

CURRICULUM VITAE

2024 November

Dong-Ha Oh  <https://ohdongha.github.io> ;  [0000-0003-1526-9814](https://orcid.org/0000-0003-1526-9814)

WORKS

- 2022 May – present : **Bioinformatic Data Wrangler**, Computercraft / Contractor ([C]), National Center for Biotechnology Information (**NCBI**), Bethesda, MD
- 2014 Jan – 2022 Apr : Assistant professor-research; Biological Sciences (BS), Louisiana State University (LSU), Baton Rouge, LA (Host faculty: Maheshi Dassanayake)
- 2013 Feb – Dec : Senior post-doctoral researcher; BS, LSU (Advisor: M. Dassanayake)
- 2010 Jun – 2013 Jan : Post-doc. research associate; Plant Biology, Univ. of Illinois at Urbana-Champaign (UIUC), Urbana, IL (Advisors: Hans J. Bohnert & John C. Cheeseman)
- 2005 Apr – 2010 Mar : Visiting scientist; Horticulture and Landscape Architecture, Purdue Univ., West Lafayette, IN (Advisors: H. J. Bohnert & Ray A. Bressan)
- 2003 Sep – 2005 Mar : Post-doc. researcher; Biological Sciences (BS), Korea Advanced Institute of Science and Technology (KAIST), Daejeon, South Korea (Advisor: Won-Il Chung)

EDUCATION

- 2003 Aug : **Ph.D.** Biological Sciences (BS), Korea Advanced Institute of Science and Technology (**KAIST**), Daejeon, S. Korea
Dissertation: Identification of the *cis*-element and transcription factors responsible for the ER-stress response in *Arabidopsis* (Advisor: Won-Il Chung)
- 1998 Feb : M.S. BS, KAIST
Dissertation: Purification and N-terminal sequence analysis of 60 and 31 kDa fruit-specific proteins from Apple (*Malus domestica* cv. Fuji) (Advisor: Won-Il Chung)
- 1996 Feb : B.S. Life Science, KAIST

CURRENT (PERSONAL) RESEARCH / DEVELOPMENT INTERESTS

- Accurate and scalable eukaryotic genome annotation especially for non-model organisms
- Human health-related biological questions explored using comparative genomics frameworks
- Methods and cases to use multiple or pan-genome references for GWAS-like studies
- Multi-genome alignment, multi-genome browser, and orthologs that are scalable and useful
- Comparative genomics resources that assist analysis and annotation of novel genomes by users
- Methods to detect modifications in, and model the evolution of, gene regulatory networks

BIOINFORMATICS RESOURCE CONTRIBUTIONS

- [Eukaryote genome annotation pipeline \(EGAP\)](#) (under continuous refinement): assisting the testing of parameters and tools within the NCBI EGAP, especially for non-model organisms.
- [Ortholog reporting for RefSeq genomes](#) (under continuous expansion): assisting the exploration of effective and scalable ortholog reporting for rapidly growing NCBI RefSeq genome resources.

- [A multi-genome viewer](#) (2024-): assisting the design and development of underlying data, logics, and design for a viewer of multi-genome alignments.
- [Gene Ontology analysis for NCBI RefSeq genomes](#) (2023-): contributed to the development of a pipeline to report Gene Ontology for protein-coding genes in non-model RefSeq genomes.
- [Comparative Genome Viewer \(CGV\)](#) (2023-): contributed to the development, testing, and production per user requests, of pairwise whole genome alignments for CGV and other applications, with methods adjusted based on pairwise MASH distances and genome sizes.
- [Phylogenetically informed profiling \(PiP\)](#) (2022): a method to detect gene sets with lineage(s)-specific modifications among multiple species, with presence and absence of correlations in gene regulation superimposed to the species tree and ranked for their significance.
- [Reference genome of *Phragmites australis* ssp. *australis* \(common reed\)](#) (2021): the reference genome for the invasive *P. australis* and endophyte-responsive RNA-seq tracks
- [Genome annotation of *Sisymbrium irio* v. 0.3](#) (2020): updated *S. irio* gene models based on BUSCO-based training parameters for gene prediction and hints from new RNA-seq data
- [Genome annotation of *Schrenkiella parvula*, v. 2.2](#) (2020): the genome annotation for *S. parvula* v. 2.1 were further polished to v. 2.2 in the Phytozome database (genome ID: 574).
- [CLfinder-OrthNet](#) (2018): a comparative genomics toolbox to (1) encode co-linearity among ortholog pairs in multiple genomes as ortholog networks (OrthNets) and (2) detect OrthNets with a shared evolutionary history using network topology search
- [Ice plant epidermal bladder cell \(EBC\) transcriptome](#) (2015): a cell type-specific reference transcriptome of the extremophyte *Mesembryanthemum crystallinum* (ice plant) EBC and its salt-responses; in collaboration with Bronwyn Barkla, Southern Cross Univ., Australia
- [Genome assembly and annotation of *S. parvula*, v. 2.1](#) (2014): updated genome assembly and annotation for *S. parvula*, based on additional RNA-Seq and comparative analyses

INVITED TALKS AND PRESENTATIONS

- D-H Oh "NCBI Refseq and Orthologs to Support Arthropod Comparative Genomics (tentative)," for the Arthropod Genomics and Genome Biology workshop at the Plant & Animal Genomes conference (PAG) 2025 (scheduled 2025 Jan 12, San Diego, CA, USA)
- D-H Oh "NCBI Comparative Genomics Resources to Explore Arthropod Pest Genomes (tentative)," for the workshop "Beyond the Usual Suspects: Genomic Advances in Non-Model Arthropod Pests" at the PAG 2025 (scheduled 2025 Jan 10, San Diego, CA, USA)
- D-H Oh "NCBI Orthologs: Scalability and Precision supporting Biodiversity Genomics," presented in the session "Beenomes and Badnoms: Advances in applied insect Genomics," Biodiversity Genomics 2024 (2024 October 28, virtual)
- D-H Oh "Visualizing insect genome alignments in NCBI Comparative Genome Viewer (CGV)," workshop presentation, AGSx Virtual Symposium Spring 2024 (2024 May 21, virtual)
- D-H Oh "Comparative genomics of 'extremophyte' Arabidopsis relatives," invited lecture, Biological Sciences at Seoul National Univ. (2022 July 25, virtual)

D-H Oh, KP Kowalski, Q Quach, C Wijesinghege, P Tanford, M Dassanayake, K Clay “What does the *Phragmites australis* genome tell us about its invasiveness?” Joint Aquatic Sciences Meeting (JASM) 2022 (2022 May 16, virtual)

D-H Oh, Y Sun, JR Dinneny, M Dassanayake “Phylogenetically informed Profiling (PiP) to identify gene functions showing lineage(s)-specific modifications,” Arabidopsis Informatics workshop at the PAG 2022 (2022 Jan 10, virtual)

D-H Oh, KP Kowalski, C Wijesinghege, Q Quach, P Tanford, M Dassanayake, K Clay “Novel genome characteristics contribute to the invasiveness of *Phragmites australis* (common reed),” Invasion Genomics 2021 (2021 Aug 10, Lafayette, LA, USA / virtual)

D-H Oh and M Dassanayake “CLfinder-Orthnet: creating comparative genomics framework for closely-related genomes using co-linearity networks,” Next-generation Genome Annotation and Analysis workshop at the PAG 2019 (2019 Jan 12, San Diego)

D-H Oh and M Dassanayake “Systematic detection of orthologous gene groups sharing an evolutionary history, using network topology,” Systems Genomics workshop at the PAG 2019 (2019 Jan 15, San Diego)

D-H Oh and M Dassanayake “CLfinder-OrthNet: encoding evolutionary history of a gene locus as network topology,” Digital Tools and Resources workshop at the PAG 2019 (2019 Jan 16, San Diego, CA)

D-H Oh, “Landscape of gene transposition-duplication events in the Brassicaceae family and their implications in adaptation,” invited lecture, Biology at Duke Univ. (2017 Nov 17, Durham, NC)

D-H Oh, “Genome structures and transcriptomes signify evolutionary trajectories for multi-ion tolerance and niche adaptation in *Schrenkiella parvula* (formerly *Thellungiella parvula*),” Gene Expression Analysis workshop at the PAG 2014 (2014 Jan 14, San Diego)

D-H Oh, “Genome evolution of crucifers (Brassicaceae): insights and questions,” invited lecture for BMB/CDIB seminar series, Biological Sciences at LSU (2013 Nov 4, Baton Rouge, LA)

D-H Oh, “Evolution of crucifer genomes: insights and questions from comparative studies,” invited lecture, Chinese Academy of Tropical Agricultural Sciences (2013 Oct 14, Haikou, China)

D-H Oh, “Riddles in plant genome evolution: comparative studies on halophyte crucifer genomes,” invited lecture, Plant Biology at UIUC (2012, Sep 12, Urbana, IL)

D-H Oh, “Life in extreme environments: learning from crucifer genomes,” invited lecture, Gregor Mendel Institute (2012, Feb 13, Vienna, Austria)

D-H Oh, M Dassanayake, H Hong, A Kropornicka, JM Cheeseman and HJ Bohnert. “Neofunctionalization among tandem duplicated stress-relevant genes in *Thellungiella* species,” Abiotic Stress workshop at the PAG 2012 (2012 Jan 15, San Diego)

PUBLICATIONS ([Google Scholar](#) all time citations: 2417 h-index: 26; i10-index: 42)

(**bold** if served as a lead or a corresponding author *equal contribution; #corresponding author)

T Goldfarb*, VK Kodali*, S Pujar, V Brover, B Robbertse, CM Farrell, D-H Oh, A Astashyn, O Ermolaeva, D Haddad, W Hlavina, J Hoffman, JD Jackson, VS Joardar, D Kristensen, P Masterson,

- KM McGarvey, R McVeigh, E Mozes, MR Murphy, SS Schafer, A Souvorov, B Spurrier, PK Strope, H Sun, AR Vatsan, C Wallin, D Webb, JR Brister, E Hatcher, A Kimchi, W Klimke, A Marchler-Bauer, KD Pruitt, F Thibaud-Nissen, TD Murphy (2024) NCBI RefSeq: reference sequence standards through 25 years of curation and annotation. *Nucleic Acids Res* ([doi:10.1093/nar/gkae1038](https://doi.org/10.1093/nar/gkae1038))
- SH Rangwala[#], DV Rudnev, VV Ananiev, D-H Oh, A Asztalos, B Benica, EA Borodin, N Bouk, VI Evgeniev, VK Kodali, V Lotov, E Mozes, MV Omelchenko, S Savkina, E Sukharnikov, J Virothaisakun, TD Murphy, KD Pruitt, VA Schneider (2024) The NCBI Comparative Genome Viewer (CGV) is an interactive visualization tool for the analysis of whole-genome eukaryotic alignments. *PLoS Biol* 22:e3002405 ([doi:10.1371/journal.pbio.3002405](https://doi.org/10.1371/journal.pbio.3002405))
- K-N Tran^{*}, P Pantha^{*}, G Wang^{*}, N Kumar^{*}, C Wijesinghege, D-H Oh, S Wimalagunasekara, N Duppen, H Li, H Hong, JC Johnson, R Kelt, MG Matherne, TT Nguyen, JR Garcia, A Clement, D Tran, C Crain, P Adhikari, Y Zhang, M Foroozani, G Sessa, JC Larkin, AP Smith, D Longstreth, P Finnegan, C Testerink, S Barak, M Dassanayake[#] (2023) Balancing growth amidst salt stress - lifestyle perspectives from the extremophyte model *Schrenkiella parvula*. *Plant J* 116:921-941 ([doi:10.1111/tpj.16396](https://doi.org/10.1111/tpj.16396))
- X Huang^{*}, H Tian^{*}, J Park^{*}, D-H Oh, J Hu, R Zentella, H Qiao, M Dassanayake, T-P Sun[#] (2023) The master growth regulator DELLA binding to histone H2A is essential for DELLA-mediated global transcription regulation. *Nat Plants* 9:1291–1305 ([doi:10.1038/s41477-023-01477-y](https://doi.org/10.1038/s41477-023-01477-y))
- P Pantha, D-H Oh, D Longstreth, M Dassanayake[#] (2023) Living with high potassium: a balance between nutrient acquisition and stress signaling during K-induced salt stress. *Plant Physiol* 191:1102-1121 ([doi:10.1093/plphys/kiac564](https://doi.org/10.1093/plphys/kiac564))
- DL Lindsay, J Freeland, P Gong, X Guan, NE Harms, KP Kowalski, RF Lance, D-H Oh, BT Sartain, DL Wendell (2022) Genetic analysis of North American *Phragmites australis* guides management approaches. *Aquat Bot* 184:103589 ([doi:10.1016/j.aquabot.2022.103589](https://doi.org/10.1016/j.aquabot.2022.103589))
- G Eshel^{*}, N Duppen^{*}, G Wang, D-H Oh, Y Kazachkova, P Herzyk, A Amtmann, M Gordon, V Chalifa-Caspi, MO Arland, S Bar-David, A Marshall-Colon, M Dassanayake[#], S Barak[#] (2022) Positive selection and heat-response transcriptomes reveal adaptive features of the Brassicaceae desert model, *Anastatica hierochuntica*. *New Phytol* 236:1006-1026 ([doi:10.1111/nph.18411](https://doi.org/10.1111/nph.18411))
- Y Sun^{*}, D-H Oh^{*}, L Duan, P Ramachandran, A Bartlett, K-N Tran, G Wang, M Dassanayake, JR Dinneny[#] (2022), Divergence in a stress regulatory network underlies differential growth control. *Nat Plants* 8:549-560 ([doi:10.1038/s41477-022-01139-5](https://doi.org/10.1038/s41477-022-01139-5))
- D-H Oh[#], KP Kowalski[#], C Wijesinghege, Q Quach, P Tanford, M Dassanayake[#], K Clay[#] (2022), Novel genome characteristics contribute to the invasiveness of *Phragmites australis* (common reed). *Mol Ecol* 31:1142-1159 ([doi:10.1111/mec.16293](https://doi.org/10.1111/mec.16293))
- K-N Tran, G Wang, D-H Oh, JC Larkin, AP Smith, M Dassanayake[#] (2021) Multiple paths lead to salt tolerance - pre-adaptation vs dynamic responses from two closely related extremophytes. *bioRxiv* ([doi:10.1101/2021.10.23.465591](https://doi.org/10.1101/2021.10.23.465591))

- G Wang G, SF DiTusa, D-H Oh, AD Herrmann, MA O'Neill, AP Smith, M Dassanayake[#] (2021), Cross species multi-omics reveals cell wall sequestration and elevated global transcript abundance as mechanisms of boron tolerance in plants. *New Phytol* 230:1985-2000 ([doi:10.1111/nph.17295](https://doi.org/10.1111/nph.17295))
- P Pantha, S Chalivendra, D-H Oh, B Elder, M Dassanayake[#] (2021), A tale of two transcriptomic responses in agricultural pests via host defenses and viral replication. *Int J Mol Sci* 22:3568 ([doi:10.3390/ijms22073568](https://doi.org/10.3390/ijms22073568))
- G Wang, D-H Oh, M Dassanayake[#] (2020), GOMCL: a tool to cluster Gene Ontology based functions. *BMC Bioinformatics* 21:139 ([doi:10.1186/s12859-020-3447-4](https://doi.org/10.1186/s12859-020-3447-4))
- SY Park, JH Choi, D-H Oh, JC Johnson, M Dassanayake, DH Jeong, MH Oh[#] (2020) Genome-wide analysis of brassinosteroid responsive small RNAs in *Arabidopsis thaliana*. *Genes Genomics* 42:957-969.
- M Foroozani, S Zahraeifard, D-H Oh, G Wang, M Dassanayake[#], AP Smith[#] (2020), Low-phosphate chromatin dynamics predict a cell wall remodeling network in rice shoots. *Plant Physiol* 182:1494-1509 ([doi:10.1104/pp.19.01153](https://doi.org/10.1104/pp.19.01153))
- MV Cruz, GM Mori, D-H Oh, M Dassanayake, MI Zucchi, RS Oliveira, AP de Souza[#] (2020), Molecular responses to freshwater limitation in the mangrove tree *Avicennia germinans* (Acanthaceae). *Mol Ecol* 29:344-362.
- MV Cruz, GM Mori, CS Müller, CC da Silva, D-H Oh, M Dassanayake, MI Zucchi, RS Oliveira, AP de Souza[#] (2019), Local adaptation of a dominant coastal tree to freshwater availability and solar radiation suggested by genomic and ecophysiological approaches. *Sci Rep* 9:19936.
- D-H Oh[#] and M Dassanayake[#] (2019), Landscape of gene transposition-duplication within the Brassicaceae family. *DNA Res* 26:21-36 ([doi:10.1093/dnares/dsy035](https://doi.org/10.1093/dnares/dsy035))
- G Wang, P Pantha, K-N Tran, D-H Oh[#], M Dassanayake[#] (2019), Plant growth and agrobacterium-mediated floral-dip transformation of the extremophyte *Schrenkiella parvula*. *J Vis Exp* 143:e58544.
- Q Zhang, D-H Oh, SF DiTusa, MV RamanaRao, N Baisakh, M Dassanayake[#], AP Smith[#] (2018), Rice nucleosome patterns undergo remodeling coincident with stress-induced gene expression. *BMC Genomics* 19:97.
- S Shrestha, D-H Oh, JK McKowen, M Dassanayake, CM Hart[#] (2018), 4C-seq characterization of Drosophila BEAF binding regions provides evidence for highly variable long-distance interactions between active chromatin. *PLoS One* 13:e0203843.
- S Zahraeifard, M Foroozani, A Sepehri, D-H Oh, G Wang, V Mangu, B Chen, N Baisakh, M Dassanayake, AP Smith[#] (2018), Rice H2A.Z negatively regulates genes responsive to nutrient starvation but promotes expression of key housekeeping genes. *J Exp Bot* 69:4907-4919.
- R Wu, L Duan, JL Pruneda-Paz, D-H Oh, M Pound, S Kay, JR Dinneny[#] (2018), The 6xABRE synthetic promoter enables the spatiotemporal analysis of ABA-mediated transcriptional regulation. *Plant Physiol* 177:1650-1665.
- B Shrestha, D-H Oh, M Dassanayake, JH Ham[#] (2018), Analysis of genome sequence variations among three us rice varieties showing differential quantitative disease resistance to bacterial panicle blight and sheath blight. *Int J Genom Data Min IJGD*-122.

- J Park, D-H Oh, M Dassanayake, KT Nguyen, J Ogas, G Choi, T-P Sun[#] (2017), Gibberellin signaling requires chromatin remodeler pickle to promote vegetative growth and phase. *Plant Physiol* 173: 1463–1474 ([doi:10.1104/pp.16.01471](https://doi.org/10.1104/pp.16.01471))
- B Lambert, M Dassanayake[#], D-H Oh, SB Garrett, SY Lee, GS Pettis[#] (2016), A novel phase variant of the cholera pathogen shows stress-adaptive cryptic transcriptomic signatures. *BMC Genomics* 17:914.
- A Ali, N Raddatz, R Aman, S Kim, HC Park, M Jan, D Baek, IU Khan, D-H Oh, SY Lee, RA Bressan, KW Lee, A Maggio, JM Pardo, HJ Bohnert, DJ Yun[#] (2016), A single amino acid substitution in the sodium transporter HKT1 associated with plant salt tolerance. *Plant Physiol* 171: 2112–2126.
- D-H Oh, BJ Barkla[#], R Vera-Estrella, O Pantoja, SY Lee, HJ Bohnert, M Dassanayake[#] (2015), Cell type-specific responses to salinity - the epidermal bladder cell transcriptome of *Mesembryanthemum crystallinum*. *New Phytol* 207:627–644 ([doi:10.1111/nph.13414](https://doi.org/10.1111/nph.13414))
- Q Wang, CM Nowak, A Korde, D-H Oh, MDassanayake, D Donze[#] (2014), Compromised RNA Polymerase III complex assembly leads to local alterations of intergenic RNA Polymerase II transcription in *Saccharomyces cerevisiae*. *BMC Biol* 12:89.
- D-H Oh^{*}, H Hong^{*}, SYLee, D-J Yun, HJ Bohnert, M Dassanayake[#] (2014), Genome structures and transcriptomes signify niche adaptation for the multi-ion tolerant extremophyte *Schrenkiella parvula*. *Plant Physiol* 164:2123–2138 ([doi:10.1104/pp.113.233551](https://doi.org/10.1104/pp.113.233551))
- G Batelli, D-H Oh, MP D'Urzo, F Orsini, M Dassanayake, JK Zhu, HJ Bohnert, RA Bressan, A Maggio[#] (2014), Using Arabidopsis-related model species (ARMS): growth, genetic transformation, and comparative genomics. *Methods Mol Biol* 1062:27–51.
- Jl Kim, D Baek, HC Park, HJ Chun, D-H Oh, MK Lee, JY Cha, WY Kim, MC Kim, WC Chung, HJ Bohnert, SY Lee, RA Bressan, SW Lee, DJ Yun[#] (2013), Overexpression of Arabidopsis YUCCA6 in potato results in high-auxin developmental phenotypes and enhanced resistance to water deficit. *Mol Plant* 6:337–349.
- D-H Oh^{*}, M Dassanayake^{*}, HJ Bohnert and JM Cheeseman[#] (2012), Life in the extreme: lessons from genomics. *Genome Biol* 13:241 ([doi:10.1186/gb4003](https://doi.org/10.1186/gb4003))
- RA Bressan, HC Park, F Orsini, D-H Oh, M Dassanayake, G Inan, DJ Yun, HJ Bohnert, A Maggio[#] (2013), Biotechnology for mechanisms that counteract salt stress in extremophile species: a genome-based view. *Plant Biotechnol Rep* 7:27–37
- H-J Wu^{*}, Z Zhang^{*}, J-Y Wang^{*}, D-H Oh^{*}, M Dassanayake^{*}, B Liu^{*}, Q Huang^{*}, HX Sun, R Xia, Y Wu, Y Wang, Z Yang, Y Liu, W Zhang, H Zhang, J Chu, C Yan, S Fang, J Zhang, Y Wang, F Zhang, G Wang, SY Lee, JM Cheeseman, B Yang, B Li, J Min, L Yang, J Wang, C Chu, SY Chen, HJ Bohnert, JK Zhu, XJ Wang, Q Xie (2012), Insights into salt tolerance from the genome of *Thellungiella salsuginea*. *Proc Natl Acad Sci USA* 109:12219–12224 ([doi:10.1073/pnas.1209954109](https://doi.org/10.1073/pnas.1209954109))
- Z Ali^{*}, A Ali^{*}, HC Park^{*}, D-H Oh^{*}, R Aman, A Kropornicka, H Hong, RA Bressan, HJ Bohnert, W-Y Kim, SY Lee, and D-J Yun[#] (2012), TsHKT1;2, a HKT1 homolog from the extremophile *Arabidopsis*-relative *Thellungiella salsuginea*, shows K⁺-specificity in the presence of NaCl. *Plant Physiol* 158:1463–1474. ([doi:10.1104/pp.111.193110](https://doi.org/10.1104/pp.111.193110))

- M Dassanayake, D-H Oh, D-J Yun, RA Bressan, JM Cheeseman, and HJ Bohnert. "The Scope of Things to Come - New Paradigms in Biotechnology" in: Plant biotechnology 2010: prospects for the 21st Century, eds. PM Hasegawa and A Altman, Elsevier, Amsterdam, Netherland (2011) (Book chapter).
- M Dassanayake^{**}, D-H Oh^{**}, JS Haas, A Hernandez, H Hong, S Ali, D-J Yun[#], RA Bressan, J-K Zhu, HJ Bohnert and JM Cheeseman (2011), The genome of the extremophile crucifer *Thellungiella parvula*. *Nat Genet* 43:913-918 ([doi:10.1038/ng.889](https://doi.org/10.1038/ng.889))
- MH Oh, J Sun, D-H Oh, RE Zielinski, SD Clouse, SC Huber[#] (2011), Enhancing Arabidopsis leaf growth by engineering the BRASSINOSTEROID INSENSITIVE1 receptor kinase. *Plant Physiol* 157:120-131.
- W Choi, D Baek, D-H Oh, J Park, H Hong, WY Kim, HJ Bohnert, RA Bressan, HC Park, DJ Yun (2011), NKS1, Na⁺- and K⁺-sensitive 1, regulates ion homeostasis in an SOS-independent pathway in Arabidopsis. *Phytochemistry* 72:330-336.
- M Dassanayake, D-H Oh, H Hong, HJ Bohnert, and JM Cheeseman (2011), Transcription strength and halophytic lifestyle. *Trends Plant Sci*16:1-3.
- D-H Oh^{*}, M Dassanayake^{*}, JS Haas, A Kropornicka, C Wright, MP D'Urzo, H Hong, S Ali, A Hernandez, GM Lambert, G Inan, DW Galbraith, RA Bressan, D-J Yun, J-K Zhu, JM Cheeseman, and HJ Bohnert[#] (2010), Genome structures and halophyte-specific gene expression of the extremophile *Thellungiella parvula* in comparison with *Thellungiella salsuginea* (*Thellungiella halophila*) and Arabidopsis. *Plant Physiol* 154:1040-1052 ([doi:10.1104/pp.110.163923](https://doi.org/10.1104/pp.110.163923))
- F Orsini, MP D'Urzo, G Inan, S Serra, D-H Oh, MV Mickelbart, F Consiglio, X Li, JC Jeong, D-J Yun, HJ Bohnert, RA Bressan, and A Maggio[#] (2010), A comparative study of salt tolerance parameters in 11 wild relatives of *Arabidopsis thaliana*. *J Exp Bot* 61:3787-3798.
- D-H Oh, SY Lee, RA Bressan, D-J Yun, and HJ Bohnert[#] (2010), Intracellular consequences of SOS1 deficiency during salt stress. *J Exp Bot* 61:1205-1213 ([doi:10.1093/jxb/erp391](https://doi.org/10.1093/jxb/erp391))
- D-H Oh, A Zahir, DJ Yun, RA Bressan, HJ Bohnert[#] (2009), SOS1 and halophytism. *Plant Signal Behav* 4:1081-1083.
- D-H Oh, E Leidi, Q Zhang, S-M Hwang, Y Li, FJ Quintero, X Jiang, MP D'Urzo, SY Lee, Y Zhao, JD Bahk, RA Bressan, D-J Yun, JM Pardo, and HJ Bohnert[#] (2009), Loss of halophytism by interference with SOS1 expression. *Plant Physiol* 151:210-222 ([doi:10.1104/pp.109.137802](https://doi.org/10.1104/pp.109.137802))
- D-H Oh, Q Gong, A Ulanov, Q Zhang, Y Li, W Ma, D-J Yun, RA Bressan, and HJ Bohnert[#] (2007), Sodium stress in the halophyte *Thellungiella halophila* and transcriptional changes in a *thsos1*-RNA interference line. *J Integr Plant Biol* 49:1484-1496
- SJ Noh, CS Kwon, D-H Oh, JS Moon, Chung WI[#] (2003), Expression of an evolutionarily distinct novel BiP gene during the unfolded protein response in *Arabidopsis thaliana*. *Gene* 311:81-91.
- D-H Oh, CS Kwon, H Sano, WI Chung[#], N Koizumi[#] (2003), Conservation between animals and plants of the cis-acting element involved in the unfolded protein response. *Biochem Biophys Res Commun* 301:225-230.

D-H Oh, KJ Song, YU Shin, WI Chung[#] (2000), Isolation of a cDNA encoding a 31-kDa, pathogenesis-related 5/thaumatin-like (PR5/TL) protein abundantly expressed in apple fruit (*Malus domestica* cv. Fuji). *Biosci Biotechnol Biochem* 64:355-362.

RESEARCH GRANTS (amount awarded; PI; my role) *roles transferred to a colleague by 2022 May

- 2023 – 2026 : DOE-BER; Using an evolutionary perspective to discover and predict stress-associated gene functions in the Brassicaceae family (\$2.7M; José Dinneny, Stanford; Co-PI*)
- 2022 – 2025 : USDA-NIFA; Deciphering the role of the quorum-sensing master regulator, *qsmR*, in social behaviors of *Burkholderia glumae* for bacterial pathogenesis in rice plants (\$682,232; Jong Hyun Ham, LSU; Collaborator*)
- 2022 – 2023: DOE-JGI; Resequencing nuclear genome, mitochondrial genome and transcriptome for Brassicaceae species to facilitate stress tolerance research (Sequencing and assembly services; Song Li, Virginia Tech.; Co-PI*)
- 2020 – 2022 : COPIA Foundation, Israel; Mining seagrasses to develop salt-tolerant crops, as an international collaboration with Ben-Gurion Univ. of the Negev (\$200,000 to LSU; Simon Barak, Ben Gurion Univ., Israel; Key personnel*)
- 2019 – 2022 : DOE-BER; Discovering innovations in stress tolerance through comparative gene regulatory network analysis and cell-type specific expression maps (\$2.2M; José Dinneny, Stanford; Co-PI*)
- 2019 – 2023 : NSF-BSF-EDGE; Developing functional genomics tools for emerging extremophyte models (\$1,000,000; Maheshi Dassanayake, LSU; Co-PI*)
- 2019 – 2022 : USGS- Great Lakes Coastal Wetland Restoration program, Cooperative Ecosystem Studies Units (CESU) G19AC0046; The *Phragmites australis* genome project (Not determined; Kurt Kowalski, U.S. Geological Survey; Key personnel*)
- 2017 – 2020 : USDA-NIFA; Improving the quality of rice by identifying targets to restrict arsenic accumulation (\$500,000; Aaron P. Smith, LSU; Key personnel)
- 2016 – 2020 : NSF-MCB; Is abiotic stress tolerance achieved by network restructuring or invention of new genetic modules? (\$900,000; Maheshi Dassanayake, LSU; Co-PI)
- 2015 – 2018 : Theragen BIO, S. Korea; Consultation on the tartary buckwheat genome project (\$95,000; M. Dassanayake; Key personnel)
- 2013 – 2017 : RDA-Biogreen 21, S. Korea; Genomic variations for stress adaptation in extremophyte wild-relatives of crops (\$300,000; Sang-Yul Lee, Gyeongsang National Univ., S. Korea; International collaborator)

TEACHING and MENTORING

Teaching and consultation activities

Guest instructor

- 2019 Fall : BIOL7800 Comparative Genomics, Biological Sciences, LSU
- 2018 Fall : BIOL3400 Evolution, Biological Sciences, LSU
- 2017 Spring : BIOL7061 Plant growth and development, Biological Sciences, LSU
- 2016 Fall : BIOL7800 Genomics, Biological Sciences, LSU

- 2014 Fall : BIOL7800 Genomics, Biological Sciences, LSU
- 2012 Fall : IB199 Undergraduate Open Seminar, Integrative Biology, UIUC, Urbana, IL

Workshops organized and consultations

- 2021 May 27 - Jul 7 : “Comparative RNA-seq bootcamp,” a 6-week workshop for research groups in LSU and McMaster Univ. Canada, as an NSF EDGE-funded outreach activity
- 2016 Apr 7 : “Using clustering to understand a 2-factor RNA-seq data: a case study,” mini-workshop for plant research groups in Biological Sciences, LSU
- 2012 Apr 19 : “On Cassava genome assembly,” consultation for Drs. Pinghua Li and Binxiao Feng at Chinese Cassava Genomics and Biotechnology Consortium
- 2011 Jun 1-2 : “On genome and transcriptome assembly, annotation and analysis using next-gen. sequencing tools,” workshop for Plant Biology and Animal Biology, UIUC

Undergraduate teaching fellowship

- Fellow of the National Academies Summer Institute on Undergraduate Education, 2015

Mentoring as a doctoral advisory committee member

- 2016 – 2022* : Chathura Wijesinghe (PhD advisee of Maheshi Dassanayake, LSU); * role transferred to a colleague on 2022 May.
- 2016 – 2021 : Kieu-Nga Tran (same as above)
- 2015 – 2021 : Pramod Pantha (same as above)
- 2014 – 2020 : Guannan Wang (same as above)
- 2014 – 2016 : Teresa DeLeon (PhD advisee of Prasanta Subudhi, AgCenter, LSU)

Mentoring as part of a collaboration

At LSU (PI in parentheses; Biological Sciences unless indicated otherwise)

- Thu T Nguyen (Maheshi Dassanayake): genome editing in extremophyte crucifers
- Samadhi Wimalagunasekara (M Dassanayake): salt stress and flowering interactions
- Matthew Vandal (A Smith): functions of metallothioneins in plant copper nutrition
- Jifeng Li (A Smith): comparative omics analyses of plant Li⁺ toxicity responses
- Prava A Pantha (John C Larkin): comparative genomics of leaf development
- Jifeng Li (Aaron Smith): bulk segregation QTL-Seq for reduced rice seed arsenic content
- Maryam Foroozani (Aaron Smith): rice ChIP-Seq and interpretation
- Sarah Zahraeifard (Aaron Smith): rice RNA-Seq analysis
- Shraddha Shrestha (Craig Hart): *Drosophila* HiC-Seq analysis
- Qi Zhang (Aaron Smith): rice MNase-Seq analysis
- Qing Wang (David Donze): yeast RNA-Seq analysis
- Bliss Lambert (Gregg Pettis) *Vibrio cholerae* RNA-Seq analysis

Outside of the LSU campus (PI and affiliation in parentheses)

- Prashanth Ramachandran (José Dinneny, Plant Biology, Stanford Univ., Palo Alto, CA): on multi-species DAP-seq analysis to identify AREB/ABF binding events
- Michelle Arland (Gidon Winters and Simon Barak, Desert Research, Ben-Gurion Univ. of the Negev, Israel): interspecies comparative analyses of seagrass transcriptomes
- Haoran Jia and Solmaz Irani (Elizabeth Weretilnyk, Biology, McMaster Univ., Hamilton, ON,

- Canada): comparison of extremophyte responses to salt stress and phosphate deficiency
- Ying Sun (former PhD advisee of José Dinneny, Stanford): interspecies comparative DAP-Seq and RNA-Seq on Brassicaceae species
- Mariana Vargas Cruz (Anete Pereira de Souza, Plant Biology, Univ. Est de Campinas, Brazil): on interspecies comparative analyses of mangrove tree transcriptomes
- Jeongmoo Park (former post-doc. advisee of Tai-Ping Sun, Biology, Duke Univ., Durham, NC); Arabidopsis RNA-Seq and ChIP-Seq analyses
- Gil Echel (former PhD advisee of Simon Barak, Desert Research, BGU, Israel); transcriptome assembly, multi-factor RNA-Seq, and phylogenomic analyses among extremophyte crucifers
- Aktar Ali and Zahir Ali (former PhD advisees of Dae-Jin Yun, Applied life sciences, Gyeongsang National Univ./GNU, Jinju, S. Korea); comparative analyses of extremophyte HKT1 homologues
- Hyewon Hong (former PhD advisees of D.-J. Yun, Applied life sciences, GNU, S. Korea); interspecies comparative RNA-Seq on *Schrenkiella parvula* and Arabidopsis

Undergraduate research mentoring (resulted in a publication/conference presentation)

Within the LSU Biological Sciences

- John C Jonson; plant small RNA regulations in response to the brassinosteroid hormone
- Kieu-Nga T Tran, John C Jonson, and Stephanie Presedo; flowering habits of extremophytes
- Matt Johnson; identification of deep paralogs based on the arrangement of short motifs
- Madison Boudreaux; ammonium toxicity-responses of *S. parvula*
- Ross Kelt; halotropism of root growth of *S. parvula*

Outside of the LSU campus

- Anna Kropornicka - former undergraduate student at Plant Biology, UIUC, IL; comparative analysis of HKT1 homologous in extremophyte plant species

OTHER PROFESSIONAL ACTIVITIES

Professional training received

- 2022 Oct 3-5: “Nextflow and nf-core” training
- 2022 Jul 26-28: “Adopting and Adapting Agility” training

Invited reviewer of scientific manuscripts, grants, and applications

- [Invited reviewer](#) (numbers of manuscripts reviewed) for: *Nature Genetics* (4 manuscripts; 8 including revisions), *Journal of Experimental Botany* (5), *BMC Genomics* (3), *Genes & Genomics* (2), *Molecular Plant* (2), *New Phytologist* (2), *Physiologia Plantarum* (2), *Plant Physiology* (2), *Australian Journal of Botany* (1), *BMC Plant Biology* (1), *Bioinformatics* (1), *DNA Research* (1), *Journal of Plant biology* (1), *Journal of Plant Physiology* (1), *Molecular Ecology* (1), *Plant Cell Reports* (1), *Plant Molecular Biology Reporter* (1), *Plant Pathology Journal* (1), and *PLoS ONE* (1)
- Review editor for *Frontiers in Plant Sciences* (2016 Sep – 2022 Mar; 17 reviewed, 11 published)
- Invited as a reviewer for NSF: 2017, 2020, 2021 (2 programs), and 2022 (2 programs)
- Served as a reviewer for NSF: 2020 and 2021