



CURRICULUM VITAE

November, 2018

Dong-Ha Oh

Homepage: <https://www.lslugenomics.org/dong-ha-oh>

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

GitHub: <https://github.com/ohdongha>

PROFESSIONAL BACKGROUND

- 2014 Jan – Present : Assistant professor-research; Biological Sciences (BS), Louisiana State University (LSU), Baton Rouge, LA (Host faculty: Maheshi Dassanayake)
- 2013 Feb – 2013 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 (Advisor: Hans J. Bohnert)
- 2005 Apr – 2010 Mar : Visiting scientist; Horticulture and Landscape Architecture, Purdue University, West Lafayette, IN (Advisor: Ray A. Bressan)
- 2003 Sep – 2005 Mar : Post-doc. researcher; Biological Sciences, Korea Advanced Institute of Science and Technology (KAIST), Daejeon, South Korea (Advisor: Won-Il Chung)

EDUCATIONAL BACKGROUND

- 2003 Aug : **Ph.D.** Biological Sciences (BS), KAIST; 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: W.-I. Chung)
- 1996 Feb : **B.S.** Life Science, KAIST

RESEARCH GRANTS

Awarded (amount awarded; PI; my role)

- 2019 – 2021 : COPIA Foundation, Israel; Mining seagrasses to develop salt-tolerant crops, as an international collaboration with Ben-Gurion University of the Negev (\$200,000; Simon Barak, Ben Gurion Univ., Israel; 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 (\$80,000; M. Dassanayake; Key personnel)
- 2013 – 2017 : RDA-Biogreen 21, South Korea; Genomic variations for stress adaptation in extremophyte wild-relatives of crops, as an international collaboration with Gyeongsang National University, South Korea (\$300,000; M. Dassanayake; Key personnel and acting project manager)

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

- 2019 – 2022 : USDA-NIFA-AFRI; Physiological mechanisms driving the accumulation of high levels of iron in common bean (*Phaseolus vulgaris*) (pending \$474,523; David Mendoza-Cózatl, Univ. of Missouri, Columbia, MO; Key personnel)
- 2019 : DOE-JGI-Community Science Program; Genes evolved for adaptations to saline environments in a model extremophyte (pending 500 Gb sequencing grant; M. Dassanayake; Key personnel)
- 2019 – 2021 : NSF-PGRP-TRTech-PGR; Systematic detection of orthologous gene groups sharing an evolutionary history using network topology search (in preparation; Dong-Ha Oh; PI)

BIOINFORMATICS TOOLS AND RESOURCES

- [CLfinder-OrthNet](#) (2018): a comparative genomics toolbox to (1) encode co-linearity among orthologous gene loci in multiple genomes as networks of orthologs (OrthNets) and (2) systematically detect gene loci with a shared evolutionary history using OrthNet topology search
- [Co-linearity matrix and OrthNets for six crucifer genomes](#) (2018): co-linearity, copy number, evolutionary history, and basal-level expression rank information for all orthologs in six Brassicaceae plant genomes, including *Arabidopsis thaliana* and its two extremophyte relatives
- [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-responsive expression; 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*, version 2.0](#) (2014): Updated genome assembly and annotation for *S. parvula*, based on additional RNA-Seq and comparative analyses. Version 2.1 is currently under development using a combination of RNA-Seq and Iso-Seq data

MENTORING, TEACHING, AND CONSULTATION

Mentoring as a doctoral advisory committee member

- 2016 – Present : Chathura Wijesinghege (PhD advisee of Maheshi Dassanayake, LSU)
- 2016 – Present : Kieu-Nga Tran (same as above)
- 2015 – Present : Pramod Pantha (same as above)
- 2014 – Present : Guannan Wang (same as above)
- 2014 – 2016 : Teresa DeLeon (PhD advisee of Prasanta Subudhi, School of Plant, Environmental, & Soil Sciences, LSU)

Mentoring as a part of collaborative research, on-going

At LSU Biological Sciences

- Maryam Foroozani - PhD advisee of Aaron Smith; rice ChIP-Seq and interpretation
- Duhon, Mark - PhD advisee of Mike Helberg; mollusk transcriptome assemblies and analyses
- Zachary Rodriguez - PhD advisee of Chris Austin; transcriptome and phylogenomics of lizards

Outside of the LSU campus

- Ying Sun - PhD advisee of José Dinneny (Plant Biology, Carnegie Institute, Stanford, CA); interspecies comparative DAP-Seq and RNA-Seq on Brassicaceae species
- Michelle Arland - PhD advisee of Gidon Winters and Simon Barak (Desert Research, Ben-Gurion University of the Negev, Israel); interspecies comparative analyses of seagrass transcriptomes
- Mariana Vargas Cruz - PhD advisee of Anete Pereira de Souza (Plant Biology, Univ. Est de Campinas, Brazil); on interspecies comparative analyses of mangrove tree transcriptomes

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

At LSU (Biological Sciences unless indicated otherwise)

- Sarah Zahraeifard - former PhD advisee of Aaron Smith; rice RNA-Seq analysis
- Shraddha Shrestha - former PhD advisee of Craig Hart; *Drosophila* HiC-Seq analysis
- Bishnu Shrestha - former PhD advisee of Jong Ham (Plant Pathology); genomic variations among rice cultivars
- Qi Zhang - former PhD advisee of Aaron Smith; rice MNase-Seq analysis
- Qing Wang - former Ph.D. advisee of David Donze; yeast RNA-Seq analysis
- Bliss Lambert – PhD advisee of Gregg Pettis; *Vibrio cholerae* RNA-Seq analysis
- Dongfang Hu – PhD advisee of Zhi-Yuan Chen (Plant Pathology); soybean RNA-Seq analysis

Outside of the LSU campus

- 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., Junju, 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

Teaching activities

Guest instructor

- 2018 Fall : BIOL3400 Evolution, Biological Sciences, LSU, Baton Rouge, LA

- 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

- 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 30 – May 2 : “On NGS technology and analyses,” for Dr. Mohamed Saad at AEGIS, Egypt, to assist development of a National Core NGS facility in Egypt, UIUC, Urbana, IL
- 2012 Apr 19 : “On Cassava genome assembly,” consultation for Drs. Pinghua Li and Binxiao Feng at Chinese Cassava Genomics and Biotechnology Consortium, UIUC
- 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

OTHER PROFESSIONAL ACTIVITIES

- [Invited reviewer](#) (numbers of manuscripts reviewed in parentheses) for: *Nature Genetics* (8), *BMC Genomics* (3), *Journal of Experimental Botany* (3), *Molecular Plant* (2), *Physiologia Plantarum* (2), *Bioinformatics* (1), *Plant Cell Reports* (1), *PLoS ONE* (1), *Journal of Plant Physiology* (1), *Plant and Soil* (1), *Plant Molecular Biology Reporter* (1), and *Australian Journal of Botany* (1)
- 2016 Sep – Present : Review editor for *Frontiers in Plant Sciences* (9 reviewed, 4 published)
- Invited reviewer for NSF (2017)

PUBLICATIONS

[Google scholar stats](#)

- All-time : total citations: **1529**; h-index: **19**; i10-index: **20**
- Since 2013 : total citations: 1237; h-index: 18; i10-index:19

Journal articles (*equal contribution; #corresponding author)

MV Cruz, GM Mori, CS Müller, CC da Silva, **D-H Oh**, M Dassanayake, MI Zucchi, RS Oliveira, AP de Souza[#] (2019), Local adaptation to water-deficit and light limitation suggested from genomic and ecophysiological approaches in a coastal habitat-forming tree. **New Phytol**, *in review*.

S-J Kim*, H-B Sohn*, **D-H Oh****, Y-J Hwang, YH Yoon, Y-Y Lee, S-G Park, K Markkandan, D Lee, HJ Kwon, P Pantha, M Dassanayake, B-C Koo, S Lee[#], Y-H Kim[#] (2019), A draft genome and comparative genome analyses reveal gene copy number variations as signatures of specialized metabolism and adaptation in tartary buckwheat. **Plant J**, *in revision*.

G Wang, P Pantha, K-N Tran, **D-H Oh**[#], M Dassanayake[#] (2018), Plant growth and agrobacterium-mediated floral-dip transformation of the extremophyte *Schrenkiella parvula*. **J Vis Exp**, *in press*.

- D-H Oh**[#] and M Dassanayake[#] (2018), Landscape of gene transposition-duplication within the Brassicaceae family. **DNA Res**, [doi:10.1093/dnares/dsy035](https://doi.org/10.1093/dnares/dsy035)
- 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.
- 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.
- 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.
- 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

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.

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.

D-H Oh^{*}, M Dassanayake^{*}, HJ Bohnert and JM Cheeseman[#] (2012), Life in the extreme: Lessons from Genomics. **Genome Biol**, 13:241.

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.

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.

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. ^{**}Recommended by members of "Faculty of 1000" (<http://f1000.com/5704964>).

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.

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.
- 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 Intgr 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.

Book chapter

- 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).

INVITED TALKS AND PRESENTATIONS

Invited talks

- 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 International Plant & Animal Genomes (PAG 2019) conference (scheduled 2019 Jan 16, San Diego, CA)
- 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 conference (scheduled 2019 Jan 15, San Diego, CA)
- 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 conference (scheduled 2019 Jan 12, San Diego)
- 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 conference (2014 Jan 14, San Diego, CA)
- 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 conference (2012 Jan 15, San Diego)

Poster presentations

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, CA)

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 (2011 Jan, San Diego)

Co-authored presentations listed in a conference proceeding

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 (PAG 2019) conference, (2019 Jan, San Diego, CA)

C Wijesinghe, **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 conference, (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 conference, (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, TX)
- N Kumar, **D-H Oh**, M Dassanayake. "Comparative transcriptomics reveal convergent evolution in diverse halophytes," ASPB meeting (2016 Jul, Austin, TX)

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, TX)

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, TX)

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 conference (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)

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