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EDUCATION

University of California, Riverside, Plant Biology, Ph.D. 2005
Punjab Agricultural University, India, Plant Breeding and Genetics, B.S. 2000

APPOINTMENTS

2019-present	Heuermann Chair of Agronomy, University of Nebraska-Lincoln (UNL)
2015-present	Associate Professor, Department of Agronomy and Horticulture, UNL
2010-2015	Assistant Professor, Department of Agronomy and Horticulture, UNL
2008-2010	Postdoctoral Associate, Department of Plant Pathology, University of California-Davis
2006-2008	Postdoctoral Associate, Genome Center, University of California-Davis

AFFILIATIONS

Center for Plant Science Innovation, UNL
School of Biological Sciences, UNL
Faculty Fellow, Daugherty Water for Food Institute, University of Nebraska
Wheat and Rice Center for Heat Resilience
Nebraska Food for Health Center

PUBLICATIONS (Citations: 3141, h-index: 25, i10-index: 31)

1. Dhatt BK, Abshire N MT, Paul P, Hasanthika K, Sandhu J, Zhang Q, Obata T, **Walia H**. Metabolic dynamics of developing rice seeds under high night temperature stress. 2019, *Frontier in Plant Science*

2. Momen M, Campbell MT, **Walia H**, Morota G. Utilizing trait networks and structural equation models as tools to interpret multi-trait genome-wide association studies. 2019, *Plant Methods* 159(107)

3. Momen M, Campbell MT, **Walia H**, Morota G. Predicting Longitudinal Traits Derived from High-Throughput Phenomics in Contrasting Environments Using Genomic Legendre polynomials and B-splines. 2019, *G3: Genes, Genomes, Genetics*

4. Du Q, Campbell MT, Yu H, Liu K, **Walia H**, Zhang Q, Zhang C. Network-based feature selection reveals substructures of gene modules responding to salt stress in rice. 2019, *Plant Direct* 12;3(8)

5. Yu H, Campbell MT, Zhang Q, **Walia H**, Morota G. Genomic Bayesian confirmatory factor analysis and Bayesian network to characterize a wide spectrum of rice phenotypes. 2019, *G3: Genes, Genomes, Genetics*

6. Campbell MT, **Walia H**, Morota G. Leveraging breeding values obtained from random regression models for genetic inference of longitudinal traits. 2019, *The Plant Genome*

7. Razzaque S, Elias SM, Haque T, Biswas S, Jewel GMNA, Rahman S, Weng X, Ismail AM, **Walia H**, Juenger TE, Seraj ZI. Gene Expression analysis associated with salt stress in a reciprocally crossed rice population. 2019, *Scientific Reports* 3;9(1)

8. Campbell MT, **Walia H**, Morota G. Utilizing random regression models for genomic prediction of a longitudinal trait derived from high-throughput phenotyping. 2018, *Plant Direct* 2(9)

9. Zhu F, Thapa S, Gao T, Ge Y, **Walia H**, Yu H. 3D Reconstruction of Plant Leaves for High-Throughput Phenotyping. 2018, *IEEE Big Data Conference*

10. Begcy K, Sandhu J, **Walia H.** Transient Heat Stress During Early Seed Development Primes Germination and Seedling Establishment in Rice. 2018, *Frontiers in Plant Science*

11. Hussain W, Campbell MT, **Walia H**, Morota G ShinyAIM: Shiny-based Application of Interactive Manhattan Plots for Longitudinal Genome-Wide Association Studies. 2018, *Plant Direct* 2(10)

12. Campbell MT, Du Q, Liu K, Brien CJ, Berger B, Zhang C, **Walia H**. A Comprehensive Image-based Phenomic Analysis Reveals the Complex Genetic Architecture of Shoot Growth Dynamics in Rice (Oryza sativa). 2017, *The Plant Genome*

13. Campbell MT, Nonoy Bandillo N, Al Shiblawi F, Sharma S, Liu K, Du Q, Schmitz AJ, Zhang C, Véry AA, Lorenz AJ, **Walia H**, Allelic variants of OsHKT1;1 underlie the divergence between Indica and Japonica subspecies of rice (Oryza sativa) for root sodium content. 2017, *PLOS Genetics*

14. Razzaque S, Haque T, Elias SM, Rahman MS, Biswas S, Schwartz S, Ismail AM, **Walia H**, Juenger TE, Seraj ZI. Reproductive stage physiological and transcriptional responses to salinity stress in reciprocal populations derived from tolerant (Horkuch) and susceptible (IR29) rice. 2017, *Scientific Reports*

15. Geng B, Blecha S, Ge Y, **Walia H**, Phansak P. Characterizing wheat response to water limitation using multispectral and thermal imaging. 2016, *ASABE*

16. Knecht AC, Campbell MT, Caprez A, Swanson DR, **Walia H**, Image Harvest: An open source platform for high-throughput plant image processing and analysis. 2016, *Journal of Experimental Botany*

17. Chen C, Begcy K, Liu K, Folsom JJ, Wang Z, Zhang C, **Walia H**, Molecular characterization of rice endosperm development under heat stress identifies OsMADS87 as a determinant of seed size and thermal sensitivity. 2016, *Plant Physiology*

18. Campbell MT, Knecht AC, Berger B, Brien CJ, Wang D, **Walia H**, Integrating image-based phenomics and association analysis to dissect the genetic architecture of temporal salinity responses in rice. 2015, *Plant Physiology* 168(4):1476-89

19. Begcy K, **Walia H**, Drought stress delays endosperm development and misregulates genes associated with cytoskeleton organization and grain quality proteins in developing wheat seeds. 2015, *Plant Science*

20. Schmitz AJ, Begcy K, Sarath G, **Walia H**, Rice Ovate Family Protein 2 (OFP2) alters hormonal homeostasis and vasculature development. 2015, *Plant Science*

21. Campbell MT, Proctor CA, Dou Y, Schmitz AJ, Phansak P, Kruger GR, Zhang C, **Walia H**, Genetic and molecular characterization of submergence response identifies Subtol6 as a major submergence tolerance locus in maize. 2015, *PLoS One*

22. Folsom JJ, Begcy K, Xiaojuan H, Wang D, **Walia H**, Rice *FIE1* regulates seed size under heat stress by controlling early endosperm development. 2014, *Plant Physiology*

23. Placido DF, Campbell MT, Jin J, Cui X, Kruger GR, Baenziger PS, **Walia H**, Introgression of novel traits from a wild wheat relative improves drought adaptation in wheat. 2013, *Plant Physiology*

24. Schmitz A, Jin J, Jikamaru Y, Ronald P, **Walia H**, *SUB1A*-mediated submergence tolerance response in rice involves differential regulation of the brassinosteroid pathway. 2013, *New Phytologist*

25. Baenziger PS, Bakhsh A, Lorenz A, **Walia H**, Bridging conventional breeding and genomics for a more sustainable wheat production. 2013, Advances in Genomics of Plant Genetic Resources, Springer

26. Peleg Z, **Walia H**, Blumwald E, Integrating genomics and genetics to accelerate development of drought and salinity tolerant crops. 2012, Plant Biotechnology and Agriculture: Prospects for the 21st Century

27. Seo YS, Chern M, Bartley LE, Han M, Jung KH, Lee I, **Walia H**, Richter T, Xu X, Cao P, Bai W, Ramanan R, Amonpant F, Arul L, Canlas, PE, Ruan R, Park CJ, Chen X, Hwang S, Jeon JS, Ronald PC, Towards establishment of a rice stress response interactome. 2011, *PLOS Genetics*

28. Cotsaftis O, Plett D, Johnson AA, **Walia H**, Wilson C, Ismail AM, Close TJ, Tester M, Baumann U, Root-specific transcript profiling of contrasting rice genotypes in response to salinity stress. 2011, *Molecular Plant*

29. Peleg Z, Reguera M, **Walia H**, Blumwald E, Cytokinin mediated source-sink modifications improve drought tolerance and increase grain yield in rice under water stress. 2010*, Plant Biotechnology Journal*

30. Laurent JM, Vogel C, Kwon T, Craig SA, Boutz DR, Huse HK, Nozue K, **Walia H**, Whiteley M, Ronald PC, Marcotte EM, Protein abundances are more conserved than mRNA abundances across diverse taxa. 2010, *Proteomics*

31. Rivero RM, Gimeno J, Van Deynze A, **Walia H**, Blumwald E. Enhanced cytokinin synthesis in tobacco plants expressing PSARK::IPT prevents the degradation of photosynthetic protein complexes during drought. 2010, *Plant Cell Physiology*

32. Jeon JS, Ryoo N, Hahn TR, **Walia H**, Nakamura Y, Starch biosynthesis in cereal endosperm. 2010, *Plant Physiol Biochem.*

33. Jung KH, Seo YS, **Walia H**, Cao P, Fukao T, Canlas PE, Amonpant F, Bailey-Serres J, Ronald PC. The submergence tolerance regulator Sub1A mediates stress-responsive expression of AP2/ERF transcription factors. 2010, *Plant Physiology*

34. **Walia H**, Josefsson C, Dilkes B, Kirkbride R, Harada J, Comai L, Dosage-dependent deregulation of an AGAMOUS-LIKE GENES cluster contributes to interspecific incompatibility. 2009, *Current Biology*

35. **Walia H**, Wilson C, Ismail AM, Close TJ, Cui X, Comparing genomic expression patterns across plant species reveals highly diverged transcriptional dynamics in response to salt stress. 2009, *BMC Genomics*

36. Kim SH, Bhat PR, Cui X, **Walia H**, Xu J, Wanamaker S, Ismail AM, Wilson C, Close TJ, Detection and validation of single feature polymorphisms using RNA expression data from a rice genome array. 2009, *BMC Plant Biology*

37. **Walia H**, Wilson C, Condamine P, Ismail A, Zeng L, Xu J, Cui X, Close TJ, Array-Based Genotyping and Expression Analysis of Barley cv. Maythorpe and Golden Promise. 2007, *BMC Genomics*

38. **Walia H**, Wilson C, Liu X, Ismail A, Close TJ, Transcriptional profiling of rice under salinity stress during panicle initiation stage. 2007, *Plant Molecular Biology*

39. **Walia H**, Wilson C, Condamine P, Liu X, Close TJ, Role of jasmonic acid in improving salinity tolerance of barley revealed by physiological and large scale gene expression studies. 2007, *Plant, Cell and Environment*

40. **Walia H**, Wilson C, Condamine P, Liu X, Ismail A, Zeng L, Wanamaker S I, Mandal J, Cui X, Xu J, Close TJ, Comparative transcriptional profiling of two contrasting rice (*Oryza sativa* L.) genotypes under salinity stress during vegetative growth stage. 2005, *Plant Physiology*

41. Rostoks N, Mudie S, Cardle L, Russell J, Ramsay L, Booth A, Svensson JT, Wanamaker SI, **Walia H**, Rodriguez EM, Hedley PE, Liu H, Morris J, Close TJ, Marshall DF, Waugh R, Genome-wide SNP discovery and linkage analysis in barley based on genes responsive to abiotic stress. 2005, *Mol Genet Genomics*

PREPRINT IN bioRxiv

1. Campbell MT, Du Q, Liu K, Sharma S, Zhang C, **Walia H**, The genetic basis of cis-regulatory divergence between the subspecies of cultivated rice (Oryza sativa). *bioRxiv* 511550; doi: https://doi.org/10.1101/511550

2. Campbell MT, Grondin A, **Walia H**, Morota G, Leveraging genome-enabled growth models to study shoot growth responses to water deficit in rice. *bioRxiv* 690479; doi: https://doi.org/10.1101/690479

3. Baba T, Momen M, Campbell MT, **Walia H**, Morota G, Multi-trait random regression models increase genomic prediction accuracy for a temporal physiological trait derived from high-throughput phenotyping. *bioRxiv* 772038; doi: https://doi.org/10.1101/772038

PATENTS

- Patent Application for "SUB1-Interacting Proteins", 2013
- US Patent US10036034B2 "Drought tolerance gene in wheat and rice," 2018

TEACHING & MENTORING

- ***Multidisciplinary Team Teaching***: Co-led the efforts to develop a team-taught graduate course in "Plant Phenomics" as part of NSF funded EPSCoR Track 2 award to build graduate level expertise in data integration approaches for plant phenomics and other omics approaches.
- ***Science Communication***: As part of developing science communication skills among undergraduate student, the plant physiology course integrates group presentations and departmental poster sessions focused on climate change and agriculture.
- ***Undergraduate Research Mentoring***: Mentored 15 undergraduate students in plant biology research from several departments, including underrepresented students.
- ***Phenomics Workshops*****:** Conducted plant phenomics workshops for undergraduate students and graduate students in Nebraska, Arkansas, Israel. The workshops in Arkansas (2013-2016) were specially focused on under-represented minority students.
- ***Graduate Committee Service***: Served on graduate committee for eight departments at UNL; serving on PhD committees from Arkansas State University (3 students) and Hebrew University; Currently advising four Ph.D. students, one MS student, two postdoctoral scholars, and five undergraduate students.
- ***Early Career Faculty Mentoring***: A major broader impact of the EPSCoR Track 2 grant that I lead is to mentor early career faculty. I have been actively engaged in mentoring four participating faculty under this program. Two of these faculty have received the prestigious NSF CAREER Awards.

REPRESENTATIVE PROFESSIONAL & UNIVERSITY SERVICE

- Chair, American Society of Plant Biologists for Midwest Section (2019-2020)
- Vice Chair of the American Society of Plant Biologists for Midwest Section (2018-2019)
- Grant review panelist: NSF (6), USDA-NIFA (2), USAID-PEER (1)
- *Ad hoc* reviewer for international peer reviewed journals, including *Plant Physiology*, *BMC Genomics*, *Plant*, *Cell and Environment*, *Nucleic Acids Research*, *Nature Biotechnology*, *PLOS Genetics*, *Nature Communications*, *New Phytologist*, and *Rice*
- Served as Associate Editor for *BMC Plant Biology, Rice* and *Frontiers of Plant Sciences*
- Member, UNL Building Bioinformatics Capacity Task Force
- Served on the ASPB Awards Committee for Stephen Hales Prize (2017-2019)
- Chair, search committee for Plant Phenomics Facility Manager
- Member, search committee for UNL VC for Research and Economic Development
- Member, search committee for Executive Director for Water for Food Institute, NU

AWARDS AND DISTINCTIONS

- Heuermann Chair of Agronomy (2019), UNL
- Dinsdale Family Junior Faculty Award for Excellence in Research and Teaching (2013), Institute of Agriculture and Natural Resources (IANR), UNL
- Student nomination for Best Teacher Award (2012), IANR, UNL
- Rice research video featured on national media at "science360.gov" (2014)
- Chancellor's Distinguished Fellowship, University of California, Riverside (2000-2004)

REPRESENTATIVE INVITED PRESENTATIONS

- KSBS and Kyung Hee University, South Korea (2019)
- Plant and Animal Genome, San Diego (2019)
- University of Tokyo, Japan (2018)
- Global Science Week, Tsukuba University, Japan (2018)
- Hebrew University of Jerusalem, Israel (2018)
- Crop Science Society of America, Baltimore (2018)
- Daugherty Water for Food Global Institute Conference, Lincoln (2017)
- Abiotic Stress Tolerance Symposium, Hebrew University, Israel (2017)
- International Rice Functional Genomics Symposium, South Korea (2017)
- Gordon Research Conference, Salt and Water Stress, Switzerland (2016)
- Danforth Center Annual Symposium, Saint Louis (2016)
- Kansas State University (2016)
- Crop Systems Biology, University of Melbourne, Australia (2015)
- International Rice Congress, Thailand (2014)
- Colorado State University, Fort Collins (2014)
- Plant and Animal Genome, (2 presentations), San Diego (2014)
- Plenary talk – International Rice Functional Genomics Symposium, Tucson (2014)
- CSIRO, Canberra, Australia (2013)
- Purdue University, West Lafayette (2013)
- Indian Agriculture Research Institute, India (2012)
- BASF, Research Triangle Park, North Carolina (2012)
- KeyGene Inc., Wageningen, Netherlands (2011)
- Punjab Agricultural University, India (2011)