

Daisie Iris Huang

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Education

Ph.D., Botany, Rancho Santa Ana Botanic Garden at Claremont Graduate University (2010).
Concentrations: Population genetics, plant molecular biology, phylogenetics, plant systematics.

B.A., Computer Science, University of California at Berkeley (2000).

B.S., Plant Biology, University of California at Berkeley (2000).

Academic Experience

Postdoctoral Research Fellow, University of British Columbia, 6/2012 to 6/2015. Worked on the POPCAN project funded by Genome Canada to explore genomic and phenotypic variability in poplar. Under the supervision of Dr. Quentin Cronk, I investigated phylogenetic relationships in the genus *Populus* and its relatives in the Salicaceae by using whole plastome and chondrome data, with eventual scaling to multilocus nuclear genes in a coalescent framework. Additionally, I developed software pipelines for efficient targeted assembly of next-generation sequencing libraries and was involved in several collaborative open-source software projects.

Postdoctoral Researcher, University of California at Santa Barbara. 10/2010 to 5/2012. Worked with Dr. Scott Hodges in conducting population genetics and genomic research in the genus *Aquilegia* (Ranunculaceae). Used next-generation sequencing data, investigating functional differences in the anthocyanin biosynthetic pathway in order to understand how flower color affects species differentiation and adaptation. Implemented the VIGS transformation protocol developed at Dr. Elena Kramer's lab for knockdown expression of genes in *Aquilegia*. Created mRNA-seq libraries for Illumina next-generation sequencing. Genotyped individuals from a large pollen-competition study involving over 1000 genetic individuals and analyzed the resulting dataset. Developed a method for extracting genomic DNA from inviable *Aquilegia* seeds, allowing genetic data to be obtained from materials previously thought to be unusable.

Teaching Assistant, Rancho Santa Ana Botanic Garden, Claremont, CA, 1/2008 to 5/2008. Assisted Dr. Elizabeth A. Friar in teaching Advanced Population Genetics. Assigned and graded weekly problem sets. Assisted Dr. Friar in designing and grading midterm and final exams. Assisted Dr. Friar in preparing lectures. Conducted weekly discussion sessions and office hours. Maintained a web site for the class.

Molecular Systematics Research Assistant, Rancho Santa Ana Botanic Garden, Claremont, CA, 1/2006 to 8/2008. Work was performed for Dr. Jennifer Cruse-Sanders and Dr. Elizabeth A. Friar's research (NSF Award Number 0519546). Developed silica-based method of extracting genomic DNA from polysaccharide-rich plant tissue. Extracted DNA from preserved samples of *Stenocereus stellatus*. Amplified and scored microsatellite markers for *S. stellatus* samples. Amplified and sequenced data from chloroplast markers in *S. stellatus*.

Herbarium Research Assistant, Rancho Santa Ana Botanic Garden, Claremont, CA, 8/2005 to 12/2005. Assisted with reidentifications of RSA-POM specimens for Dr. John Kartesz's Biota of North America. Mounted, filed, and databased specimens. Wrote scripts to update 4000+ recalcitrant entries in the herbarium's main Filemaker Pro database.

Employment History

Software Developer, Dryad Digital Repository, Durham, NC, 5/2014 to present. Worked with another colleague on a major initiative to move Dryad from a legacy university IT platform to a cloud-based, modern solution using AWS. Leveraged OpsWorks, EC2, S3, and Lambda, among other services, to create our system. This cloud migration was strategically important to Dryad for reliability and cost savings. As part of this migration, automated our deployment process using the virtualization technologies Vagrant and Ansible, creating a more robust and reproducible system and enabling consistent test environments. Refactored and scaled the Duraspace-based code base and added many features to automate curation and journal integration processes. Currently working with our new partner, the California Digital Library, to merge our two disparate systems by migrating to a Dash-based, Rails-based platform.

Associate Science Director, California Institute for Biodiversity, Oakland, CA, 9/2004 to 8/2005. Researched and wrote for *Coast Alive!*, an educational multimedia project focusing on the Southern California coast, targeted at 7th through 10th grades. Wrote and developed a large multimedia presentation on fire ecology, basic Mendelian genetics, and plant identification, based on a theoretical fire in the coastal sage scrub habitat of southern California. Edited Teacher Resource Guide for scientific accuracy.

Software Engineer, Apple Computer, Inc., Cupertino, CA, 6/2000 to 8/2004. Maintained KEXT Management code inside OS X, fixing flaws and adding features. Designed and implemented KEXT integrity verification system. Designed architecture for KEXT management features in Mac OS X 10.4. Designed and implemented thermal architecture for new portable hardware (U.S. patent numbers 7,451,332 and 8,237,386).

Awards and Honors

National Science Foundation microMORPH RCN Grant, Spring 2011.

Fletcher Jones Foundation Predoctoral Fellowship, Fall 2009, Spring 2010.

Rancho Santa Ana Botanic Garden: Phoebe and Howard Brown Graduate Program Fund, 2008-2009.

Southern California Botanists: SCB Annual Grant, 2007.

CNPS Bristlecone Chapter: Mary DeDecker Botanical Grant, 2007.

Rancho Santa Ana Botanic Garden: Goldhamer Scholarship, 2006-2007.

California Native Plant Society: G. Ledyard Stebbins Award for research in evolutionary botany, 2006.

Member of Upsilon Pi Epsilon (International Honor Society for Computer Science), UC Berkeley chapter.

Publications

Turner, KG, DI Huang, QCB Cronk, LH Rieseberg (2017) Homogenization of Populations in the Wildflower, Texas Bluebonnet (*Lupinus texensis*). *Journal of Heredity*, esx094.

<https://doi.org/10.1093/jhered/esx094>

Allen, JM, B Boyd, NP Nguyen, P Vachaspati, T Warnow, DI Huang, PG Grady, KC Bell, QCB Cronk, L Mugisha, BR Pittendrigh, LM Soledad, DL Reed, KP Johnson (2017) Phylogenomics from Whole Genome Sequences Using aTRAM. *Systematic Biology*, syw105. doi:

10.1093/sysbio/syw105

Huang, DI and QCB Cronk (2015) Plann: A Command-Line Application for Annotating Plastome Sequences. *Applications in Plant Sciences*, 3: 1500026. doi: 10.3732/apps.1500026

Allen, JM, DI Huang, QC Cronk, KP Johnson (2015) aTRAM – automated target restricted assembly method: a fast method for assembling loci across divergent taxa from next-generation sequencing data. *BMC Bioinformatics*, 16: 98. doi:10.1186/s12859-015-0515-2

Huang, DI, CA Hefer, N Kolosova, C Douglas, QC Cronk (2014) Whole plastome sequencing reveals deep plastid divergence and cytonuclear discordance between closely related balsam poplars, *Populus balsamifera* and *P. trichocarpa* (Salicaceae). *New Phytologist*, 204: 693–703. doi: 10.1111/nph.12956

Huang, DI and H Lapp (2013) Software Engineering as Instrumentation for the Long Tail of Scientific Software. Contributed paper for the Workshop on Sustainable Software for Science: Practice and Experiences at SC13, Denver, CO.

Huang, DI (2013) A conservation plan for *Lupinus ludovicianus* (San Luis Obispo County Lupine, Fabaceae). Rancho Santa Ana Botanic Garden Occasional Publications 13.

Cruse-Sanders, JM, KC Parker, EA Friar, DI Huang, S Mashayekhi, LM Prince, A Otero-Arnaiz, A Casas (2013) Managing diversity: Domestication and gene flow in *Stenocereus stellatus* Riccob. (Cactaceae) in Mexico. *Ecology and Evolution*, 3, 1340-1355. doi: 10.1002/ece3.524

Huang, DI and EA Friar (2011). Relationships in the *Lupinus albifrons* species complex (Fabaceae) based on two highly variable chloroplast regions. *Systematic Botany*, 36, 362-70. doi: 10.1600/036364411X569543

Huang, DI, CA Hefer, N Kolosova, C Douglas, Q Cronk. In prep. Whole plastome phylogeography of two widespread balsam poplars, *Populus balsamifera* and *P. trichocarpa* (Salicaceae) in North America. To be submitted to *American Journal of Botany*.

Presentations

Huang, DI, JM Allen, KP Johnson, and Q Cronk (2014). Phylogenomic exploration with aTRAM. Presented at Evolution 2014, Raleigh, NC.

<http://dx.doi.org/10.6084/m9.figshare.1066958>

Huang, DI (2013). Panel subpresentation on Implementing Policy in Sustainable Software. Presented at WSSSPE 2013, Denver, CO. <http://www.slideshare.net/DaisieHuang/implementing-policy-wssspe>

Huang, DI and Q Cronk (2013). Plastome phylogenetics in *Populus*. Presented at Evolution 2013, Snowbird, UT. <http://www.slideshare.net/DaisieHuang/plastome-phylogenomics-in-populus>

Huang, DI and EA Friar (2010). Incomplete lineage sorting above the species level in *Lupinus* (Fabaceae). Presented at Evolution 2010, Portland, OR.

Huang, DI and EA Friar (2009). Perennial *Lupinus* of western North America: Challenges in defining species boundaries in a recent radiation. Presented at Botany 2009, Snowbird, UT, and Evolution 2009, Moscow, ID.

Huang, DI (2008). Untangling relationships in the perennial lupines of California. Invited talk, Bristlecone Chapter of the California Native Plant Society, Bishop, CA.

Huang, DI and EA Friar (2008). Monophyly in western North American *Lupinus*. Presented at Botany 2008, Vancouver, BC.

Huang, DI and EA Friar (2007). Phylogenetics in three groups of perennial *Lupinus* in California. Presented at Botany and Plant Biology Joint Congress, Chicago, IL.

Huang, DI, LA McDade, and EA Friar (2007). Chloroplast inheritance in *Lupinus*. Poster presented at Botany and Plant Biology Joint Congress, Chicago, IL.

Cruse-Sanders, JM, EA Friar, KC Parker, DI Huang, and A Casas (2007). Geographically based analysis of genetic diversity in wild, managed and cultivated populations of the columnar cactus *Stenocereus stellatus* in Central Mexico. Poster presented at Botany and Plant Biology Joint Congress, Chicago, IL.

Professional Service

Instructor and repository maintainer for Software Carpentry

Reviewer for Plant Systematics and Evolution, Molecular Phylogenetics and Evolution, Molecular Ecology Resources, PLOS One.

Reviewer for NSF Division of Environmental Biology

Code contributor to BioPerl and Mesquite, open-source bioinformatics projects

Organizing committee member for iEvoBio 2014, Raleigh, NC, in June 2014.

Participant at Phylotastic 2 hackathon, January 2013, hosted by NESCent at iPlant in Tucson, AZ.

Participant at TaxonWorks hackathon, September 2013, at the Illinois Natural History Survey, Champaign, IL.

Participant at Tree-For-All hackathon, September 2014, at the University of Michigan at Ann Arbor.

Participant at FuturePhy hackathon, February 2016, at the University of Florida at Gainesville.

Professional Affiliations

American Society of Plant Taxonomists

Botanical Society of America

Society for the Study of Evolution