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SHORT BIOGRAPHY

I am an Assistant Professor in the Plant and Wildlife Sciences department at Brigham Young University (BYU). I received my B.S. and M.S. degrees from BYU and my Ph.D. from the University of Arizona. Prior to coming to BYU in 2017, I was a post-doctoral fellow at King Abdullah University of Science and Technology (KAUST). I have experience in molecular biology, genetics, and genomics. My research interests focus on the development of genomic tools that can aid in the agronomic improvement of understudied crops such as quinoa. Of particular interest is improving the ability of these crops to grow in marginal environments, such as areas containing high levels of soil salinity.

EDUCATION

- University of Arizona, Ph.D.**, Plant Sciences (Advisor Dr. Karen Schumaker) 2014
Minor: Molecular and cellular biology
Dissertation: *Functional and evolutionary analysis of CATION/PROTON ANTIporter-1 genes in Brassicaceae adaptation to salinity*
- Brigham Young University, M.S.**, Genetics and Biotechnology (Advisor Dr. Eric Jellen) 2006
Thesis: *Simple sequence repeat development, polymorphism and genetic mapping in quinoa (Chenopodium quinoa Willd.)*
- Brigham Young University, B.S.**, Biotechnology 2004

EXPERIENCE

- Assistant professor, Dept. of Plant and Wildlife Sciences, BYU 2017 - present
Post-doctoral fellow, King Abdullah University of Science and Technology 2014 - 2017

AWARDS, SCHOLARSHIPS, FELLOWSHIPS, AND SOCIETIES

- Outstanding Dissertation Award, School of Plant Sciences, University of Arizona 2014
Graduate and Professional Student Council (GPSC) Travel Grant Award, University of Arizona 2013
University of Arizona Graduate College Research Fellowship 2011, 2012, 2013
Registration Award, 22nd International Conference on Arabidopsis Research 2011
College of Agriculture and Life Sciences Meritorious Graduate Teaching Award, University of Arizona 2009
National Science Foundation Integrative Graduate Education and Research Traineeship (NSF-IGERT) Fellowship in Genomics 2006 - 2008
Brigham Young, Plant and Animal Sciences Faculty, University, and Bicentennial Scholarships 1998 - 2006

COMMITTEE AND PROFESSIONAL ACTIVITIES

Professional Service

- Co-organizer and instructor, IAEA International Genomics and Bioinformatics Analysis Workshop, BYU, UT (Aug. 6 – 31) 2018
- Workshop organizer, Quinoa and Close Relatives, Plant and Animal Genome XXV, San Diego, CA 2017 - present
- Participant in the “Plant Sciences at the University of Arizona” booth at the 6th Annual Math, Science, and Technology Funfest for local 4th – 8th grade students, Tucson, AZ 2008
- Participant in the “Plant Science Family Night” for local middle school students, Tucson, AZ 2012 & 2013
- Judge, Southern Arizona Regional Science and Engineering Fair, Tucson, AZ 2013

Department, College, and University

- Judge, Department Review Committee for CURA Proposals 2018
- Judge, College Review Committee for ORCA Proposals 2017
- Faculty Advisor, Genetics and Biotechnology Club 2017 - present

TEACHING EXPERIENCE

BYU (faculty)

My primary teaching responsibilities include PWS 468 (Genomics) and PWS 288 (Molecular Genetics Lab).

Course ID	Credits	Semester	No. of students	Composite student rating (out of 5)	GPA
PWS 468	3	Fall 2018	48		3.05
PWS 288	2	Winter 2018	15	4.7	3.55

University of Arizona (graduate student)

- Plant and Animal Genetics (PLS 312)
Lab Coordinator Spring 2011
Teaching Assistant Spring 2009, Spring 2010
- Plant Biology (PLS 240)
Teaching Assistant Fall 2012
- Plants and Our World (NATS 104)
Teaching Assistant Fall 2008, Fall 2010

BYU (graduate student)

- Genetics (PWS 340)
Teaching Assistant Fall 2004, Winter 2005, Fall 2005
- Co-instructor, Universidad Autónoma del Estado de México
“The Use of Molecular Markers in Plant Improvement” Workshop. June 6-16, 2006

SCHOLARSHIP ([Google Scholar](#))

Refereed Journal Publications

Graduate and Undergraduate students are underlines and italicized, respectively.

- Maughan PJ, Chaney L, Lightfoot DJ, Cox BJ, Tester M, Jellen EN, **Jarvis DE**. Mitochondrial and chloroplast genomes provide insights into the evolutionary origins of quinoa (*Chenopodium quinoa* Willd.). *Sci Reports* (accepted)
- Ward B, Brien C, Oakey H, Pearson A, Negrão S, Schilling RK, Taylor J, **Jarvis D**, Timmins A, Roy SJ, Tester M, Berger B, van den Hengel A. High-throughput 3D modelling to dissect the genetic control of leaf elongation in barley (*Hordeum vulgare*). *Plant J* doi: 10.1111/tpj.14225 (2019)
- Lightfoot DJ*, **Jarvis DE***, Ramaraj T, Lee R, Jellen EN, Maughan PJ. Single-molecule sequencing and Hi-C-based proximity-guided assembly of amaranth (*Amaranthus hypochondriacus*) chromosomes provide insights into genome evolution. *BMC Biology* 15:74 (2017)
- *These authors contributed equally to this work.
- Schmöckel SM, Lightfoot DJ, Razali R, Tester M, **Jarvis DE**. Identification of putative transmembrane proteins involved in salinity tolerance in *Chenopodium quinoa* by integrating physiological data, RNAseq, and SNP analyses. *Frontiers in Plant Science* 8:1023 (2017)
- Jarvis DE***, Ho YS*, Lightfoot DJ*, Schmöckel SM*, Li B*, Borm T, Ohyanagi H, Mineta K, Michell CT, Saber N, Kharbatia NM, Rupper RR, Sharp AR, Dally N, Boughton BA, Woo YH, Gao G, Schijlen E, Guo X, Momin AA, Negrão S, Al-Babili S, Gehring C, Roessner U, Jung C, Murphy K, Arold ST, Gojobori T, van der Linden CG, van Loo EN, Jellen EN, Maughan PJ, Tester M. The genome of *Chenopodium quinoa*. *Nature* 542:307 (2017)
- *These authors contributed equally to this work.
- Jarvis DE**, Ryu C-H, Beilstein MA, Schumaker KS. Distinct roles for *SOS1* in the convergent evolution of salt tolerance in *Eutrema salsugineum* and *Schrenkiella parvula*. *Molecular Biology and Evolution* 31:2094-2107 (2014)
- Yang R*, **Jarvis DE***, Chen H, Beilstein MA, Grimwood J, Jenkins J, Shu S, Prochnik S, Xin M, Ma C, Schmutz J, Wing RA, Mitchell-Olds T, Schumaker KS, Wang X. The reference genome of the halophytic plant *Eutrema salsugineum*. *Frontiers in Plant Science* 4:46 doi: 10.3389/fpls.2013.00046 (2013)
- *These authors contributed equally to this work.
- Haudry A, Platts AE, Vello E, Hoen DR, Leclercq M, Williamson RJ, Forczek E, Joly-Lopez Z, Steffen JG, Hazzouri KM, Dewar K, Stinchcombe JR, Schoen DJ, Wang X, Schmutz J, Town CD, Edger PP, Pires JC, Schumaker KS, **Jarvis DE**, Mandakova T, Lysak MA, van den Bergh E, Schranz ME, Harrison PM, Moses AM, Bureau TE, Wright SI, Blanchette M. An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. *Nature Genetics* 45:891-898 (2013)
- Jarvis DE**, Kopp O, Jellen EN, Mallory MA, Bonifacio A, Coleman CE, Stevens MR, Fairbanks DJ, Maughan PJ. Simple sequence repeat marker development and genetic mapping in quinoa (*Chenopodium quinoa* Willd.). *Journal of Genetics* 89:39–51 (2008)
- Maughan PJ, Bonifacio A, Jellen EN, Stevens MR, Coleman CE, Ricks M, Mason SL, **Jarvis DE**, Gardunia BW, Fairbanks DJ. A genetic linkage map of quinoa (*Chenopodium quinoa*) based on AFLP, RAPD and SSR markers. *Theoretical and Applied Genetics* 109:1188–1195 (2004)

Book Chapters

- Murphy KM, Matanguihan JB, Fuentes FF, Gómez-Pando LR, Jellen EN, Maughan PJ, **Jarvis DE**. Quinoa breeding and genomics. In *Plant Breeding Reviews, Volume 42*. 257-320 (2018)
- Schmöckel SM and **Jarvis DE**. Salt stress. In *Encyclopedia of Applied Plant Sciences (Second Edition)*. 40-43 (2017)

Invited Scholarly Presentation

- Jarvis DE.** An updated chromosome-scale assembly of quinoa using Hi-C. Plant and Animal Genome XXVI, San Diego, CA (2018)
- Jarvis DE.** The genome of the salt tolerant species *Chenopodium quinoa*. Quinoa for Future Food and Nutrition Security in Marginal Environments, Dubai, UAE (2016)
- Jarvis DE.** The genome of *Chenopodium quinoa*. Plant and Animal Genome XXIV, San Diego, CA (2016)
- Jarvis DE.** Identification of novel salt tolerance genes in the halophyte *Thellungiella halophila* by sense-RNAi. Southwest Consortium on Plant Genetics and Water Resources Symposium, Albuquerque, NM (2009)
- Jarvis DE.** The development of molecular tools for improvement of quinoa (*Chenopodium quinoa* Willd.). Plant and Animal Genome XIV, San Diego, CA (2006)

Published Abstracts

- Jarvis DE, Maughan PJ, Jellen EN, Tester M.** An updated chromosome-scale assembly of quinoa using Hi-C. 13th Annual Sequencing, Finishing, and Analysis in the Future (SFAF) Meeting, Santa Fe, NM (2018)
- Hansen H, Jellen EN, **Jarvis DE**, Maughan PJ. A PacBio and Hi-C based proximity guided assembly of *Chenopodium pallidiculae*. Plant and Animal Genome XXVI, San Diego, CA (2018)
- Van Loo EN, **Jarvis DE**, Borm TJA, Ho YS, Schmoeckel SM, Jellen EN, Kharbatia NM, Li B, Lightfoot DJ, Saber NO, Schijlen E, van der Linden CG, Maughan PJ, Tester MA. The chromosome scaffold based quinoa genome: its building and its use to find the non-bitter mutations in quinoa. Plant and Animal Genome XXV, San Diego, CA (2017)
- Jarvis DE**, Ho YS, Lightfoot DJ, Schmoeckel SM, Li B, Michell CT, Mineta K, Ohyanagi H, Gojobori T, Jellen EN, Maughan PJ, Tester M. The genome of the salt-tolerant species *Chenopodium quinoa*. Gordon Research Conference (Salt and Water Stress in Plants), Les Diablerets, Switzerland (2016)
- Jarvis DE**, Ryu C-H, Barrero-Gil J, Schumaker KS. Regulatory changes in *SOS1* contribute to the extreme salt tolerance of *Eutrema salsugineum*. Gordon Research Conference (Salt and Water Stress in Plants), Newry, ME (2014)
- Jarvis DE**, Ryu C-H, Barrero-Gil J, Beilstein MA, Schumaker KS. Regulatory and functional changes in *SOS1* contribute to the extreme salt tolerance of *Eutrema salsugineum*. Keystone Symposia on Molecular and Cellular Biology (Plant Abiotic Stress and Sustainable Agriculture: Translating Basic Understanding to Food Production), Taos, NM (2013)
- Jarvis DE**, Barrero-Gil J, Schumaker KS. Functional and evolutionary analysis of plant adaptation to salinity. 22nd International Conference on Arabidopsis Research, Madison, WI (2011)
- Jarvis DE**, Kopp OR, Jellen EN, Mallory MA, Pattee J, Bonifacio A, Coleman CE, Stevens MR, Fairbanks DJ, Maughan PJ. Simple sequence repeat development, polymorphism and genetic mapping in quinoa (*Chenopodium quinoa* Willd.). McKnight Foundation, Collaborative Crop Research Program Biennial Grantees Conference, Paris, France (2007)
- Stevens MR, Maughan PJ, Bonifacio A, Coleman CE, Jellen EN, Geary BD, Fairbanks DJ, Balzotti MB, Christensen SA, Gardunia BW, **Jarvis DE**, Kolano BA, Larson EM, Mason SL, Pratt C, Ricks MD. The development of molecular tools for improvement of the South American high plains underdeveloped crop quinoa (*Chenopodium quinoa* Willd.) International Conference on "Plant Genomics and Biotechnology: Challenges and Opportunities." Raipur, Chhattisgarh, India (2005)
- Jellen EN, **Jarvis DE**, Loskutov I, Jannink J-L, Ames DC, Raymond FD, Maughan PJ. Molecular variation in the secondary and distant primary oat gene pools (*Avena* spp.). Plant and Animal Genome XIII, San Diego, CA (2005)

Jellen EN, **Jarvis DE**, Ames DC, Loskutov IG, Raymond FD, Maughan PJ. Genetic variation in the secondary and distant primary oat gene pools. American Society of Agronomy Conference, Seattle, WA (2004)

Ricks MD, **Jarvis DE**, Jones RB, Stewart E, Butler DC, Stevens MR, Jellen EN, Coleman CE, Maughan PJ. Genetic linkage map of quinoa (*Chenopodium quinoa*). Plant and Animal Genome XII, San Diego, CA (2004)

Jellen EN, Stevens MR, Maughan PJ, Coleman CE, Bonifacio A, Mason SL, Ricks MD, Pratt C, **Jarvis DE**, Butler DC, Christensen SA, Coles ND, Jones RB, Maffei T, Nelson PT, Rasmussen AG, Stewart EW, Thompson CL, Gardunia BW, Fairbanks DJ. Genetic mapping and polymorphism in quinoa. American Society of Agronomy Conference, Denver, CO (2003)

MENTORING

Supervision of graduate students as advisor

Brian Cox M.S. 2018 – present

Supervision of graduate students as a committee member

Rebekah Lee M.S. 2017

Chris Hanson M.S. 2017

Hayley Hanson M.S. 2017 – present

Spencer Hunt M.S. 2017 – present

HOSTING VISITING SCIENTISTS

Drs. Mariusz and Lukasz Jaremko, Oct 2018, King Abdullah University of Science and Technology, Saudi Arabia

Dr. Elodie Rey, Jan 2019, King Abdullah University of Science and Technology, Saudi Arabia

RESEARCH GRANTS

External

Jarvis DE, Maughan PJ, Jellen EN (2018). Improving quinoa productivity through the use of wild relatives and induced variation. USDA-NIFA \$485,400 (pending)

Internal

Zach Jaramillo (2018). Evaluation of *Chenopodium berlandieri* as a source of novel traits for the agronomic improvement of quinoa. CURA. \$3,000

Jarvis DE (2017). The development of a mutant population in quinoa as a tool to identify genes regulating saponin biosynthesis in quinoa and as a resource for future functional studies. College of Life Sciences Start-up Grant. \$20,000.

Chaston JM, Jarvis DE, Coleman CE (2017). An experiment in multi-semester experiential learning for Genetics, Genomics, & Biotechnology students. Teaching Enhancement Grant. \$2,316.