

# 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? These molecular interactions, called “biological networks”, are crucial for all living organisms to maintain cellular homeostasis. My long-term research goal is to characterize gene networks underlying significant biological pathways and apply the findings to translational research.

## PROFESSIONAL APPOINTMENTS

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**Assistant Professor - Fixed Term** 2022 – Present

MSU-DOE Plant Research Laboratories  
Great Lakes Bioenergy Research Center  
Department of Plant Biology, Michigan State University, MI, USA.

- Hosted by Dr. Federica Brandizzi
- Research summary: Investigating into how genes respond to environmental stresses in both model and non-model plant species using the single-cell genomics technologies.

**Postdoctoral Research Associate** 2017 – 2022

MSU-DOE Plant Research Laboratories  
Great Lakes Bioenergy Research Center, Michigan State University, MI, USA.

- Advisor: Dr. Federica Brandizzi
- Research summary: Investigated gene regulatory networks in plant unfolded protein response using multi-omics approaches. Explored cell wall biogenesis and differentiation in bioenergy crops through gene regulatory network modeling and functional characterization. Aimed to provide a systems-level understanding of these processes.

**Postdoctoral Research Associate** 2016 – 2017

Department of Plant Biology, Michigan State University, MI, USA.

- Advisor: Dr. C. Robin Buell
- Research summary: Identified unintended consequences of genome modification methods in clonally propagated diploid potato, addressing 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, TX, USA. 2009 – 2016

- Department of Molecular Biosciences (Major: Plant Biology)
- Advisor: Dr. 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 maize heterosis using a functional genomics approach covering a broad array of molecular techniques.

**M.S.** Seoul National University, Seoul, South Korea. 2006 – 2008

- Department of Biological Sciences
- Advisor: Dr. 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, Seoul, South Korea. 2000 – 2006

- Department of Crop Science

## PUBLICATIONS

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### ***Published in Peer-Reviewed Articles (17 total: 9 first authorships; 8 co-authorships)***

1. **Ko DK**, Brandizzi F (2024). Dynamics of ER stress-induced gene regulation in plants. ***Nature Reviews Genetics***. DOI: 10.1038/s41576-024-00710-4
2. **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(8), 1333-1346.
  - Featured in Spotlight by Varshney et al. (2023), *Trends in Plant Science* 2023 Dec 14:S1360-1385(23)00388-6.
  - Highlight in MSUTODAY (<https://rb.gy/7oapjq>)
  - Interview video (<https://shorturl.at/kwL36>)
3. 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.
4. **Ko DK**, Brandizzi F (2022). Transcriptional competition shapes proteotoxic ER stress resolution. ***Nature Plants*** 8(5), 481-490.
  - Highlight in MSU-PRL Bulletin (<https://shorturl.at/vAHS6>)
5. **Ko DK**, Brandizzi F (2022). Advanced genomics identifies growth effectors for proteotoxic ER stress recovery in *Arabidopsis thaliana*. ***Communications Biology*** 5, 16.
  - Highlight in MSU-PRL Bulletin (<https://shorturl.at/esuR1>)
  - Interview video (<https://shorturl.at/lpMQ2>)
6. 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.
7. 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.

8. 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.
  - Highlight in MSU-PRL Bulletin (<https://rb.gy/hvc1s4>)
10. **Ko DK**, Brandizzi F (2020). Network-based approaches for understanding gene regulation and function in plants. **The Plant Journal** Oct;104(2):302-317.
  - Featured in the Society for Experimental Biology's Spring Bulletin (<https://shorturl.at/qBQU8>)
11. 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.
12. 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.
13. 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 in Plant Science** 8;10:110.
14. **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.
15. \***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.
16. 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.
17. **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.**

1. **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.
3. **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***

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

1. **Ko DK**, Brandizzi F. Defining transcriptomic dynamics in sorghum in multiple abiotic stresses. The anticipated submission is in March 2024.
2. **Ko DK**, Sun X, Kim SJ, Brandizzi F. Understanding trade-off between mixed-linkage glucan production and growth fitness in *Brachypodium*. The anticipated submission is in April 2024.

## **FUNDING AND FELLOWSHIPS**

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**(Pending) Project GREEN** (Generating Research and Extension to meet Economic and Environmental Needs) **Award**, Michigan State University

- Project title: “Unveiling Abiotic Stress-Inducible Transcriptional Networks in Sorghum through Pooled CRISPR Screening”
- Role: PI
- Budget: \$97,498
- Starting-Ending date: 07/01/2024 – 12/31/2026

**(Pending) NSF Plant Genome Research Program**

- Project title: “Unveiling Systems-Level Mechanisms of Arabidopsis bZIP Transcription Factors for Resilience to Virus Infection”
- Role: Co-PI (PI: Dr. Jeanmarie Verchot)
- Budget: \$1,349,609 (\$711,650 will go to the Ko Lab, if funded)
- Starting-Ending date: 07/01/2024 – 06/30/2028

**DOE-JGI Bioenergy Research Center grant** (Proposal ID: 509513)

- Project title: “The DNA Binding Landscape of Sorghum TFs in Response to Abiotic Stress”
- Description: Supporting DNA synthesis of 142 TF genes and DNA Affinity Purification and sequencing.
- Role: PI
- Award year: 2023

**Project GREEN** (Generating Research and Extension to meet Economic and Environmental Needs) **Award**, Michigan State University

- Project title: “Accessing the Impact of Abiotic Stress on Activities of Gene Regulatory DNA Sequences in Sorghum at Single-cell Resolution”
- Role: PI
- Amount: \$30,000
- Starting-Ending date: 07/01/2022 – 12/31/2023

### DOE-JGI Bioenergy Research Center grant (Proposal ID: 508271)

- Project title: "Transcriptome Analysis Under Abiotic Stress in Sorghum"
- Description: Supporting RNA-seq library construction of 104 samples and next-generation sequencing.
- Role: PI
- Award year: 2021

### MSU Cloud Computing Fellowship

- Description: Supporting a cloud computing system (Microsoft Azure) for the awardee's research projects and providing hands-on training and participating in public activities)
- Starting-Ending date: 11/01/2020 – 04/30/2021
- Public Announcement: <https://rb.gy/z56d0g>

<b>Travel grant</b> , The Plant Resilience Institute, Michigan State University (\$1,000).	2020
<b>NSF travel grant</b> for Plant Cell Dynamics VIII 22nd Plant Biology Symposium (\$405).	2019
<b>Bennett Memorial Graduate Fellowship</b> , The University of Texas at Austin (\$1,000).	2015
<b>Travel award</b> , Graduate School, The University of Texas at Austin (\$500).	2014
<b>Summer Research Fellowship</b> , The University of Texas at Austin.	2013 – 2014
<b>Pre-emptive Fellowship</b> , The University of Texas at Austin.	2009 – 2010
<ul style="list-style-type: none"> <li>• Full scholarship for selected 1<sup>st</sup>-year graduate students</li> </ul>	

### HONORS

The 2 <sup>nd</sup> place prize for Best Poster, the 2 <sup>nd</sup> Plant Cell Atlas Symposium.	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

### LEADERSHIP, SERVICE & PUBLIC OUTREACH

NASA Open Science Data Repository Workshop, Washington D.C. Invited.	Nov 2003
Core Member of the Plant Cell Atlas initiative ( <a href="https://www.plantcellatlas.org">https://www.plantcellatlas.org</a> ).	2021 – Present
Active Member of the NASA GeneLab Plants Analysis Working Group.	2023 – Present
Active Member of the NASA GeneLab Multi-omics Analysis Working Group.	2023 – Present
Organizer for Crop Engineering Community of Practice in GLBRC.	2023 – Present
2024 GLBRC Annual Science Meeting Planning Committee.	2023 – Present
2023 GLBRC Annual Science Meeting Session Organizing Committee.	2022 – 2023
2022 GLBRC Annual Science Meeting Session Organizing Committee.	2021 – 2022
DOE-BRC Workshop on AI-ML for Biosystems Design, Washington D.C. Invited.	Feb 2020
Hosting MSU Department seminar, Speaker: Dr. Vladimir Gligorijevic (Flatiron Institute).	Dec 2019
Family Day Weekend in The University of Texas at Austin, Austin, TX.	Oct 2012
Hosting UT-Austin Department seminar, Speaker: Dr. Zachary B. Lippman (CSHL).	Apr 2012
DOE panel reviewer: DOE SBIR/STTR	2020
JGI panel reviewer: Community Science Program (CSP) Functional Genomics	2024

Journal Peer Reviewer: PNAS, Science Signaling, 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, Data in Brief.

Special issue topic editor: Frontiers in Plant Science (<https://shorturl.at/elpx4>).

## TEACHING EXPERIENCE

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**Teaching Assistant, Department of Molecular Biosciences, The University of Texas at Austin**  
BIO327 Genomics Spring 2016

- Graduate lecture course (30 students)
- Instructor – Dr. Z. Jeffrey Chen
- Responsibilities: Conducted weekly discussion sessions where I delivered concise 10-minute lecture summaries. Evaluated exams containing diverse question formats, including multiple choice, short answer, and essays. Assisted group presentations. Facilitated office hours by appointment.

BIO395 Genetics Spring 2014

- Upper division lecture course (23 students)
- Instructors – Drs. Jeffrey Gross & Z. Jeffrey Chen
- Responsibilities: Conducted weekly discussion sessions where I delivered concise 10-minute lecture summaries. Evaluated exams containing diverse question formats, including multiple choice, short answer, and essays. Facilitated office hours by appointment.

BIO325 Genetics Fall 2010, Spring/Summer 2011, Spring/Summer/Fall 2012, Spring/Fall 2013

- Sophomore lecture course (121, 83, 56, 77, 52, 109, 49, or 35 students in each semester)
- Instructor (one per semester): Drs. Inder M. Saxena, Sibum Sung, and Beverly Finklea
- Responsibilities: Conducted weekly discussion sessions where I delivered concise 10-minute lecture summaries. Evaluated exams containing diverse question formats, including multiple choice, short answer, and essays. Facilitated office hours by appointment.

BIO205L Laboratory Experiments in Cell and Molecular Biology Spring 2011

- Introductory laboratory course (29 students)
- Instructors – Dr. A. William Allen
- Responsibilities: Conducted weekly lab sessions where I delivered concise 10-minute lecture for specified experiments and demonstrated hands-on experiments. Collaborated with the instructor and undergraduate helpers in designing lab experiments and assessed weekly reports, exams, and term papers.

**Teaching Assistant, Department of Biological Sciences, Seoul National University**

010.323-003 General Biology Experiment Fall 2007

- Introductory laboratory course (52 students)
- Responsibilities: Conducted weekly lab sessions where I delivered concise 10-minute lecture for specified experiments and demonstrated hands-on experiments. Assessed weekly reports, exams, and term papers.

### Guest Lectures

Guest speaker for Gene Network Workshop, Chung-Ang Univ., South Korea. Virtual. Apr 2023

Guest speaker for Coexpression Network Workshop, Chung-Ang Univ., South Korea. Virtual. Oct 2022

Guest speaker for ChIP-seq Workshop, Chung-Ang Univ., South Korea. Virtual. Apr 2022

Guest speaker for PLB801 Foundation of Plant Biology (graduate course), MSU. Virtual. Oct 2020

- Instructor: Dr. Jiming Jiang

Guest speaker for BIO325 Genetics, UT-Austin Oct 2012



- Instructor: Dr. Inder M. Saxena

## MENTORING

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Zachary Smith, GLBRC Research Assistant.	2022 – Present
Joshua Deradoorian, GLBRC Research Assistant.	2022 – 2023
Chloe Hollidays, MSU Undergraduate Student.	2022 – 2023
Xiaohe (Sherry) Sun, GLBRC Summer Undergraduate Research Program	May – Jul 2022
• Online Blog describing her experiences with my mentorship ( <a href="https://rb.gy/erul98">https://rb.gy/erul98</a> )	
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.	May – Jun 2014

## SEMINAR ORAL PRESENTATIONS

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Center for Sorghum Improvement 2024 Seminar Series. Virtual.	Mar 2024
• Title: “Network-Enhanced Gene Discovery Pipeline (NEEDLE) for Non-Model Plant Species”	
NASA GeneLab Plants AWG meeting. Virtual.	Nov 2023
• Title: “Network-Enhanced Gene Discovery Pipeline (NEEDLE) for Non-Model Plant Species”	
Biological Research Information Center Webinar Series. Virtual.	Oct 2023
• Title: “Unleashing Cellular Destiny: IRE1-Proteasome Signaling Governs Plant ER Proteotoxic Stress”	
• Record: <a href="https://rb.gy/d6w241">https://rb.gy/d6w241</a>	
Department of Horticulture, Chung-Ang University, South Korea. Virtual.	Jul 2021
• Title: “Network-Enabled Understanding of Gene Regulation in Response to Abiotic Stress”	
Tuesday Noon Seminar, MSU-DOE Plant Research Laboratories, East Lansing, MI.	Feb 2020
• Title: “A Temporal Hierarchy Underpins the Transcription Factor-DNA Interactome of the Maize UPR”	
Plant Resilience Brown Bag, MSU, East Lansing, MI. Virtual.	Dec 2019
• Title: “A Systems-Level Approach to Understand Transcriptional ER Stress Response in Plants”	
Department of Horticulture, Chung-Ang University, South Korea.	Jul 2019
• Title: “Systems-Level Approach to Understand UPR Gene Regulation in Arabidopsis”	
Systems & Synthetic Agrobiotech Center, Gyeongsang National University, South Korea.	Jul 2019
• Title: “Systems-Level Approach to Understand UPR Gene Regulation in Arabidopsis”	
Tuesday Noon Seminar, MSU-DOE Plant Research Laboratories, East Lansing, MI.	Apr 2019
• Title: “Systems-Level Approach to Discover Architecture and Dynamics of ER Stress Gene Networks”	
Monsanto Company, Chesterfield, MO	Aug 2017
• Title: “Genome Editing Methods in Potato”	
Plant Luncheon Seminar Series, The University of Texas at Austin, Austin, TX	Mar 2014
• Title: “Early Establishment of Growth Vigor in Maize Hybrids by Circadian Regulators”	

## INVITED/SELECTED CONFERENCE TALKS

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Phytochemical Society of North America (PSNA) Annual Meeting, East Lansing, MI.	Jul 2023
• Selected talk	

- Title: “Unleashing Cellular Destiny: IRE1-Proteasome Signaling Governs Plant ER Proteotoxic Stress”
- Great Lake Bioenergy Research Center (GLBRC) - Annual Science Meeting, Geneva, WI. May 2023
- Invited talk
  - Title: “Network-Enabled Gene Discovery Pipeline (NEEDLE) for Bioenergy Research”
- American Society of Plant Biologists (ASPB) Midwest Conference, Ames, IA. Apr 2023
- Selected talk
  - Title: “A Signaling Cohort of IRE1 and Proteasome System Controls Cell Fate Determination in Unresolved Proteotoxic Stress of the Plant Endoplasmic Reticulum”
- Biotechnology and Environmental Technology Symposium, South Korea. Virtual. Dec 2022
- Invited talk
  - Title: “Network-Enabled Regulatory Dissection of the Mixed-Linkage Glucan Synthase Genes in Grasses”
- 2<sup>nd</sup> International Seminar for the Recent Advances in New Agro Food Research. Virtual. July 2022
- Invited talk
  - Title: “Transcriptional Competition Shapes Proteotoxic ER Stress Resolution”
- Great Lake Bioenergy Research Center Sustainability Meeting. Virtual. Feb 2022
- Invited talk
  - Title: “Network Modeling of Dynamic Transcriptomes Underlying the Development of *B. distachyon* and *S. bicolor*”
- Plant Cell Dynamics VIII 22<sup>nd</sup> Plant Biology Symposium, State College, PA. Jun 2019
- Selected talk
  - Title: “Gene Networks in the Endoplasmic Reticulum Stress”

## CONFERENCE POSTER PRESENTATION

- Advances in Genome Biology and Technology Agricultural Meeting, Phoenix, AZ. Apr 2024
- Title: “Unraveling Gene Expression Dynamics in Bioenergy Crops Under Environmental Stress Challenges”
- Genomic Science Program Annual Principal Investigator Meeting, Washington D.C. Apr 2023
- Title: “Defining Transcriptomic Dynamics in Sorghum in Multiple Abiotic Stresses”
- International Conference on Arabidopsis Research, Virtual. Jun 2022
- Title: “Transcriptional competition shapes proteotoxic ER stress resolution”
- Plant Cell Atlas Symposium Dec 2022
- Title: “Network-Enabled Regulatory Dissection of the Mixed-Linkage Glucan Synthase Genes in Grasses”
- Joint Genome Institute User Meeting Aug 2022
- Title: “Network-Enabled Dissection of Conserved and Diverged Regulation of the Mixed-Linkage Glucan Synthase Gene in Bioenergy Crops”
- Plant Cell Atlas Symposium Dec 2021
- Title: “Understanding Gene Regulatory Networks Underlying Plant ER Stress: Insights from Bulk Cells to Single Cell”
- Plant Biology Worldwide Summit, Virtual. July 2021
- Title: “Gene-Regulatory Network-Enabled Identification of Effectors Controlling Organ Growth During Recovery from Endoplasmic Reticulum Stress”
- International Conference on Arabidopsis Research, Virtual. Jun 2021
- Title: “Gene-Regulatory Network-Enabled Identification of Effectors Controlling Organ Growth During Recovery from Endoplasmic Reticulum Stress”
- EMBO Workshop - International Plant Systems Biology, Virtual. Apr 2021



- Title: “Gene-Regulatory Network-Enabled Identification of Effectors Controlling Organ Growth During Recovery from Endoplasmic Reticulum Stress”

BRC Workshop: AI and Machine Learning for Biosystems Design, Washington D.C. Feb 2020

- Title: “Systems-Level Analysis of ER Stress Gene Networks in Plants”

59th Annual Maize Genetics Conference, Saint Louis, MO. Mar 2017

- Title: “Expansion of the Wisconsin Diversity Panel to Further Document the Maize Pan-Transcriptome”

CSHL Meeting - Plant Genomes & Biotechnology: From Genes to Networks, Woodbury, NY. Dec 2021

- Title: “Circadian-Mediated Regulation of Morning-Phased Genes Contributes to Biomass Heterosis in Maize Hybrids”

Botany & Plant Biology Joint Congress, Chicago, IL. Jul 2021

- Title: “Functional Analysis of Heat Shock Protein 70 in Flooding-Stressed *Nicotiana tabacum*”

## PROFESSIONAL SOCIETIES

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Active member of the American Society of Plant Biologists (ASPB)

Active member of the Phytochemical Society of North America (PSNA)

Active member of the Korean American Scientists and Engineers Association (KSEA)