







# Dae Kwan Ko

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## RESEARCH INTERESTS

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I am an early-career researcher who is passionate about addressing critical biological questions at the systems-level with a hypothesis-driven approach using the power of genomics. Do genes and proteins interact with each other in cells as we do in society? Then, what could be the functional consequences of those interactions in regulating biological pathways? I believe that these molecular interactions, called “biological networks”, are crucial for all living organisms to maintain cellular homeostasis. My long-term research goal is toward characterizing gene networks underlying significant biological pathways and applying the findings to translational research.

## PROFESSIONAL APPOINTMENTS

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### **Assistant Professor - Fixed Term** (Dec 2022 – present)

Plant Research Laboratory, Department of Plant Biology, Great Lakes Bioenergy Research Center, Michigan State University, USA (funded by Federica Brandizzi and independent grants)

Research summary: Investigating how genes respond to environmental stresses through a comprehensive systems-level approach involving gene regulatory network modeling and functional characterization. This research spans across both model and non-model plant species.

### **Postdoctoral Research Associate** (Dec 2017 – Nov 2022)

Plant Research Laboratories, Great Lakes Bioenergy Research Center, Michigan State University, USA  
Advisor: Federica Brandizzi

Research summary: (1) Understanding gene regulatory networks in plant unfolded protein response: utilizing multi-omics approaches combined with forward genetics, my work focused on unraveling the intricate gene regulatory networks governing the unfolded protein response in plants. This research aimed to provide a systems-level understanding of this critical cellular process. (2) Cell wall biogenesis and differentiation in bioenergy crops: employing gene regulatory network modeling and functional characterization, I investigated the mechanisms behind cell wall biogenesis and differentiation during the growth of bioenergy crops. This holistic approach allowed for a comprehensive exploration of these crucial aspects of plant development.

### **Postdoctoral Research Associate** (June 2016 – Nov 2017)

Department of Plant Biology, Michigan State University, USA

Advisor: C. Robin Buell

Research summary: Identifying unintended consequences of genome modification methods in clonally propagated diploid potato. This work addressed critical concerns related to genome editing and its implications within the context of crop improvement.

## EDUCATION

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### **Ph.D.** The University of Texas at Austin (Plant Biology), USA (Sept 2009 – Aug 2016)

Advisor: Z. Jeffrey Chen

Thesis title: *Clock-regulatory networks contribute to growth vigor in maize hybrids*

Research summary: Investigating the molecular link of the circadian clock with growth vigor in maize hybrids using functional genomics approach covering a broad array of molecular techniques

### **M.S.** Seoul National University (Biological Sciences), Republic of Korea (Sept 2006 – Aug 2008)

Advisor: Choo Bong Hong

Thesis title: *Submergence-inducible and circadian rhythmic transcriptional networks in Nicotiana tabacum*  
Research summary: Characterizing clock-regulated transcription factor genes in response to abiotic stress in *Nicotiana tabacum*

**B.S.** Konkuk University (Crop Science), Republic of Korea (Mar 2000 – Aug 2006)

## PUBLICATIONS

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### ***Published in Peer-Reviewed Articles (16 total: 8 first authorships; 8 co-authorships)***

16. **Ko DK**, Kim JY, Thibault EA, Brandizzi F (2023). A signaling cohort of IRE1 and proteasome system controls cell fate determination in unresolved proteotoxic stress of the plant endoplasmic reticulum. **Nature Plants** 9, 1333-1346. ([Highlighted in MSUToday](#))

15. Bhandari DD, **Ko DK**, Kim SJ, Nomura K, He SY, Brandizzi F (2023). Defense against phytopathogens relies on efficient anti-microbial protein secretion mediated by the microtubule-binding protein TGNap1. **Nature Communications** 14, 6357.

14. **Ko DK**, Brandizzi F (2022). Transcriptional competition shapes proteotoxic ER stress resolution. **Nature Plants** 8, 481-490. ([Highlighted in the PRL Bulletin](#))

13. **Ko DK**, Brandizzi F (2022). Advanced genomics identifies growth effectors for proteotoxic ER stress recovery in *Arabidopsis thaliana*. **Communications Biology** 5, 16. ([Highlighted in the PRL Bulletin](#))

12. York LM, Cumming JR, Trusiak A .... **Ko DK** .... Yang WH (2022). Bioenergy Belowground: challenges and opportunities for phenotyping roots and the microbiome for sustainable bioenergy crop production. **Plant Phenome Journal** 5: e20028.

11. Plant Cell Atlas Consortium, Ghosh Jha S, Borowsky AT .... **Ko DK** ... Rhee SY (2021). Science Forum: Vision, challenges and opportunities for a Plant Cell Atlas. **eLife** 10:e66877.

10. Angelos E, **Ko DK**, Zemelis-Durfee S, Brandizzi F (2021). Relevance of the Unfolded Protein Response to Spaceflight-Induced Transcriptional Reprogramming in Arabidopsis. **Astrobiology** 1;21(3);367-380.

9. **Ko DK**, Brandizzi F (2021). A temporal hierarchy underpins the transcription factor-DNA interactome of the maize UPR. **The Plant Journal** 105(1);254-270. ([Highlighted in the PRL Bulletin](#))

8. **Ko DK**, Brandizzi F (2020). Network-based approaches for understanding gene regulation and function in plants. **The Plant Journal** Oct;104(2):302-317. ([Highlighted in the Society for Experimental Biology's Spring Bulletin](#))

7. Rice S, Fryer E, Ghosh Jha S...The Plant Cell Atlas Consortium (including **Ko DK**) (2020). First plant cell atlas workshop report. **Plant Direct** 00:1–10.

6. Pastor-Cantizano N, **Ko DK**, Angelos E, Pu Y, Brandizzi F (2019). Functional diversification of ER stress responses in Arabidopsis. **Trends in Biochemical Sciences** 18;45(2):123-136.

5. Nadakuduti SS, Starker CG, **Ko DK**, Jayakody TB, Buell CR, Voytas DF, Douches DS (2019). Evaluation of Methods to Assess in vivo Activity of Engineered Genome-Editing Nucleases in Protoplasts. **Frontiers Plant Science** 8;10:110.

4. **Ko DK**, Nadakuduti SS, Douches DS, Buell CR (2018). Transcriptome profiling of transgenic potato plants provides insights into variability caused by plant transformation. **PLoS One** 8;13(11):e0206055.

3. \***Ko DK**, \*Rohozinski D, Song Q, Taylor SH, Juenger TE, Harmon FG, \*Chen ZJ (2016). Temporal shift of circadian-mediated gene expression and carbon fixation contributes to biomass heterosis in maize hybrids. **PLoS Genetics** 28;12(7):e1006197. \*These authors contributed equally to this work.

2. Shi X, Zhang C, **Ko DK**, Chen ZJ (2015). Genome-wide dosage-dependent and -independent regulation contributes to gene expression and evolutionary novelty in plant polyploids. **Molecular Biology and Evolution** 32(9):2351-66.

1. **Ko DK**, Lee MO, Hahn JS, Kim BG, Hong CB (2009). Submergence-inducible and circadian rhythmic basic helix-loop-helix protein gene in *Nicotiana tabacum*. **Journal of Plant Physiology** 1;166(10):1090-100.

### ***Book Chapters and Editorial***

3. **Ko DK**, Brandizzi F (2023). Multi-omics resources for understanding gene regulation in response to ER stress in plants. *Plant Endoplasmic Reticulum: Methods and Protocols*, Second Edition. Methods in Molecular Biology *In press*

2. **Ko DK**<sup>#</sup>, Sanchez-Ballesta MT (2023). Editorial: methods, applications, and protocols in plant science: network modeling-guided understanding of gene regulation in plants. *Frontiers in Plant Science* 14:1171846. <sup>#</sup>Corresponding author.

1. **Ko DK**, Brandizzi F (2022). Coexpression network construction and visualization from transcriptomes underlying ER stress responses. In: Lois, L.M., Trujillo, M. (eds) *Plant Proteostasis*. Methods in Molecular Biology, vol 2581. Humana, New York, NY.

### ***In Review/In Revision***

4. **Ko DK**, Brandizzi F. Dynamic gene regulation in the plant unfolded protein response - a systems biology perspective. Review article invited by **Nature Reviews Genetics**.

3. **Ko DK**, Brandizzi F. NEEDLE: network-enabled gene discovery pipeline for non-model plant species. *Under review*

2. Choi D, **Ko DK**, Kim DH. Transcriptome analysis revealed that Arabidopsis model plants invokes the activation of heat shock proteins and ER stress response against cesium stress. *Under review*

1. Choi D, Lee SW, **Ko DK**, Kim DH. Dynamic histone modifications establish dual modes of transcriptional response of Arabidopsis glucosinolate pathway genes under wounding stress. *Under review*

### ***In Preparation***

2. **Ko DK**, Brandizzi F. Defining transcriptomic dynamics in sorghum in multiple abiotic stresses. The anticipated submission in Nov 2023.

1. **Ko DK**, Sun X, Kim SJ, Brandizzi F. Understanding trade-off between mixed-linkage glucan production and growth fitness in *Brachypodium*. The anticipated submission in Nov 2023.

### **FUNDING AND FELLOWSHIPS**

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**DOE Bioenergy Research Center grant** (proposal ID: 509513), "The DNA binding landscape of sorghum TFs in response to abiotic stress", supporting DNA synthesis of 142 TFs and DAP-seq analyses in Joint Genome Institute, Role: **PI** (2023)

**Project GREEN (Generating Research and Extension to meet Economic and Environmental Needs) Award**, Michigan State University, “Assessing the impact of abiotic stress on activities of gene regulatory DNA sequences in sorghum at single-cell resolution”, Role: **PI** (\$30,000) (2022 – 2023)  
**DOE Bioenergy Research Center grant** (proposal ID: 508271), “Transcriptome analysis under abiotic stress in sorghum”, supporting RNA-seq library construction of 104 samples and next-generation sequencing in Joint Genome Institute, Role: **PI** (2021)

**MSU Cloud Computing Fellowship** (funded to work on research projects in a cloud computing system, Microsoft Azure, receiving hands-on training and participating in public activities) (2020 – 2021)  
([Announcement](#))

**Travel grant**, The Plant Resilience Institute, Michigan State University (\$1,000) (2020)

**NSF travel grant** for Plant Cell Dynamics VIII 22nd Plant Biology Symposium (\$405) (2019)

**Bennett Memorial Graduate Fellowship**, The University of Texas at Austin (\$1,000) (2015)

**Travel award**, Graduate School, The University of Texas at Austin (\$500) (2014)

**Summer Research Fellowship**, The University of Texas at Austin (2013 – 2014, summer semester)

**Pre-emptive Fellowship** (for selected 1<sup>st</sup>-year students), The University of Texas at Austin (2009 – 2010)

## HONORS

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**The 2<sup>nd</sup> place prize for Best Poster**, the 2<sup>nd</sup> Plant Cell Atlas Symposium, virtual (2022)

**Nomination for Teaching Assistant Award**, The University of Texas at Austin (2013)

**Honor in Great Teaching Assistant**, School of Biological Sciences, Seoul National University (2007)

## SERVICE, COMMUNITY & PUBLIC OUTREACH

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NASA Open Science Data Repository (NASA-OSDR) Analysis Working Group Workshop, Washington D.C., Nov 2023 ([fully funded invitation by NASA Ames Research Center](#))

Core Member of the Plant Cell Atlas initiative (2021 – present) ([Public web page](#))

Member of the NASA GeneLab Plants Analysis Working Groups (2023 – present)

Organizing Committee of concurrent session of Bioenergy Crop Improvement in Great Lake Bioenergy Research Center Annual Science Meeting, Lake Geneva, WI, May 2022

Organizing Committee of Great Lake Bioenergy Research Center Sustainability Meeting (virtual), Feb 2022

Organizing Committee of Great Lake Bioenergy Research Center Machine Learning/AI Workshop (virtual), Feb 2021

DOE-Bioenergy Research Centers (DOE-BRC) Workshop on Artificial Intelligence and Machine Learning for Biosystems Design ([fully funded invitation by DOE](#)), Washington D.C., Feb 2020

Grant Panel Reviewer: Department of Energy, Small Business Innovation Research/Small Business Technology Transfer (DOE SBIR/STTR), 2020

Hosting Machine Learning Seminar speaker (Dr. Vladimir Glorigijevic from Simons Foundation's Flatiron Institute) at Michigan State University, Dec 2019

Scientific outreach: Family Day Weekend in The University of Texas at Austin, Austin, TX, Oct 2012  
Hosting Plant Biology Graduate Seminar speaker (Dr. Zachary B. Lippman from Cold Spring Harbor Laboratory) at the University of Texas at Austin, Austin, TX, Apr 2012

Journal Peer Reviewer: New Phytologist, The Plant Journal, Communications Biology, Plant Communications, Frontiers in Plant Sciences (serving as a Review Editor), IEEE/ACM Transactions on Computational Biology and Bioinformatics, Genes, Plants, International Journal of Molecular Sciences, Cells, Agronomy

Topic Editor in "Frontiers in Plant Sciences" (2022 – 2023) ([Public web page](#))

## **TEACHING EXPERIENCE**

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Guest lecture, Gene Network Workshop Lecture, Department of Horticulture, Chung-Ang University, Republic of Korea (virtual), Apr 2023

Guest lecture, WGCNA Workshop Lecture, Department of Horticulture, Chung-Ang University, Republic of Korea (virtual), Oct 2022

Guest lecture, ChIP-seq Workshop Lecture, Department of Horticulture, Chung-Ang University, Republic of Korea (virtual), Apr 2022

Guest lecture, PLB801 Foundation of Plant Biology (graduate course), MSU, East Lansing, Oct 2020

Teaching Assistant, BIO395F Genetics (graduate course), The University of Texas at Austin, Austin TX, Spring 2014

Teaching Assistant, BIO325 Genetics, The University of Texas at Austin, Austin, TX 2010 – 2013 (7 long and 2 summer semesters)

Guest lecture, BIO325 Genetics, The University of Texas at Austin, Austin, TX, Oct 2012

Laboratory Instructor, BIO205L Cell & Molecular Biology, The University of Texas at Austin, Austin, TX, Spring 2011

Teaching Assistant, 010.323-003 General Biology Experiment, Seoul National University, Republic of Korea, Fall 2007

## **MENTORING**

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Joshua Deradoorian, GLBRC Research Assistant (2022 – present)

Chloe Hollidays, MSU Undergraduate Student (2022 – 2023)

Xiaohe (Sherry) Sun, GLBRC Summer Undergraduate Research Program (2022 May – Jul)

Rita E. Barr, MSU Undergraduate Student (2021 – 2022)

Sara Knapp, GLBRC Research Assistant (2020 – 2021)

Elizabeth Selby, MSU Research Assistant (2019 – 2020)

Rebecca Selby, MSU Research Assistant (2018 – 2019)

Michael Cadell, UT-Austin Undergraduate Student (2012 – 2014)

Krystal Chi-Shuan Chang, UT-Austin REU (2014)

## **INVITED SEMINARS**

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"Unveiling the Mysteries of Plant Gene Regulation: Harnessing Systems-Level Approaches, Biochemistry, Genetics, and Beyond" Department of Molecular Biosciences and Bioengineering at the University of Hawai'i at Mānoa, Jun 2023

"Network-enabled understanding of gene regulation in response to abiotic stress" Department of Horticulture, Chung-Ang University, Republic of Korea (virtual), Jul 2021

"A temporal hierarchy underpins the transcription factor-DNA interactome of the maize UPR" Tuesday Noon Seminar, MSU-DOE Plant Research Laboratories, East Lansing, MI, Feb 2020

"A systems-level approach to understand transcriptional ER stress response in plants" Plant Resilience Brown Bag, MSU, East Lansing, MI

"Systems-level approach to understand UPR gene regulation in Arabidopsis" Department of Horticulture, Chung-Ang University, Republic of Korea, Jul 2019

"Systems-level approach to understand UPR gene regulation in Arabidopsis" Systems & Synthetic Agrobiotech Center, Gyeongsang National University, Republic of Korea, Jul 2019

"A systems-level approach to discover architecture and dynamics of ER stress gene networks" Tuesday Noon Seminar, MSU-DOE Plant Research Laboratories, East Lansing, MI, Apr 2019

"Genome editing methods in potato" Monsanto Company, Chesterfield, MO, Aug 2017

"Circadian-mediated regulation of morning-phased genes contributes to biomass heterosis in maize hybrids" The Center for Genomics and Systems Biology, New York University, New York, NY, Aug 2015

"Early establishment of growth vigor in maize hybrids by circadian regulators" Plant Luncheon, Department of Molecular Biosciences, The University of Texas at Austin, Austin, TX, Mar 2014

## INVITED/SELECTED CONFERENCE TALKS

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"Unleashing Cellular Destiny: IRE1-Proteasome Signaling Governs Plant ER Proteotoxic Stress" Selected talk, Phytochemical Society of North America (PSNA) Annual Meeting, East Lansing, MI, Jul 2023

"Network-enabled gene discovery pipeline (NEEDLE) for bioenergy research" Invited talk, Great Lake Bioenergy Research Center - Annual Science Meeting, Geneva, WI, May 2023

"A signaling cohort of IRE1 and proteasome system controls cell fate determination in unresolved proteotoxic stress of the plant endoplasmic reticulum" Selected talk, ASPB Midwest Conference, Ames, IA, Apr 2023

"Network-enabled regulatory dissection of the mixed-linkage glucan synthase genes in grasses" Invited talk, Biotechnology and Environmental Technology Symposium organized by Chung-Ang University, Republic of Korea (virtual), Dec 2022

"Transcriptional competition shapes proteotoxic ER stress resolution" Invited talk, 2<sup>nd</sup> International Seminar for the Recent Advances in New Agro Food Research organized by Chung-Ang University, Republic of Korea (virtual), Jul 2022

"Network modeling of dynamic transcriptomes underlying the development of *B. distachyon* and *S. bicolor*" Invited talk, Great Lake Bioenergy Research Center Sustainability Meeting (virtual), Feb 2022

"Network-enabled understanding of gene regulation in response to ER stress" Selected talk, MSU-DOE Plant Research Laboratories Retreat, East Lansing, MI, Oct 2021

"Gene networks in the endoplasmic reticulum stress" Selected talk, Plant Cell Dynamics VIII 22nd Plant Biology Symposium, Penn State University, State College, PA, Jun 2019

### **Professional Societies**

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Member of American Society of Plant biologists (ASPB)

Member of Phytochemical Society of North America (PSNA)

Member of Korean-American Scientists and Engineers Association (KSEA)