







Dae Kwan Ko

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RESEARCH INTERESTS

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

Assistant Professor - Fixed Term (Dec 2022 – present)

Plant Research Laboratory, Department of Plant Biology, Great Lakes Bioenergy Research Center, Michigan State University, USA

Research summary: Investigate how genes respond to environmental stress using a systems-level approach of gene regulatory network modeling and functional characterization in 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 underlying the unfolded protein response in plants (*Arabidopsis* and maize) at systems-level using multi-omics approaches combined with the forward genetics, (2) Characterizing the mechanisms for cell wall biogenesis and differentiation during growth of bioenergy crops at systems-level using gene regulatory network modeling and functional characterization

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

EDUCATION

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

15. **Ko DK**, Brandizzi F (2022). Transcriptional competition shapes proteotoxic ER stress resolution. *Nature Plants* 8, 481-490. ([Highlighted in the PRL Bulletin](#))
14. **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](#))
13. **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.
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.

In submitted

Ko DK, Kim JY, Thibault EA, Brandizzi F. A signaling cohort of IRE1 and proteasome system controls cell fate determination in unresolved proteotoxic stress of the plant endoplasmic reticulum.

In preparation

Ko DK, Kim SJ, Brandizzi F. Network-enabled dissection of conserved and diverged regulation of the mixed-linkage glucan synthase gene in bioenergy crops. The anticipated submission Jan 2023.

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

FUNDING, HONORS AND FELLOWSHIPS

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)

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

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

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

SERVICE, COMMUNITY & PUBLIC OUTREACH

Journal Peer Reviewer: New Phytologist, The Plant Journal, Communications Biology, Plant Communications, Frontiers in Plant Sciences, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Genes, International Journal of Molecular Sciences, Plants

Serving as Topic Editor in "Frontiers in Plant Sciences" (2022 - present) ([Public web page](#))

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

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

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

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

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

Hosting Machine Learning Seminar speaker in Michigan State University (Dec 9th, 2019), Speaker: Dr. Vladimir Glorigijevic (Simons Foundation's Flatiron Institute)

Scientific outreach: Family Day Weekend in The University of Texas at Austin (Oct 27th, 2012)

Hosting Plant Biology Graduate Seminar speaker in The University of Texas at Austin (Apr 30th, 2012), Speaker: Dr. Zachary B. Lippman (Cold Spring Harbor Laboratory)

TEACHING EXPERIENCE

Invited lecture – Genomics workshop for ChIP-seq analyses, Department of Horticulture, Chung-Ang University, Republic of Korea, virtual (April 12, 2022)

Invited lecture – PLB801 Foundation of Plant Biology (graduate course), Michigan State University (Oct 6th, 2020)

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

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

Invited lecture – BIO325 Genetics, The University of Texas at Austin (Oct 11th, 2012)

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

Teaching Assistant, 010.323-003 General Biology Experiment, Seoul National University (Fall semester, 2007)

MENTORING

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

Joshua Deradoorian, GLBRC Research Assistant (2022 – present)

Chloe Hollidays, MSU Undergraduate Student (2022 – present)

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

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)

ORAL PRESENTATIONS

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

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

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

"Network-enabled understanding of gene regulation in response to ER stress" MSU-DOE PRL retreat, MI (2021)

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

"Systems-level approach to understand UPR gene regulation in Arabidopsis" **Invited talk**, Department of Horticulture, Chung-Ang University, Republic of Korea (2019)

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

"Gene networks in the endoplasmic reticulum (ER) stress" Plant Cell Dynamics VIII 22nd Plant Biology Symposium, Penn State University, PA (2019)

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

"Genome editing methods in potato" **Invited talk**, Monsanto Company, MO (2017)

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

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