



CURRICULUM VITAE

December, 2021

Dong-Ha Oh

Google Scholar: <https://scholar.google.com/citations?user=nueqysEAAAAJ>

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PROFESSIONAL AND EDUCATIONAL BACKGROUND

- 2014 Jan – Present : 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, University 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 University, 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)

EDUCATIONAL BACKGROUND

- 2003 Aug : **Ph.D.** Biological Sciences (BS), Korea Advanced Institute of Science and Technology (KAIST), Daejeon, South 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

RESEARCH GRANTS

Awarded (amount awarded; PI; my role)

- 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 University 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 (\$2,200,000; Jose Dinneny, Stanford Univ., CA; Co-Investigator)

- 2019 – 2022 : NSF-BSF-EDGE; Developing Functional Genomics Tools for Emerging Extremophyte Models (\$1,000,000; Maheshi Dassanayake, LSU; Co-PI)
- 2019 – 2021 : 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 – 2019 : 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, South Korea; Consultation on the tartary buckwheat genome project (\$95,000; M. Dassanayake; Key personnel)
- 2013 – 2017 : RDA-Biogreen 21, South Korea; Genomic variations for stress adaptation in extremophyte wild-relatives of crops (\$300,000; Sang-Yul Lee, Gyeongsang National University, S. Korea; International collaborator)

Pending and in preparation (current status; PI; my role)

- 2023 – : The invasive European Frog-bit (*Hydrocharis morsus-ranae* L.) genome project (Pending; Kurt Kowalski, U.S. Geological Survey; Key personnel)

PUBLICATIONS ([Google scholar](#) all time citations: **2472**; h-index: **22**; i10-index: **30**)

Publications a first/corresponding author (*equal contribution; #corresponding author)

- Y Sun*, **D-H Oh***, L Duan, P Ramachandran, A Bartlett, M Dassanayake, JR Dinneny# (2021), Divergence in a stress regulatory network underlies differential growth control. *bioRxiv* ([doi:10.1101/2020.11.18.349449](#))
- D-H Oh**#, KP Kowalski#, C Wijesinghege, Q Quach, P Tanford, M Dassanayake#, K Clay# (2021), Novel genome characteristics contribute to the invasiveness of *Phragmites australis* (common reed). *Mol Ecol* ([doi:10.1111/mec.16293](#))
- 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](#))
- 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.
- 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](#))
- 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](#))
- 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))
- 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))
- 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))
- 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))
- 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
- 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.

Publications as a co-author (*equal contribution; #corresponding author)

- K-N Tran*, P Pantha*, G Wang*, N Kumar*, C Wijesinghege, **D-H Oh**, N Duppen, H Li, H Hong, JC Johnson, R Kelt, MG Matherne, 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[#] (2021) Balancing growth amidst salinity stress-lifestyle perspectives from the extremophyte model *Schrenkiella parvula*. *bioRxiv* ([doi:10.1101/2021.08.27.457575](https://doi.org/10.1101/2021.08.27.457575))
- P Pantha, **D-H Oh**, D Longstreth, M Dassanayake[#] (2021) Living with high potassium: an asset or a hindrance. *bioRxiv* ([doi:10.1101/2021.07.01.450778](https://doi.org/10.1101/2021.07.01.450778))
- 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[#] (2021) Positive selection and heat-response transcriptomes reveal adaptive features of the Arabidopsis desert relative, *Anastatica hierochuntica*. *bioRxiv* ([doi:10.1101/2021.05.23.445339](https://doi.org/10.1101/2021.05.23.445339))
- 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 Elderd, 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))
- 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.
- 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))
- 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.
- 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.
- 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.
- 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.
- J Park, **D-H Oh**, M Dassanayake, KT Nguyen, J Ogas, G Choi, T 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.
- 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.
- 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.
- JI 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.
- 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
- 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.

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).

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.

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.

BIOINFORMATICS RESOURCES (* release withheld until publication of the manuscript)

- [Reference genome of *Phragmites australis* ssp. *australis* \(common reed\)](#) (2021): The genome for the invasive *P. australis* and selected endophyte-responsive RNA-seq tracks from both invasive and native genotypes in the CoGe and EPIC-CoGe (genome ID 59768)
- [Phylogenetically informed profiling \(PiP\)*](#) (2021): To detect gene sets with lineage(s)-specific modifications among multiple species, presence and absence of correlations in gene regulation are superimposed to the species tree, and ranked for their significance.
- [Genome annotation of *Sisymbrium irio* v. 0.3*](#) (2020): The gene models of *S. irio* were updated based on BUSCO-based training parameters for *ab initio* gene prediction and hints from new RNA-seq and sequence homology 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
- [Variations signifying niche adaptation of *Schrenkiella parvula*](#) (2014): Comparison of copy numbers and basal level expression of orthologues between the extremophyte *S. parvula* and its relative model plant *A. thaliana*
- [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

Invited talks

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 International Plant & Animal Genomes conference (PAG) 2022 (scheduled 2022 Jan 10, San Diego, CA)

- D-H Oh**, KP Kowalski, C Wijesinghe, 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)

Poster presentations / lightning talks

- D-H Oh**, KP Kowalski, C Wijesinghe, Q Quach, P Tanford, M Dassanayake, K Clay “Novel genome characteristics contribute to the invasiveness of *Phragmites australis* (common reed),” Plant Genomes in a Changing Environment 2021 by the Wellcome Sanger Institute (2021 Oct 19, Virtual; lightning talk)
- D-H Oh**, and M Dassanayake. “Developing genomic resources for biocontrol of a major invasive grass *Phragmites australis* (common reed),” Plant Biology Worldwide Summit 2021 conference (2021 Jul, virtual)

- D-H Oh** and M Dassanayake. “Landscape of lineage-specific gene translocation and duplication events within the crucifer family,” International Plant & Animal Genomes (PAG 2017) conference (2017 Jan, San Diego)
- D-H Oh** and M Dassanayake. “Landscape of shared and lineage-specific tandem duplications and gene order rearrangements within the crucifer family,” American Society of Plant Biologists (ASPB) meeting (2016 Jul, Austin, TX)
- D-H Oh** and M Dassanayake. “Single cell responses to salinity: The epidermal bladder cell transcriptome of *Mesembryanthemum crystallinum*,” Gordon Research Conference for Salt and water Stress (2014 Aug, Newry, ME)
- D-H Oh**, H Hong, SY Lee, H Bohnert, M Dassanayake. “Genome structures and transcriptomes signify evolutionary trajectories for multi-ion tolerance and niche adaptation in *Schrenkiella parvula* (formerly *Thellungiella parvula*),” PAG 2014 conference (2014 Jan, San Diego)
- D-H Oh** and M Dassanayake. “Genome adaptations to multi ion tolerance,” ASPB meeting (2013 Jul, Providence, RI)
- D-H Oh**, M Dassanayake, et al. “*Thellungiella parvula*: the evolution of extremophile genome and lifestyle,” Plant Genome Evolution, A Current Opinion Conference, Elsevier (2011 Sep, Amsterdam, Netherlands)
- D-H Oh**, M Dassanayake, J Haas, A Hernandez, S Ali, H Hong, D Yun, RA Bressan, JK Zhu, HJ Bohnert, JM Cheeseman. “The genome of the extremophile Arabidopsis-relative *Thellungiella parvula*,” PAG 2011 conference (2011 Jan, San Diego)

Co-authored presentations listed in conference proceedings

- Y Sun, K-N Tran, L Duan, **D-H Oh**, A Ramirez, G Wang, M Dassanayake, JR Dinneny. “Divergence in stress tolerance mechanisms across the Brassicaceae family highlight strategies for maintaining growth and physiological balance under extreme environments,” U.S. Department of Energy, Office of Biological and Environmental Research, 2021 Biological System Sciences Division Principal Investigators' Meetings (2021 Feb 23, virtual)
- K-N Tran, **D-H Oh**, and M Dassanayake. “Extremophyte Arabidopsis relatives thrive in soils contaminated with toxic concentrations of sodium and lithium,” International Plant & Animal Genomes conference (PAG) 2019 (2019 Jan, San Diego)
- C Wijesinghege, **D-H Oh**, and M Dassanayake. “Alternative splicing adds regulatory complexity in differential orthologue expression between Arabidopsis and its extremophyte relative *Schrenkiella parvula*,” PAG 2019 (2019 Jan, San Diego)
- G Wang, **D-H Oh**, and M Dassanayake. “Comparative omics between Arabidopsis and the extremophyte, *Schrenkiella parvula*, identify candidate contributors to boron toxicity tolerance,” PAG 2019 (2019 Jan, San Diego)
- P Pantha, **D-H Oh**, and M Dassanayake. “The genome and transcriptome of the extremophyte, *Schrenkiella parvula* reveal unique adaptations to survive high K⁺ in its

- native soils,” Nepalese Agricultural Professional in America meeting (2018 May, Oklahoma City, OK)
- G Wang, **D-H Oh**, and M Dassanayake. “Can *Schrenkiella parvula*, an extremophyte relative of *Arabidopsis*, help determine a genomic blueprint in adapting to boron toxicity?” American Society of Plant Biologists (ASPB) meeting (2018 Jul, Montreal, Canada)
- P Pantha, **D-H Oh**, and M Dassanayake. “Insights into plant responses and adaptations to K⁺ toxicity gained by comparing the extremophyte, *Schrenkiella parvula*, to *Arabidopsis thaliana*,” ASPB meeting (2018 Jul, Montreal, Canada)
- K-N Tran, **D-H Oh**, and M Dassanayake. “Extremophyte *Arabidopsis* wild-relatives reveal modified salt stress response pathways,” ASPB meeting (2018 Jul, Montreal, Canada)
- K-N Tran, **D-H Oh**, and M Dassanayake. “Extremophyte *Arabidopsis* wild-relatives reveal modified salt stress response pathways,” International Conference on *Arabidopsis* Research (2018 July, Turku, Finland)
- P Pantha, **D-H Oh**, and M Dassanayake. “A comparative transcriptomic view on high K⁺ stress tolerance between *Schrenkiella parvula* and *Arabidopsis thaliana*,” The Southern Section of the American Society of Plant Biologists meeting (2018 Mar, New Orleans, LA)
- MV Cruz, GM Mori, **D-H Oh**, M Dassanayake, RS Oliveira, and AP de Souza. “Local adaptations of neotropical mangrove species to contrasting environments discovered through comparative ecophysiology, transcriptomics and genomic scan for selection,” XIX International Botanical Congress (2017 Jul, Shenzhen, China)
- G Eshel, **D-H Oh**, R Shaked, V Chalifa-Caspi, S Bar-David, A Fait, M Dassanayake, and S Barak. “Transcriptome analysis of the *Arabidopsis* Negev desert relative, *Anastatica hierochuntica* (True Rose of Jericho), reveals stress tolerance and developmental determinants that might facilitate an opportunistic extremophyte lifestyle,” XIX International Botanical Congress (2017 Jul, Shenzhen, China)
- Y Sun, **D-H Oh**, M Yee, M Dassanayake, J Dinneny. “Do changes in gene regulatory networks underlie variation in stress tolerance in the Brassicaceae?” The 28th Conference on *Arabidopsis* Research (2017 Jun, St. Louis, MO)
- K-N Tran, **D-H Oh**, M Dassanayake. “A comparative analysis of multi-ion salt stress responses among *Arabidopsis thaliana*, *Eutrema salsugineum*, and *Schrenkiella parvula*,” ASPB meeting (2016 Jul, Austin, TX)
- G Wang, **D-H Oh**, M Dassanayake. “Genomic structural variations leading to niche adaptation of the *Arabidopsis*-relative Extremophyte, *Schrenkiella parvula*,” ASPB meeting (2016 Jul, Austin)
- N Kumar, **D-H Oh**, M Dassanayake. “Comparative transcriptomics reveal convergent evolution in diverse halophytes,” ASPB meeting (2016 Jul, Austin)
- MV Cruz, GM Mori, S Bajay, C Müller, M Dassanayake, **D-H Oh**, RS Oliveira, and AP de Souza. “Evolutionary study of neotropical mangrove species through functional genomics and ecophysiology,” ASPB meeting (2016 Jul, Austin)

- P Pantha, **D-H Oh**, and M Dassanayake. "Salinity adaptation investigated by comparison of spatiotemporal gene expression between *Schrenkiella parvula* and *Arabidopsis thaliana*," ASPB meeting (2016 Jul, Austin)
- G Wang, **D-H Oh**, and M Dassanayake. "Extremophyte crucifer species: a comparative framework to study genome variations that lead to niche adaptations," PAG 2016 (2016 Jan, San Diego)
- BK Shrestha, **D-H Oh**, M Dassanayake, and JH Ham. "Identification of genome variants of rice associated with disease resistance to sheath blight and bacterial panicle blight through NGS sequencing," American Phytopathological Society Annual meeting (2015 Aug, Pasadena, CA)
- D Hu, **D-H Oh**, M Dassanayake, D Walker, and Z-Y Chen. "RNA-seq analysis of soybean near-isogenic line carrying Asian soybean rust -resistant and -susceptible alleles," American Phytopathological Association - Southern Division (2015 Feb, Atlanta, GA)
- M Dassanayake and **D-H Oh**. "Genome architecture signify evolutionary trajectories for multi-ion salt tolerance," Gordon Research Conference for Salt and water Stress (2014 Aug, Newry, ME)
- M Dassanayake and **D-H Oh**. "Genome structures and transcriptomes signify evolutionary trajectories for multi-ion salt tolerance," ASPB meeting (2014 Jul, Portland, OR)
- Q Wang, A Korde, C Nowak, **D-H Oh**, M Dassanayake, and D Donze. "Global defective RNA polymerase III complex assembly in *Saccharomyces cerevisiae* results in varied local effects on the Pol II transcriptome," International Conference on Transcription by RNA Polymerases I, III, IV, and V (2014 Jun, Ann Arbor, MI)
- B Lambert, M Dassanayake, **D-H Oh**, and GS Pettis. "RNA-Seq analysis of colonial phase variant lineages of *Vibrio cholerae* 01 El Tor N16961," American Society for Microbiology General Meeting, (2014 May, Boston, MA)
- J Larkin, **D-H Oh**, and M Dassanayake. "Evolution of the SIAMESE-related (SMR) family of cell cycle regulators," FASEB Plant Developmental Mechanisms (2013 Aug, Saxtons River, NH)
- S Chalivendra, **D-H Oh**, and M Dassanayake. "Germination adaptations to salt stress in *Thellungiella parvula*," ASPB meeting (2013 Jul, Providence, RI)
- M Dassanayake, **D-H Oh**, J Haas, A Hernandez, S Ali, H Hong, D-J Yun, RA Bressan, JK Zhu, HJ Bohnert, JM Cheeseman. "The genome of the extremophile Arabidopsis-relative *Thellungiella parvula*," Plant Abiotic Stress Tolerance Mechanisms, Water and Global Agriculture (A7) of Keystone symposia (40th meeting). (2011 Jan, Keystone, CO)
- M Dassanayake, **D-H Oh**, MP d'Urzo, G Lambert, D Galbraith, JM Cheeseman, S. Ali, A Hernandez, MV Mickelbart, D-J Yun, RA Bressan, JK Zhu, and HJ Bohnert. "Genomic characterization of *Arabidopsis thaliana* extremophile relatives: *Thellungiella parvula*," PAG 2011 (2011 Jan, San Diego)

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

Undergraduate teaching fellowship

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

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 a NSF EDGE-funded outreach activity
- 2016 Apr 7 : “Using clustering to understand a 2-factor RNAseq 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

Mentoring as a doctoral advisory committee member

- 2016 – Present : Chathura Wijesinghe (PhD advisee of Maheshi Dassanayake, LSU)
- 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 a collaboration, on-going

At LSU Biological Sciences (PI in parentheses)

- Thu T Nguyen (Maheshi Dassanayake): genome editing in extremophyte crucifers
- Samadhi Wimalagunasekara (M Dassanayake): salt stress and flowering interactions
- Rubaiat Akhand (Aaron Smith): plant salt and P deficiency stress response 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

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

- Michelle Arland (Gidon Winters and Simon Barak, Desert Research, Ben-Gurion University of the Negev, Israel): interspecies comparative analyses of seagrass transcriptomes
- Solmaz Irani (Elizabeth Weretilnyk, Biology, McMaster University, Hamilton, ON, Canada): comparative analyses of extremophyte responses to salt stress and phosphate deficiency

Mentoring as a collaboration, past (resulted in a publication/conference presentation)

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

- 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

- Ying Sun – former PhD advisee of José Dinneny (Plant Biology, Stanford University, Palo Alto, CA): 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., Jinju, South Korea); comparative analyses of extremophyte HKT1 homologues
- Hyewon Hong - former PhD advisees of D.-J. Yun (Applied life sciences, GNU, South 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

Invited reviewer of scientific manuscripts

- Review editor for *Frontiers in Plant Sciences* (17 reviewed, 11 published since 2016 Sep)
- [Invited reviewer](#) (numbers of manuscripts reviewed in parentheses) for:
Nature Genetics (8), *Journal of Experimental Botany* (5), *BMC Genomics* (3), *Molecular Plant* (2), *Physiologia Plantarum* (2), *New Phytologist* (1), *Plant Physiology* (1), *Bioinformatics* (1), *DNA Research* (1), *Plant Cell Reports* (1), *PLoS ONE* (1), *Journal of Plant*

Physiology (1), Plant and Soil (1), Plant Molecular Biology Reporter (1), Genes and Genomics (1), Journal of Plant biology (1), and Australian Journal of Botany (1)

Invited reviewer of grants and applications

- Invited as a reviewer for NSF: 2017, 2020, 2021 (2 programs), and 2022
- Served as a reviewer for NSF: 2020 and 2021