Ai Kitazumi, Ph.D.

Research Associate in Computational Genomics
Department of Plant and Soil Science
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Professional Preparation

Ph.D. (Plant and Soil Science), Texas Tech University, 2019

Ph.D. (Plant Science), University of Maine, 2014 - 2015; Degree program continued at Texas Tech University

M.S. (Botany and Plant Pathology), University of Maine, 2013

B.A. (Human Ecology), College of the Atlantic, 2010

Appointments

Research Associate (in Computational Genomics), Texas Tech University, March 2022-Present

Research Associate, Texas Tech University, September 2020-February 2022

Research Aide, Texas Tech University, October 2019- August 2020

Temp Professional Specialist, University of Maine-Orono, December 2019- May 2020

Graduate Research Assistant, Texas Tech University, January 2016-August 2019

Graduate Research/Teaching Assistant, University of Maine-Orono, January 2014-December 2015

Graduate Research/Teaching Assistant, University of Maine-Orono, July 2010- December 2013

Relevant activities and awards

Editor for “Plant Omics: Advances in Big Data Biology” with UK-CABI Publishing

Member of review editor board for Plant Breeding

Member of reviewer board Insects, Biology and Current Plant Biology

Bioinformatics contractor for metagenomic and virome analysis for USDA-ARS

Bioinformatics advisor for large scale sequencing panel and genome-wide association study for rice variant discovery in International Rice Research Institute, Philippines

Graduate School Representative for summer 2019 commencement in Texas Tech University

Key research personnel for shuttle research activities and collaboration between De los Reyes Lab at UMaine/Texas Tech and Kurata Lab at the National Institute of Genetics (NIG), Japan

Teaching assistant for Introductory Biology labs and Principal of Genetics in University of Maine

Outstanding Graduate Student in Plant Biology (SBE Fay Highland-Hilborn Prize in Plant Biology/Plant Pathology Award), School of Biology and Ecology, University of Maine, 2014

Current Project

Genetic and Physiological Novelties for Salinity Tolerance in Rice Created by Transgressive Segregation (USDA-NIFA-AFRI # 2023-67013-39541) as a lead bioinformatician

Epigenomic variation associated with fiber and stress related traits in cotton: Application of epi-QTL in stress tolerance breeding (Bayer CropScience, Texas Tech University, BASF Project Revolution Program) as a lead bioinformatician

Prevention of Pathogen Contamination in the Lettuce Production Continuum (USDA-NIFA-SCRI #2030-42000-055-007-A) as a lead scientist for bioinformatics on genomic basis of pathogenic bacteria and investigation of phage-bacteria interactions (RSA# 58-2030-0-034)

Research Interests

My role in research is to translate the advanced genomics inquiries into computational biology executables using machine learning and artificial intelligence on high performance computational center, with a particular focus on conducting full-depth genomic investigations in plants with complex heritages and agriculturally valuable traits. I specialize in analyzing genetic inheritance and gene expression patterns, including the response of repetitive regions and transposons. Currently, I am focusing on gene silencing profiling through methylation and transcriptomic studies, while inferring chromatin states to understand regulatory mechanisms. Expanding my expertise, I am leading metagenomic investigations of bacterial and phage-viral genomes, to enhance food safety and track organisms with fast mutation rates for government projects.

Publication

- Zhang Y, **Kitazumi A**, Liao YT, de Los Reyes BG, Wu VCH. Metagenomic investigation reveals bacteriophage-mediated horizontal transfer of antibiotic resistance genes in microbial communities of an organic agricultural ecosystem (2023). *Microbiol Spectr*. 2023;11(5):e0022623.
- **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*, 10-29.
- Asari M, **Kitazumi A**, Nambara E, de los Reyes BG, Yano K (2022) Plant Gene Expression Network In *Plant Omics: Advances in Big Data Biology*, 137-150
- Sanchez J, Kaur PP, Pabuayon ICM, Karampudi NBR, **Kitazumi A,** Sandhu N, Catalos M, Kumar A, De los Reyes BG (2022) *DECUSSATE* network with flowering genes explains the variable effects of qDTY12.1 to rice yield under drought across genetic backgrounds. *Plant Genome* 15(1):e20168.
- Sanchez J, Kaur PP, Pabuayon ICM, Karampudi NBR, **Kitazumi A,** Sandhu N, Catalos M, Kumar A, De los Reyes BG (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. *BioRxiv*, 2021 (Preprint).
- Shu X, Singh M, Karampudi NBR, Bridges DF, **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. *PLoS ONE*. 2021;16(10):e0256324.
- Pabuayon ICM, **Kitazumi A,** Cushman KR, et al (2021). Novel and transgressive salinity tolerance in recombinant inbred lines of rice created by physiological coupling-uncoupling and network rewiring effects. *Front Plant Sci*. 2021;12:615277.
- Suwabe K, Nagasaka K, Windari EA, Hoshiai C, Ota T, Takada M, **Kitazumi A**, Masuko-Suzuki H, Kagata Y, Yano K, Tsuchimatsu T, Shimizu KK, Takayama S, Suzuki G, Watababe M (2020). Double-locking mechanism of self-compatibility in *Arabidopsis thaliana*: the synergistic effect of

transcriptional depression and disruption of coding region in the male specificity gene. *Front Plant Sci*. 2020;11:576140.

- Kaur A, Neelam K, Kaur K, **Kitazumi A,** de los Reyes BG, Singh K. Novel allelic variation in the Phospholipase D alpha1 gene (OsPLDα1) of wild *Oryza* species implies to its low expression in rice bran (2020). *Sci Rep*. 2020 Apr 20;10(1):6571.
- Kaur A, Neelam K, **Kitazumi A**, Kaur K, Sharma P, Mangat GS, et al (2020). Novel cis-acting regulatory elements in wild *Oryza* species impart improved rice bran quality by lowering the expression of phospholipase D alpha1 enzyme (OsPLDα1) (2020). *Mol Biol Rep*. 2020 Jan;47(1):401–22.
- 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. *Front Genet*. 2020;11:594569.
- Shu X, Singh M, Karampudi NBR, **Kitazumi A**, et al (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. *Front Microbiol*. 2020;11:1122.
- **Kitazumi A**, Pabuayon ICM, Ohyanagi H, Fujita M, Osti B, Shenton MR, 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. *Nature Scientific Reports* 8:16346.
- 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.
- 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.
- 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.
- Mohanty B, **Kitazumi A**, Cheung CYM, Lakshmanan M, De los Reyes BG, Jang IC, Lee DY (2016) Identification of candidate network hubs involved in metabolic adjustments of rice under drought stress by integrating transcriptome data and genome-scale metabolic network. *Plant Science,* 242:224–239
- Chen J, **Kitazumi A**, Alpuerto J, Alyokhin A, De los reyes B. Heat-induced mortality and expression of heat shock proteins in Colorado potato beetles treated with imidacloprid. *Insect Sci.* 2016;23(4):548-54.
- **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 an andigena potato (*Solanum tuberosum* subsp. *andigena*) to salinity stress, predicted from network models in *Arabidopsis*. *Genome 58(1):* 13-24.
- Xu F, Park MR, **Kitazumi A**, Herath V, Mohanty B, 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.

Book editor

Ohyanagi H, Yano K, Yamamoto E, **Kitazumi A**, editors. Plant omics: Advances in big data biology. GB: CABI; 2022

Other relevant publications (Poster and workshop abstract)

Kitazumi A, Pabuayon I, Cushman KR, Singh RK, Kawahara Y, de los Reyes BG (2024). Reconfigured epigenomic landscapes of the transgressive segregants for salinity tolerance in indica x aus recombinant inbred population of rice. Plant and Animal Genome XXXI, San Diego, CA.

Pabuayon I, **Kitazumi A**, de los Reyes BG (2024). Mechanisms behind the novel adaptive physiology and ideotype in a transgressive segregant for salinity tolerance in rice. Plant and Animal Genome XXXI, San Diego, CA.

Cushman KR, Kitazumi A, Lim A, et al (2024). The assembled genome of landrace Cedix (SA-1766) reveals genetic potential for stress tolerance not represented in the current model of *Gossipyum hirsutum*. Plant and Animal Genome XXXI, San Diego, CA.

Mandal SN, **Kitazumi A**, Van-Beek CR, Bello OCM, Pabuayon ICM, Reyes BG de los. Unlocking of cryptic gene functions in wild species *O. rufipogon* by alien introgression into the genome of domesticated *O. sativa* ssp. Japonica to develop novel salinity-tolerant phenotypes. In: ASA-CSSA-SSSA; 2023.

Kitazimi A, Pabuayon I, Singh RK, Gregorio GB, De los Reyes BG (2019) Regulation of Recipient Parent's Genomic Structure Via Epigenetic Patterns from Donor Parent Lead to Transgressive Segregants in Rice. Plant and Animal Genome XXVII, San Diego, CA.

Kitazimi A, Pabuayon I, Osti B, Singh RK, Gregorio GB, De los Reyes BG (2018) DNA Methylation and Network Rewiring In Salt-Tolerant Transgressive Segregants from a Biparental Recombinant Inbred Population of Rice. Plant and Animal Genome XXVI, San Diego, CA.

Kitazimi A, Ohyanagi H, Pabuayon I, Fujita M, Osti B, Kakei Y, Toyoda A, Fujiyama A, Shenton MR, Kurata N, De los Reyes BG (2017). *Oryza sativa* (AA) and *Oryza Officinalis* (CC) Exhibit Both Conserved and Diverged Regulatory Networks for Low Temperature Stress Response Mechanisms Despite Their Similar Levels of Sensitivity to Cold. Plant and Animal Genome XXV, San Diego, CA.

Kitazimi A, Pabuayon I, Osti B, 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 Transcriptome Reconfiguration and Network Rewiring in Hybrids? Plant and Animal Genome XXV, San Diego, CA.

Kitazimi A, Ohyanagi H, Fujita M, Kakei Y, Toyoda A, Fujiyama A, Kurata N, De los Reyes BG (2016). AA-genome and CC-genome Complementation in *Oryza*: Comparative Regulon Reconstruction by Network Analysis and Cis-element Mining Between O. sativa and O. officinalis. 36th Rice Technical Working Group Meeting (RTWG), Galveston, TX

Kitazimi A, Ohyanagi H, Fujita M, Toyoda A, Fujiyama A, Kurata N, De los Reyes BG (2014) Comparing the compositional complexities of the low temperature stress transcriptomes of AA and CC genomes of *Oryza*. 12th International Symposium on Rice Functional Genomics, Tucson, Arizona.

Kitazimi A, De los Reyes BG, Ohyanagi H, Fujita M, Toyoda A, Fujiyama A, Kobayashi M, Yano K, Wing RA, Kurata N (2014) Investigation of Wild *Oryza* for Potential Genetic Resource to Improve Abiotic Stress Tolerance in Rice using Low Stress Response Transcriptome as an Example. Retreat of National Institute of Genetics, Japan.

Kitazimi A, Amas J, Ramos JM, Alpuerto JB, Ohyanagi H, Gregorio GB, Vera-Cruz C, Jena KK, Kurata N, De los Reyes BG (2013) Analysis of the Low Temperature Stress Transcriptome of the CC-Genome *Oryza officinalis*. Plant and Animal Genome XXII, San Diego, CA.

Kitazimi A, Kawahara Y, De Koeyer D, De los Reyes BG (2013) Integration of Stress and Growth-Related Responses by microRNAs in Andean Potatoes. Plant and Animal Genome XXII, San Diego, CA.

Kitazimi 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*. Plant and Animal Genome XX, San Diego, CA.