Reyes BG, Emendack Y, Ritchie G, Shim RA, Hayes C (2019) Phenotypic assessment of seedling cold response in *Sorghum bicolor* L. Moench: Application of a variable temperature regime. *Poster 841: Plant and Animal Genome XXVII*, San Diego, CA.

Shim J, Cushman K, Karampudi NBR, Hinze L, Sweeney M, De los Reyes BG (2018) Transcriptomic changes during progressive salt stress across two upland cotton cultivars representing the extremes of tolerance and/or avoidance mechanisms. *Poster: Annual Conference of the American Society of Agronomy and Crop Science Society of America*, Baltimore, MD.

Pal Kaur P, Karampudi NGR, Kitazumi A, Pabuayon ICM, Sandhu N, Catolos M, Gendron J, Kumar A, De los Reyes BG (2018) Genetic basis of synergistic and antagonistic interactions between *qDTY12.1* and genetic background of rice cultivar IR64 as inferred from transcriptomic data. *Poster: National Association of Plant Breeders Annual Meeting*, Ontario, Canada.

Champaco ER, Kitazumi A, Karampudi NBR, Larkin RP, Tavantzis S, De los Reyes BG (2018) Potential role of small noncoding RNAs in regulating hypovirulence in *Rhizoctonia solani* anastomosis group-3. *Poster 559: International Congress of Plant Pathology*, Boston, MA.

Cushman KR, Hinze L, Pabuayon ICM, Sweeney M, De los Reyes BG (2018) Role of transporters in vertical distribution of excess Na⁺ and its association to salt-tolerance in tetraploid *Gossypium* germplasm. *Oral presentation CS-C2: Symposium of the Southern Section of the American Society of Plant Biologists*, New Orleans, LA.

Pabuayon ICM, Kitazumi A, Cushman K, Singh RK, Gregorio G, De los Reyes BG (2018) Novel adaptive mechanisms for transgressive salinity tolerance revealed through transcriptome analysis of rice recombinant inbred lines from genetically diverse parents. *Oral Presentation CS-C5: Southern Section of the American Society of Plant Biologists*, New Orleans, LA.

Cushman K, Hinze L, Pabuayon ICM, Sweeney M, De los Reyes BG (2018) Regulation of vertical Na⁺ transport and partitioning and its contributions to natural variation for salt tolerance across the cultivated tetraploid *Gossypium* germplasm. *Poster 610: Plant and Animal Genome XXVI*, San Diego, CA.

Gendron JM, Kaprampudi NBR, Kitazumi A, Cushman K, Pabuayon ICM, Singh RK, De los Reyes BG (2018) A case study on a novel dehydration stress tolerance mechanism in transgressive recombinant inbred lines of IR29 x Pokkali: Phenotypic and transcriptomic analyses. *Poster 951: Plant and Animal Genome XXVI*, San Diego, CA.

Karampudi NBR, Gendron JM, Kitazumi A, Pabuayon ICM, de los Reyes BG (2018) Uncovering distinctive spatio-temporal transcriptome signatures across genotypes, stress regimes, and developmental stages in rice: Assumptions and strategies. *Poster 927: Plant and Animal Genome XXVI*, San Diego, CA.

Kitazumi A, Pabuayon ICM, Singh RK, Gregorio G, de los Reyes BG (2018) DNA methylation and network rewiring in salt-tolerant transgressive segregants from a biparental recombinant inbred population of rice. *Poster 952: Plant and Animal Genome XXVI*, San Diego, CA.

Pabuayon ICM, Kitazumi A, Singh RK, Gregorio G, de los Reyes BG (2018) Distinctive transcriptome signatures in recombinant inbred lines of rice derived from genetically diverse parents lead to novel adaptive mechanisms and transgressive salinity tolerance. *Poster 924: Plant and Animal Genome XXVI*, San Diego, CA.

Pal Kaur P, Kaprampudi NBR, Kitazumi A, Pabuayon ICM, Sandhu N, Catolos M, Kumar A, de los Reyes BG (2018) Biological and physiological implications of qDTY12.1 introgression to basal growth and developmental processes in rice cv. IR64 as inferred from transcriptome signatures. *Poster 920: Plant and Animal Genome XXVI*, San Diego, CA.

Cushman KR, Hinze L, Pabuayon ICM, Sweeney M, De los Reyes BG (2017) Accessing stress phenotypic diversity in the tetraploid cotton germplasm through the *Gossypium* Diversity Reference Set. *Poster 571: Plant and Animal Genome XXV*, San Diego, CA.

Cushman KR, Hinze L, Pabuayon ICM, Sweeney M, De los Reyes BG (2017) Diversity for salinity tolerance across the tetraploid cotton germplasm in tetraploid cotton based on the *Gossypium* Diversity Reference Set. *Joint Conference of the American Society of Plant Taxonomists and Botanical Society of America*, Fort Worth, TX.

Gendron JM, Pabuayon ICM, Kitazumi A, Cushman K, Singh RK, Gregorio G, De los Reyes BG (2017) Understanding the molecular basis of transgressive phenotypes in rice: A case study on novel dehydration stress tolerance mechanisms in RILs derived from dehydration-sensitive parents. *Poster 780: Plant and Animal Genome XXV*, San Diego, CA.

Gendron JM, Karampudi B, Kitazumi A, Cushman K, Pabuayon ICM, Singh RK, De los Reyes BG (2017) Molecular basis of transgressive dehydration tolerance in RILs of rice from dehydration-sensitive parents. *Poster: Joint Conference of the American Society of Plant Taxonomists and Botanical Society of America*, Fort Worth, TX.

Kitazumi A, Ohyanagi H, Pabuayon ICM, Fujita M, Osti B, Kakei Y, Toyoda A, Fujiyama A, Shenton MR, Kurata N, de los Reyes BG (2017) *Oryza sativa* (AA-genome) and *Oryza Officinalis* (CC-genome) exhibit both conserved and diverged regulatory networks for low temperature stress response mechanisms despite their similar levels of sensitivity to cold. *Poster 0139: Plant and Animal Genome XXV*, San Diego, CA.

Kitazumi A, Pabuayon ICM, Osti B, Gendron JM, Singh RK, Gregorio GB, De los Reyes BG (2017) Patterns of salinity-induced ncRNA expression across the genomes of sibling recombinant inbred lines of rice: What do they tell us about network rewiring in hybrids? *Poster 0140: Plant and Animal Genome XXV*, San Diego, CA.

Pabuayon ICM, Kitazumi A, Gendron JM, Cushman KR, Singh RK, Gregorio GB, De los Reyes BG (2017) Novel transcriptional and physiological profiles in recombinant inbred lines of rice exhibiting transgressive traits for salinity tolerance: miRNA-mediated network rewiring. *Poster 0141: Plant and Animal Genome XXV*, San Diego, CA.

De los Reyes BG (2016) Cold stress response genetic networks in rice: Complementation, epistasis, epialleles, and transgressive phenotypes. *36th Rice Technical Working Group Meeting*, Galveston, Texas, USA.

De los Reyes BG (2016) Network rewiring and transgressive stress tolerance phenotypes: New paradigms for a classical concept in rice breeding. *14th International Symposium on Rice Functional Genomics (ISRFG 2016)*, September 26 to 28, 2016, Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), Le Corum, Montpellier, France (<http://isrfg2016.cirad.fr/>).

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Gendron J, Kitazumi A, Pabuayon ICM, De los Reyes BG (2016) Post-transcriptional regulation of *Nuclear Factor-Yα* transcription factor by *miR169* in transgressive progenies of the salt-tolerant rice cultivar Pokkali. *36th Rice Technical Working Group Meeting*, March 1 to 4, 2016, Galveston, Texas, USA (<https://beaumont.tamu.edu/rtwg/>).

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Kitazumi A, Ramos J, Hechanova SL, Mohanty B, Jena KK, Kurata N, Brar DS, De los Reyes BG (2012) Vertical comparison of stress-related transcription factors in the genus *Oryza*. *International Plant and Animal Genome Congress XX*, P802, San Diego, California.

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Mohanty B, De los Reyes BG, Wijaya E, Lee DY (2012) Cis-regulatory information of the transcriptome of an alcohol dehydrogenase (*adh1*) mutant in rice. *International Conference on Plant Abiotic Stresses*, P74, Vienna, Austria.

Kitazumi A, Ramos JM, Hechanova SL, Mohanty B, Jena KK, Kurata N, Brar DS, De los Reyes BG (2012) Vertical comparison of stress-related transcription factors in the genus *Oryza*. *International Plant and Animal Genome Congress XX*, P0802, San Diego, California.

Herath V, Mohanty B, Wijaya E, Bajic VB, Yun SJ, De los Reyes BG (2011) Defining orthology for stress-related genes of rice based on expression profiles and cis-regulatory information content. *International Plant and Animal Genome Congress XIX, San Diego*, California.

Mukherjee A, Alyokhin A, Sewell G, Novy R, De los Reyes BG (2010) Sources of aphid resistance mechanisms from the tuber-bearing *Solanum* germplasm. *Annual Meeting of the Crop Science Society of America (CSSA)*, Long Beach, California.

Mohanty B, Yeo HC, Wijaya E, De los Reyes BG, Lee DY (2010) Promoter analysis and transcriptional regulatory network in response to anoxia/low oxygen stress in rice and *Arabidopsis*. *10th International Conference on Plant Anaerobiosis*, PA6-08, Volterra, Italy.

Xu F, Park MR, Mohanty B, Herath V, Yun SJ, De los Reyes BG (2009) Regulatory signatures of orthologous stress-related bZIP transcription factors based on phylogenetic footprints. *6th International Rice Functional Genomics and Rice Genetics Symposium*, Manila, Philippines.

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Herath V, Park MR, Yun KY, Mohanty B, Xu F, De los Reyes BG (2009) Function of *TGA10* as a regulator of oxidative mediated chilling stress transcriptional network in japonica rice. *International Plant Reactive Oxygen Congress*, Helsinki, Finland.

Herath V, Park MR, Yun KY, Magoon D, Mohanty B, Xu F, Mauleon R, Bajic V, Bruskiewich R, De los Reyes BG (2008) Regulatory clusters involved in the early responses of japonica rice to chilling. *Plant Biology 2008*, Annual Meeting of the American Society of Plant Biologists. Merida, Mexico.

De los Reyes BG, Mohanty B, Yun KY, Park MR, Herath V, Xu F, Mauleon R, Wijaya E, Bajic VB, Bruskiewich R (2008) Chilling stress transcriptome of japonica rice: Physiological and regulatory implications of induced components. *6th International Symposium of Rice Functional Genomics*, Jeju Island, Republic of Korea.

Yun KY, Magoon D, Mohanty B, De los Reyes BG (2007) Structural and functional diversity of low temperature stress-related F-box domain-containing proteins of rice based on expression and phylogenetic analyses. *5th International Rice Functional Genomics Symposium*, Tsukuba, Japan.

Yun KY, Cheng C, De los Reyes BG (2007) Assembling the low temperature transcriptional regulatory network of chilling-sensitive plants with the japonica rice as model. *International Plant and Animal Genome Congress XV*, San Diego, California.

Ballou SM, De los Reyes BG (2007) Evaluating the genetic homogeneity of commercial

potato cultivars propagated in tissue culture at the Jacob Shur Research Facility. *University of Maine Cooperative Extension Annual Meeting*. Presque Isle, Maine.

De los Reyes BG, Ballou S, Cheng C (2006) Differential expression of cold acclimation associated genes in *Solanum* species. *Plant and Animal Genome XIV*, San Diego, California.

Cheng C, De los Reyes BG, Zhang Y, Ransom H, Yulin Jia, Yun SJ (2006) Genomic analysis of the early cold stress transcriptome of developing seedlings of rice. *International Plant and Animal Genome Congress XIV*, San Diego, California.

Cheng C, Jia Y, Yun SJ, Zhang Y, Ransom H, De los Reyes BG (2006) Genomic analysis of the early responses of developing rice seedlings to cold stress. *Proceedings of the Arthur M. Sackler Colloquia of the National Academy of Sciences, USA: From Functional Genomics of Model Organisms to Crop Plants for Global Health*, Washington, DC.

De los Reyes BG, Cheng C, Yun KY, Jia Y, Ransom HW, Gibbons J, Yun SJ (2006) Candidate regulators of the cold stress response gene regulon of rice. *4th International Rice Functional Genomics Symposium*, Montpellier, France.

Cheng C, Zhang Y, Ransom H, Jia Y, Yun SY, De los Reyes BG (2005) Genomic analysis of the early responses of rice seedlings to cold stress. *Annual Meeting of the American Society of Plant Biologists*, Seattle, Washington.

Yoo NH, Park MR, Yu CY, De los Reyes BG, Yun SJ (2005) Characteristic changes in antioxidant compounds in response to oxidative stresses and hormones in paraquat-tolerant *Rehmannia glutinosa*. *Annual Meeting of the American Society of Plant Biologists*, Seattle, Washington.

Morsy M, Stewart JM, De los Reyes BG (2004) Characterization of *OsLti6*, a small family of stress-regulated rice genes, encoding low molecular weight membrane proteins. *Gordon Research Conference for Salt and Water Stress in Plants*, Hong Kong.

Morsy MR, De los Reyes BG, Stewart JM (2004) *OsLti6*: A small family of integral membrane proteins associated with abiotic stress tolerance in rice. *Proceedings of the Second International Symposium of Rice Functional Genomics*, Tucson, Arizona.

Antoine W, Stewart JM, De los Reyes BG (2004) Orthologs of the sodium/lithium tolerance (*OsSLT1*, *OsSLT2*) gene family in rice: a new class of heat shock proteins specific to plants. *Conference on Chaperones and Heat Shock Proteins*, Cold Spring Harbor Laboratory, New York.

De los Reyes BG, Antoine W, Stewart JM (2004) The *OsSLT1* gene of rice is post-translationally regulated and functions as chaperone under stress conditions. *2nd International Symposium of Rice Functional Genomics*, Tucson, Arizona.

Morsy M, De los Reyes BG (2003) *OsLti6*: A family of novel cold stress inducible proteins in developing rice seedlings. *Annual Meeting of the American Society of Plant Biologists*, Southern Division, Dallas, Texas.

SYNERGISTIC ACTIVITIES:

Journal editorial board:

Associate Editor, *FRONTIERS IN PLANT SCIENCE* (journal), Plant Breeding Section, Impact Factor = 6.627, Published by Frontiers Media S.A., Lausanne, Switzerland; October 2022 – five years term

Associate Editor, *THE PLANT GENOME* (journal), Impact Factor = 5.826, Published by the Crop Science Society of America and John Wiley and Sons, Inc., New York, USA; October 2020 – five years term

Member of Editorial Board, *SCIENTIFIC REPORTS* (journal), Genetics and Genomics section, Impact Factor = 4.996, Published by Springer-Nature, Berlin, Germany; May 2019 – June 2022

Associate Editor, *RICE* (journal), Impact Factor = 6.097, Published by Springer-Nature, BioMed Central Ltd., London, UK; 2012 – present (indefinite term)

Guest Editor, *Special Issue of the INTERNATIONAL JOURNAL OF AGRONOMY* (journal), Genome-Enabled Analysis of Abiotic Stress Tolerance Mechanisms in Food Crops, Impact Factor = 2.07, Published by Hindawi Publishing Corp., New York, USA; 2013

Grant review and evaluation panels:

National Science Foundation, Integrative Organismal System, October 2019, August 2020, November 2021, EPSCoR External Advisory Board

National Science Foundation, Integrative Organismal System, 2018, EPSCoR Program on Genome to Phenome, Scientific Advisory Panel

Israel Science Foundation, 2016, Plant biology, genomics and climate change

French National Research Agency, 2013, 2014, 2015, BIOADAPT Program

USDA-AFRI-Foundational Program, 2013, Biological Mechanisms

National Science Foundation, 2012, Basic Research for the Enhancement of Agricultural Development

American Association for the Advancement of Science (AAAS), 2011, International Plant Genetics Scientific Advisory Panel

National Science Foundation, 2006, Integrative Organismal System/Functional Cluster

Israel Science Foundation, 2005, Arabidopsis Functional Genomics Program

Natural Science and Engineering Research Council of Canada, 2005, Genome Program

Ad hoc grant review panels:

National Science Foundation, 2016, 2017, Integrative Organismal Systems-Physiology

National Science Foundation, 2010, 2017, Integrative Organismal Systems-Regulatory

National Science Foundation, 2010, 2014, 2017, Molecular and Cellular Biology

National Science Foundation, 2010, Arabidopsis 2010

National Science Foundation, 2010, 2015, Plant Genome Research Program

USDA-AFRI, 2009, 2015, Foundational Program

National Science Foundation, 2009, Basic Research for the Enhancement of Agricultural Development

USDA-NRI, 2007, 2008, 2010, 2015, Plant Responses to the Environment, Plant Genome Research Program, Plant Genetic Mechanisms

Conference Chair (recent):

Global Forum on Innovations for Marginal Environment (GFIME), International Scientific Advisory Committee Member, United Arab Emirates, September to November 2019

Discussion Panelist/Expert on a public information on the role of genomics technology to address pressing issues on global food security in the 21st century. Featured four experts from across the Atlantic and Pacific, and covered by European and Middle East Press, Dubai, United Arab Emirates, November 19-21, 2019

Journal peer review services (since 2004):

Acta Physiologiae Plantarum, African Journal of Plant Biotechnology, BMC Bioinformatics, BMC Genetics, BMC Genomics, BMC Plant Biology, Crop Science, European Journal of Plant Pathology, Frontiers in Biotechnology, Frontiers in Genetics, Frontiers in Plant Science, Functional Plant Biology, Gene, Genetics, Genetic Resources and Crop Evolution, Genome, Genome Biology, Genome Research, Heredity, International Journal of Plant Sciences, Journal of Experimental Botany, Molecular Genetics and Genomics, Nature, Naturwissenschaften, New Phytologist, Phytopathology, Planta, Plant Cell, Plant Cell and Environment, Plant and Cell Physiology, Plant Genome, Physiologia Plantarum, Plant Molecular Biology Reporter, Plant Molecular Biology, Plant Cell Reports, Plant Disease, Plant Science, Plant Physiology, Plant Journal, PLoS Biology, PLoS Genetics, PLoS One, Rice, Scientific Reports, Theoretical and Applied Genetics

Adjunct graduate faculty appointment:

Biological Sciences, Plant Science, and Biochemistry and Molecular Graduate Programs, 2016 to present, University of Maine, Orono; Interdepartmental Cell and Molecular Biology Graduate Program, 2004-2010, University of Arkansas, Fayetteville

Leadership training:

Certificate on Leadership in Science and Academia, Cornell University, 2012

HIGHLIGHTS OF RECENT RESEARCH GRANTSMANSHIP:

During the last 15 years, my research has generated more than \$15 million of funding from major agencies such as the National Science Foundation, US Department of Agriculture-NIFA-AFRI, World Food Prize Foundation, Korea Research Foundation, and the National Institute of Genetics of Japan. Examples of the most notable major funding that supported my research at Texas Tech during the last six years are as follows. Minor grants are not listed.

Probing into the role of regulatory RNA, DNA methylation and associated network rewiring in transgressive segregation for stress tolerance, National Science Foundation, Plant Genome Research Program; Total \$699,000; Principal Investigator, 2014 – 2018; \$289,900 of this total was transferred from PI De los Reyes' former position at the University of Maine to his new position at Texas Tech in January 2016.

Enhancing the safety and quality of fresh produce and low moisture foods by waterless non-thermal technologies, USDA-NIFA-AFRI-CAP; Total = \$5,000,000; Principal Investigator, 2014 to 2016; Co-Principal Investigator, 2016 – 2023; Dr. de los Reyes had to give up his role as PI of this CAP grant because Texas is not eligible for an Enhancement Award because it is not an EPSCoR state. Portion of the grant (\$185,000) was transferred to Texas Tech to support a portion of the project objectives where Dr. de los Reyes maintained a co-PI role.

The macroalgal microbiome in space and time, National Science Foundation, Dimensions of Biodiversity; Total = \$983,900; Co-Principal Investigator, 2015 – 2021; grant originated from PI's previous position at the University of Maine.

Prevention of pathogen contamination in agricultural water in the lettuce production continuum, USDA-NIFA-Special Commodity Research Initiative (SCRI); Total funds = \$200,000; Principal Investigator, 2022 to 2026

Epigenomic variation associated with fiber and stress related traits in cotton: Application of epi-QTL in stress tolerance breeding, TTU-BASF-Project Revolution; Total funds = \$795,000; Principal Investigator, 2022 – 2025

Spectrum of physiological and genomic variation across the range of salinity and drought tolerance in the cultivated tetraploid Gossypium germplasm, Bayer Project Revolution; Total funds = \$1,199,000; Principal Investigator, 2016 – present

Genetic mechanisms of bacterial resistance to abiotic intervention strategies, USDA-ARS; Total = \$124,448; Principal Investigator, 2017 – 2019

Governor's University Research Initiative (GURI) Application, Office of the Governor of Texas; Total funds = \$5,000,000; Initial Principal Investigator in conjunction with CASNR and Office of the President; 2018 to present; This initiative aimed to recruit a Member of the National Academy of Sciences (NAS) to the Plant and Soil Science faculty of Texas Tech. Dr. de los Reyes wrote the original proposal that established the *Scientific Merit*, *Vision*, and *Broader Impacts* of the original proposal, which focused on establishing a research cluster in plant genomics for semi-arid agriculture at Texas Tech. Dr. Eric Hequet facilitated all other logistics of the concept in cooperation with the Office of the President. The funded proposal allowed Texas Tech to hire Dr. Luis Herrera-Estrella and four other new faculty in the cluster. When Dr. Herrera-Estrella got on board, the full responsibility and credit for the grant was transferred to him and his other colleagues in the cluster. (Note: I should have been given more credit by the administration for this major success, but I was NOT).

Biocomputing for environmental bacterial and viral metagenomes, USDA-ARS; Total = \$494,000; Principal Investigator, 2020 – present

OVERVIEW OF CURRENT RESEARCH:

World population is projected to reach more than 10 billion by 2050, hence the 'Ten Billion People Question' (10BPQ) is considered to be the grandest of the grand challenges to agriculture in the 21st century. It raises questions on what it will take to further elevate the yield ceiling of crops amidst the limitations imposed by climate change and continuous deterioration of water resources and arable lands. Apart from what has been achieved during the last century of crop genetic improvements by breeding, genomics, and biotechnology, maximizing the limits of crop yield and adaptive potentials will have to rely on new holistic paradigms that can create genetic novelties that have not been envisioned or achieved by earlier paradigms during and after the Green Revolution.

The genus *Oryza*, which includes the Asian (*O. sativa*) and African (*O. glaberrima*) cultivated rices and 22 exotic wild species, represents 15-million years of speciation and 4,000 years of domestication history. Optimized by natural evolutionary processes, this rich biodiversity must be harnessed strategically by breeding and biotechnology to widen the genetic and epigenetic bases of cultivars, towards the much needed adaptive novelties for stress-prone ecosystems that continue to threaten world food security. To contribute to this goal, transformative research in my laboratory uses the genus *Oryza* as model system to create genetic novelties and adaptive phenotypes through holistic, non-reductionist, and systems-level approaches to genetic manipulation, guided by evolutionary principles. Inspired by the *Omnigenic Theory* and the paradigm of genomic modeling, we interface genomics, epigenomics and systems biology to elucidate the molecular underpinnings of the phenomenon of *transgressive segregation* in context of genetic network rewiring mediated by chromatin, genome, and epigenome restructuring during intra-species and inter-species hybridization.

Transgressive segregation creates rare recombinant progenies that are beyond the phenotypic range of their genetically divergent parents. To this end, we are elucidating the impact of genomic and epigenomic restructuring to transcriptional and post-transcriptional regulation, and how they create novel adaptive phenotypes. By comparative genomic, regulomic, and epigenomic analyses coupled with network modeling and functional validation by transgenics and gene editing, we aim to uncover changes in cellular regulation that configure novel physiological and/or biochemical networks in hybrids and recombinants. We are illuminating the molecular underpinnings of genetic gains and physiological drags as causes of novel adaptive phenotypes created by genome shuffling and epigenome confrontation. We are also translating the transformative knowledge from model studies to develop new breeding paradigms for other food and fiber crops for the rapidly changing ecology and climate across West Texas and beyond.

PERSONAL STATEMENT AND CONTRIBUTIONS TO PLANT SCIENCE:

I pride myself as a pragmatic yet ambitious, original, and extremely motivated scientist whose holistic visions about innovation have been shaped by well-rounded experiences in the fundamental aspects of genetics and their translations to plant breeding. At this point in my career, I could confidently say that I have seen the advances in plant genetics and genomics as they happened from the 1980s to the present time, both the science and the technology aspects, from linkage and QTL mapping to transgenics, whole genome sequencing, genomic selection, genome editing, epigenomics, and systems-biology. I have witnessed all the excitements as new technology emerged, all the paradigm shifts, and most importantly the successes and failures of over-calculating what the emerging technology and discovery paradigms in molecular genetics and genomics could realistically deliver. Having said that, I could say that I have reached my full intellectual maturity and potential as a pure-bred geneticist, and my visions on how to translate my scientific knowledge and experiences to plant breeding are strongly anchored to more than two decades of high profile interdisciplinary research. An icing-on-the-cake is my broad understanding of the various disciplines and sub-disciplines associated with plant breeding apart from genetics, which include physiology, biochemistry, molecular biology, genomics, and evolution. At this stage in my career, my experiences have given me the wisdom and strengthened my genuine desire to lead a global research and education program in plant breeding with practicality, clear vision and purpose. I believe that such an opportunity will allow me to translate my visions towards an overarching goal of cementing my future contributions to the grand challenge to food security in the 21st century.

During the last two decades of my career in the U.S., I have established myself as significant contributor of new knowledge in plant molecular genetics through transformative research. My major contributions span the areas of stress physiology and biochemistry and their genetic regulatory mechanisms, particularly the elucidation of intricate molecular networks involved in abiotic stress tolerance using *Oryza* (rice) as experimental model. The fundamental research questions that I have been addressing throughout my entire career have always been inspired by potential translations in plant breeding, be it for novel means of selection or for the discovery of novel genetic mechanisms that can illuminate our understanding of plant phenotypes and their selection during the course of breeding.

My accomplishments in research are the results of my broad experiences in both fundamental and applied aspects of plant genetics, physiology and molecular biology, which I had established during the period that I have been a faculty member at the University of Arkansas, University of Maine, and Texas Tech University. My career experiences have also been enriched by successful partnerships with various experts in experimental and computational genomics and both classical and modern genomics-assisted plant breeding in the U.S. (Georgetown University) and abroad (National University of Singapore, National Institute of Genetics-Japan, National Institute of Agrobiological Sciences-Japan, Chonbuk National University-Korea, International Rice Research Institute-Philippines, King Abdullah University of Science and Technology-Saudi Arabia, and Punjab Agricultural University-India). My research has been funded by both federal (National Science Foundation, USDA-NRI, USDA-NIFA-AFRI, USDA-ARS, USDA-FAS).

Equally important to my intellectual growth and broad vision as a scientist are my extensive experiences prior to my career in the U.S. I was a valued member of the genetics research team at the Plant Breeding, Genetics and Biotechnology Division at the International Rice Research Institute (IRRI) for about a decade under the direction of World Food Prize and Japan Food Prize Laureate Dr. Gurdev S. Khush. As part of the Rockefeller Foundation's International Program on Rice Biotechnology, my work back then focused mainly on aspects related to establishment of the basic scaffolding of the reference genome of rice, and its applications for mining the germplasm for novel genes and alleles with potential applications to the improvement of the environmental resilience and yield of rice. I started my exposure to international agricultural research early on during my graduate student years through research fellowships at the John Innes Centre in the U.K. and Japan Rice Genome Program in Tsukuba, Japan, where I took part in what is now considered the most important milestone in plant breeding, *i.e.*, the assembly of the very first '*finished*' reference genome sequence of any crop of global importance.

More recently at Texas Tech University, my research focus has transitioned from purely stress physiological genetics and genomics to elucidating the roles of *epigenetic mechanisms*, including transcriptional gene silencing (TGS) by RNA-directed DNA methylation and post-transcriptional gene silencing (TGS) by miRNAs, in fine-tuning regulatory networks that lead to transgressive quantitative traits for stress tolerance. This project is focused primarily on rice (*Oryza* spp.) as a model system but translation to a crop of great importance to West Texas agriculture (cotton) is an integral part, with parallel funding from the National Science Foundation for hypothesis-driven aspects, and Bayer CropScience Endowed Professorship for the translational aspects. Another major goal of my current research is the establishment of a pan-genomics pipeline for the application of a '*Global Allelic Panel*' that will serve as foundation for a new breeding technology which is *allele stacking by genome editing*. As the holder of one of the major endowed professorships at Texas Tech University, I also take the role of a leader among researchers working on various aspects of plant/crop genetics and breeding in my department and the college as a whole.

Pre-doctoral career. My career began when I was a part of the Rockefeller Foundation's International Program on Rice Biotechnology at the International Rice Research Institute during the late 1980's to early 1990's. The goal of my research was to understand the architecture of the rice genome using the most state-of-the-art molecular technologies for mutant analysis, genetic fingerprinting, and genome mapping that were available during that time. My contributions to such an effort include: a) establishing genetic linkage maps and associating genetic linkage groups with cytologically identifiable chromosomes using various types of mutants and aneuploids, and protein and DNA marker technologies; b) redefining the traditional species and ecotypic classification of the cultivated and wild rice germplasm consisting of more than 120,000 accessions using our understanding of genomic architecture and genetic variation; and c) using the knowledge of rice genome architecture to understand interspecies genetic introgression and preferential chromosome transmission in *Oryza* and their applications in diversifying the genetic base of cultivars by biotechnology-assisted breeding.

My research contributed to cementing the status of rice as the reference genome for the syntenic groups of grasses (Poaceae) representing more than 40 million years of evolutionary history in the plant kingdom. Much of the advanced level research in rice genetics and biotechnology that are currently on-going at IRRI and many other research institutions for rice in the world were nucleated by the early accomplishments in rice molecular genetics and genomics that I played a critical part of during my tenure at IRRI during the 1980's and 1990's. Unknown to many rice researchers around the world, the establishment of the 3K rice genomics panel that is now an important platform for discovery in rice genetics and breeding had its foundational roots from the outcomes of my early research at IRRI.

Early career. During the early part of my career as principal investigator, my research focused on uncovering the regulatory switches and/or critical biochemical processes that configure the defenses of plants (primarily rice and other plant genetic models) against the physiological perturbations caused by cold, dehydration and salinity stresses. Examples of my most important contributions to this area of plant biology include the functional characterization important transcriptional regulators and metabolic genes that contribute in a cumulative fashion to the inherent defenses of plant cells against the physiological perturbations and biochemical dysfunctions caused by stress, and how these mechanisms contribute to the expression of inherent stress tolerance potential across genotypes. My approach to these investigations made use of the paradigms of functional genomics combined with modern techniques in cellular physiology and biochemistry and then linking them to quantitative trait loci that have been uncovered by genomics-assisted plant breeding.

Mid-career: During this period, my research continued to probe into the mechanisms of cellular responses to abiotic stresses in plants (with primary emphasis on rice) one dimension deeper by examining cellular defenses within the context of genetic regulatory networks. For the body of works that I have done on this area of plant stress biology, I have combined the power of genome-enabled investigations coupled with systems-level approaches, forward and reverse genetics, protein-DNA interaction, and state-of-the-art computational genomics to elucidate the hierarchy of regulatory hubs for transcriptional networks that configure plant defenses and adaptation. The main highlights are the discovery of an oxidative-mediated regulon that configures early defenses, thereby preventing the domino effects of stress physiological perturbation. My research also contributed to the identification of some non-coding regulatory RNA molecules as fine-tuners of transcriptional networks that integrate growth and stress-related response