

CONTACT INFORMATION	Biological Sciences 2901 Main Street Lubbock, TX 79409 806-834-5750 (office)	Texas Tech University matt.johnson@ttu.edu website: mossmatters.com
EDUCATION	Ph.D. Duke University, Durham, NC Dissertation: “Evolution of Mating Systems in <i>Sphagnum</i> peatmosses” B.S. with distinction , Duke University, Durham, NC Honors Thesis: “Genetic relationships within <i>Sphagnum cribrosum</i> Lind. “wave form” and “normal form” in southeastern North Carolina using three anonymous nuclear genes.”	May, 2013 May 2006
PROFESSIONAL APPOINTMENTS	Assistant Professor Biological Sciences Texas Tech University Director E.L. Reed Herbarium (TTC) Postdoctoral Research Associate Plant Science and Conservation Research Center Chicago Botanic Garden Supervisor: Norman Wickett, Ph.D	September 2017 to present September 2017 to present June 2013 to August 2017
PUBLICATIONS	Journal Articles (34 total, 11 first-author, 2 last-author) Google Scholar Profile <ol style="list-style-type: none"> 1. S.B. Carey, J. Jenkins, J.T. Lovell, F. Maumus, A. Sreedasyam, A.C. Payton, S. Shu, G.P. Tiley, N. Fernandez-Pozo, K. Barry, C. Chen, M. Wang, A. Lipzen, C. Daum, C.A. Saski, J.C. McBreen, R.E. Conrad, L.M. Kollar, S. Olsson, S. Huttunen, J.B. Landis, J.G. Burleigh, N.J. Wickett, M.G. Johnson, S.A. Rensing, J. Grimwood, J. Schmutz, and S.F. McDaniel. The <i>Ceratodon purpureus</i> genome uncovers structurally complex, gene rich sex chromosomes. 2021. <i>Science Advances</i> 7 (27), eabh2488. doi:10.1126/sciadv.abh2488 2. N. Patel, R. Medina, M.G. Johnson, and B. Goffinet. Karyotypic diversity and cryptic speciation: Have we vastly underestimated moss species diversity? 2021. <i>Bry. Div. Evol.</i> 043 (1): 150-165. doi:10.11646/bde.43.1.12 3. M. Slimp*, L.D. Williams, H. Hale, and M.G. Johnson. On the potential of Angiosperms353 for population genomics. 2021. <i>Applications in Plant Sciences</i> doi:10.1002/aps3.11419 4. E.M. Gardner, M.G. Johnson[†], J.T. Pereira, A.S.A. Puad, D. Arifiani, S. Sahromi, N.J. Wickett, and N.J.C. Zerega. Paralogs and off-target sequences improve phylogenetic resolution in a densely-sampled study of the breadfruit genus (<i>Artocarpus</i>, Moraceae). 2021 <i>Systematic Biology</i>, 70(3) 558-575. doi:10.1093/sysbio/syaa073 	

5. Ribeiro, C. L., Conde, D., Balmant, K. M., Dervinis, C., **Johnson, M. G.**, McGrath, A. P., Szewczyk, P., Unda, F., Finegan, C. A., Schmidt, H. W., Miles, B., Drost, D. R., Novaes, E., Gonzalez-Benecke, C. A., Peter, G. F., Burleigh, J. G., Martin, T. A., Mansfield, S. D., Chang, G., Wickett, N. J. Kirst, M. (2020). The uncharacterized gene EVE contributes to vessel element dimensions in *Populus*. *Proceedings of the National Academy of Sciences of the United States of America*, 117(9), 5059-5066. doi:10.1073/pnas.1912434117
6. H. Hale, E.M. Gardner, J. Viruel, L. Pokorny, and **M.G. Johnson**. 2020. Strategies for reducing per-sample costs in target capture sequencing for phylogenomics and population genomics in plants. Invited Special Issue: *Low-cost methods in plant sciences Applications in Plant Sciences* e11337. doi:10.1002/aps3.11337.
7. A. Ghosh, **M.G. Johnson**, A.B. Osmanski, S. Louha, N.J. Bayona-Vasquez, T.C. Glenn, J. Gonorga, R.E. Green, S. Isberg, R.D. Stevens, and D.A. Ray. 2020. A high-quality reference genome assembly of the saltwater crocodile, *Crocodylus porosus*, reveals patterns of selection in Crocodylidae. *Genome Biology and Evolution* 12(1), 3635-3646. doi:10.1093/gbe/evz269.
8. S. Dodsworth[†], L. Pokorny[†], **M.G. Johnson[†]**, J.T. Kim, O. Maurin, N.J. Wickett, F. Forrest, and W.J. Baker. 2019. Hyb-Seq for Flowering Plant Systematics. *Trends in Plant Science* doi:10.1016/j.tplants.2019.07.011
9. R. Medina, **M.G. Johnson**, Y. Liu, N. Wickett, A.J. Shaw, and B. Goffinet. Phylogenomic delineation of Physcomitrium (Bryophyta: Funariaceae) based on targeted sequencing of nuclear exons and their flanking regions rejects the retention of Physcomitrella, Physcomitridium and Aphanorrhegma. *J. Systematics and Evolution* 57(4): 404-417. doi:10.1111/jse.12516
10. Y. Liu[†], **M.G. Johnson[†]**, C.J. Cox, R. Medina, N. Devos, A. Vanderpoorten, L. Hedenas, N. Bell, J.R. Shevock, B. Aguero, D. Quandt, N.J. Wickett, A.J. Shaw, and B. Goffinet. 2019. Resolution of the ordinal phylogeny of mosses using targeted exons from organellar and nuclear genomes. *Nature Communications* 10, Article number: 1485. doi:10.1038/s41467-019-09454-w
11. **M.G. Johnson[†]**, L. Pokorny[†], S. Dodsworth[†], L.R. Botigue, R.S. Cowan, A. Devault, W.L. Eiserhardt, N. Epiawalage, F. Forest, J.T. Kim, J.H. Leebens-Mack, I.J. Leitch, O. Maurin, D.E. Soltis, P.S. Soltis, G.K. Wong, W.J. Baker, and N.J. Wickett. A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using k-medoids Clustering. *Systematic Biology* 68(5): 594-606. doi:10.1093/sysbio/syy086
12. T. Villaverde, L. Pokorny, S. Olson, M. Rincon, **M.G. Johnson**, E.G. Gardner, N.J. Wickett, J. Molero, R. Riina, and I. Sanmartin. 2018. Bridging the micro-macro evolutionary gap: target sequencing with chloroplast skimming resolves phylogenetic relationships within the Rand Flora *Euphorbia balsamifera*. *New Phytologist* 220:636-650. doi:10.1111/nph.15312
13. K. LaRiccia, **M.G. Johnson**, E.G. Gardner, D. Ragone, N. Zyreg, and N.J. Wickett. 2018. A transcriptome screen for positive selection in domesticated breadfruit and its wild relatives (*Artocarpus* spp.). *American Journal of Botany* 105(5): 915-926. doi:10.1002/ajb2.1095
14. P.G. Wolf, T.A. Robison, **M.G. Johnson**, M.A. Sundue, W.L. Testo, and C.J. Rothfels. 2018. Target Sequence Capture of Nuclear-Encoded Genes for Phylogenetic Analysis in Ferns *Applications in Plant Science* e01148. doi:10.1002/aps3.1148

15. H.R. Kates[†], **M.G. Johnson[†]**, E.G. Gardner, N. Zyrega, and N.J. Wickett. 2018. Allele phasing has minimal impact on phylogenetic reconstruction from targeted nuclear gene sequences in a case study of *Artocarpus* (Moraceae) *American Journal of Botany* 105(3):404-416 *Invited Special Issue: Using and Navigating the Plant Tree of Life* doi:10.1002/ajb2.1068
16. M.R. McKain[†], **M.G. Johnson[†]**, S. Uribe-Convers[†], D. Eaton[†], and Y. Yang. 2018[†]. Practical considerations for plant phylogenomics. *Applications in Plant Sciences* 6(3):e01038. *Invited Special Issue: Methods for Exploring the Plant Tree of Life* doi:10.1002/aps3.1038
17. R. Medina, **M.G. Johnson**, Y. Liu, N. Wilding, T.A. Hedderson, N.J. Wickett, and B. Goffinet. 2018. Evolutionary Dynamism in Bryophytes: Phylogenomic Inferences Confirm Rapid Radiation in the Moss Family Funariaceae. *Molecular Phylogenetics and Evolution* 120:240-247. doi:10.1016/j.ympev.2017.12.002.
18. D.J. Weston, M.R. Turetsky, **M.G. Johnson**, G. Granath, Z. Lindo, L.R. Belyea, S.K. Rice, D.T. Hanson, K.A.M. Engelhardt, J. Schmutz, E. Dorrepaal, E.S. Euskirchen, H.K. Stenoién, P. Szovenyi, M. Jackson B.T. Piatkowski, W. Muchero, R.J. Norby, J.E. Kostka, J.B. Glass, H. Rydin, J. Limpens, E. Tuittila, K.K. Ulrich, A. Carrell, B.W. Benscoter, J. Chen, T.A. Oke, M.B. Nilsson, P. Ranjan, D. Jacobson, E.A. Lileskov, R.S. Clymo, and A.J. Shaw. 2018. The Sphagnum Project: Enabling Ecological and Evolutionary Insights through a Genus-Level Sequencing Project. *New Phytologist* 217 (1):16-25.
19. **M.G. Johnson**, E.M. Gardner, Y. Liu, R. Medina, B. Goffinet, A.J. Shaw, N.J.C. Zerega, and N.J. Wickett. 2016. HybPiper: Extracting coding sequence and introns for phylogenetics from high-throughput sequencing reads using target enrichment. *Applications in Plant Sciences*. 4(7):1600016 doi:10.3732/apps.1600016.
20. E.M. Gardner, **M.G. Johnson**, D. Ragone, N.J. Wickett, and N.J.C. Zerega. 2016. Low-coverage, whole-genome sequencing of *Artocarpus camansi* (Moraceae) for phylogenetic marker development and gene discovery. *Applications in Plant Sciences* 4(7):1600017. doi:10.3732/apps.1600017.
21. N. Brandley, **M.G. Johnson**, and S. Johnsen. 2016. Aposematic signals in North American black widows are more conspicuous to predators than to prey. *Behavioral Ecology*. 27(4):1104-1112. doi:10.1093/beheco/arw014
22. **M.G. Johnson** and A.J. Shaw. 2016. The effects of quantitative fecundity in the haploid stage on reproductive success and diploid fitness in the aquatic peat moss *Sphagnum macrophyllum*. *Heredity*. 116:523-530. doi:10.1038/hdy.2016.13.
23. **M.G. Johnson**, C. Malley, A.J. Shaw, B. Goffinet, and N.J. Wickett. 2016. A phylotranscriptomic analysis of gene family expansion and evolution in the largest order of pleurocarpous mosses (Hypnales, Bryophyta). *Molecular Phylogenetics and Evolution*. 98:29-40. doi:10.1016/j.ympev.2016.01.008
24. N. Devos, P. Szovenyi, D. Weston, C. Rothfels, **M.G. Johnson**, and A.J. Shaw. 2016. Analyses of transcriptome sequences reveal multiple ancient large-scale duplication events in the ancestor of Sphagnopsida (Bryophyta). *New Phytologist* 211(1):300-318. doi:10.1111/nph.13887.
25. **M.G. Johnson**, K. Lang, P. Manos, G.H. Golet, and K.A. Schierenbeck. 2016. Evidence for genetic pollution of a California native tree, *Platanus racemosa*, via recent, ongoing introgressive hybridization with an introduced ornamental species." *Conservation Genetics*. 17(3):593-602. doi:10.1007/s10592-015-0808-z.

26. **M.G. Johnson** and A.J. Shaw. 2015. Genetic diversity, sexual condition, and microhabitat preference determine mating patterns in *Sphagnum* (Sphagnaceae) peat-mosses. *Biological Journal of the Linnean Society*. 115(1):96-113. doi:10.1111/bij.12497
27. **M.G. Johnson**, G. Granath, T. Tahvanainen, R. Pouliot, H. Stenoien, L. Rochefort, H. Rydin, and A.J. Shaw. 2015. Evolution of niche preference in *Sphagnum* peat mosses” *Evolution*. 69(1) 90-103. doi:10.1111/evo.12547
28. E. Mikulaskova, M. Hajek, A. Veleba, **M.G. Johnson**, T. Tomas, and A.J. Shaw. 2015. Local adaptations in bryophytes revisited: the genetic structure of the calcium-tolerant peatmoss *Sphagnum warnstorffii* along geographic and pH gradients. *Ecology and Evolution*. 5(1) 229-242. doi:10.1002/ece3.1351
29. A.J. Shaw, B. Shaw, **M.G. Johnson**, N. Devos, H. Stenoien, K.I. Flatberg, and B.E. Carter. 2015. Phylogenetic structure and biogeography of the Pacific Rim clade of *Sphagnum* subgen. *Subsecunda*: haploid and allopolyploid taxa. *Biological Journal of the Linnean Society*. 116(2): 295-311. doi:10.1111/bij.12586
30. A.J. Shaw, B. Shaw, **M.G. Johnson**, M. Higuchi, T. Arikawa, Y. Hirayama, and N. Devos. 2013. Origins, genetic structure, and systematics of the narrow endemic peatmosses (*Sphagnum*): *S. triseriporum* and *S. calymmatophyllum* (Sphagnaceae). *American Journal of Botany*. 100(6) 1202-1220. doi:10.3732/ajb.1200630
31. **M.G. Johnson**, B. Shaw, P. Zhou, and A.J. Shaw. 2012. Genetic analysis of the peatmoss *Sphagnum cribrosum* indicates indepent origins of an extreme infra-specific morphology shift. *Biological Journal of the Linnean Society*. 106(1):137-153. doi:10.1111/j.1095-8312.2012.01842.x
32. A.J. Shaw, K.I. Flatberg, P. Szovenyi, M. Ricca, **M.G. Johnson**, H. Stenoien, and B. Shaw. 2012. Systematics of the *Sphagnum fimbriatum* complex: phylogenetic relationships, morphological variation, and allopolyploidy. *Systematic Botany*. 37:36-50. doi:10.1600/036364412X616585
33. M. Ricca, P. Szovenyi, E. Temsch, **M.G. Johnson**, and A.J. Shaw. 2011. Interploidal hybridization and mating patterns in *Sphagnum subsecundum* complex. *Molecular Ecology*. 20(15): 3202-3218. doi:10.1111/j.1365-294X.2011.05170.x
34. M. Ramaliya*, **M.G. Johnson**, J. Heinrichs, J. Hentschel, M. von Konrat, P. Davison, B. Shaw, and A.J. Shaw. 2010. Morphologically cryptic biological species within the liverwort *Frullania asagrayana*. *American Journal of Botany*. 97:1707-1718. doi:10.3732/ajb.1000171

(†Authors Contributed Equally; *Undergraduate Student)

IN REVIEW AND REVISION

1. L.L. Bechen*, **M.G. Johnson**, G. Broadhead, R. A. Levin, R.P. Overson, T. Jogesh, J.B. Fant, R.A. Raguso, K.A. Skogen, and N.J. Wickett. Differential gene expression associated with a floral scent polymorphism in the evening primrose *Oenothera harringtonii* (Onagraceae) *BMC Genomics (in revision)*, preprint: doi:10.1101/2021.01.12.426409
2. K.N. Krakos, **M.G. Johnson**, P.C. Hoch, W.L. Wagner, P. Huan, and P.H. Raven. Molecular phylogenetics reveals multiple transitions to self-compatibility in a primary subclade of *Oenothera*. *Taxon. (in review)*
3. W. Freyman, **M.G. Johnson** and C.J. Rothfels. homologizer: Phylogenetic phasing of gene copies into polyploid subgenomes preprint doi:10.1101/2020.10.22.351486

4. A. Patsis*, R.P. Overson, K.A. Skogen, N.J. Wickett, **M.G. Johnson**, W.L. Wagner, R.A. Raguso, J.B. Fant, and R.A. Levin. Elucidating the Evolutionary History of Oenothera Sect. Pachylophus (Onagraceae): A Phylogenomic Approach to Inference of Taxon Relationships. *Systematic Botany* (accepted, in press)
 5. J.B. Beck, M.L. Markley, M.G. Zielke, J.R. Thomas, H.J. Hale, L.D. Williams, and **M.G. Johnson**. Is Palmers elm leaf goldenrod real? The Angiosperms353 kit provides within-species signal in *Solidago ulmifolia* s.l. *Systematic Botany* accepted, in press, preprint: doi:10.1101/2021.01.07.425781
- (* Undergraduate Student)

NON-REFERREED

1. W.J. Baker, S. Dodsworth, F. Forest, S.W. Graham, **M.G. Johnson**, A. McDonnell, L. Pokorny, J.A. Tate, S. Wicke, and N.J. Wickett. 2021. Exploring Angiosperms353: an open, community toolkit for collaborative phylogenomic research on flowering plants *American Journal of Botany* (accepted, in press).
2. A. McDonnell, W.J. Baker, S. Dodsworth, F. Forest, S.W. Graham, **M.G. Johnson**, L. Pokorny, J.A. Tate, S. Wicke, and N.J. Wickett. 2021. Exploring Angiosperms353: Developing and Applying a Universal Toolkit for Flowering Plant Phylogenomics . *Applications in Plant Sciences*. (accepted, in press)

EXTERNAL RESEARCH GRANTS

Principal Investigator: Collaborative Research: Diversity of *Physcomitrium pyriforme* in North America and Europe: significance of autopolyploidy within a phylogenomic and experimental framework. *National Science Foundation Division of Environmental Biology*. 2018-2021. Awarded Amount: \$417,685. DEB-1753800

Subaward: Progress toward solving the silvery-thread moss issue in cool-season putting greens. *United States Golf Association*. 2019-2021. Total Awarded Amount: \$119,991. Sub-award: \$12,000. Lead Principal Investigator: Lloyd Stark, University of Nevada Las Vegas. Collaborator: Zane Raudenbush, Ohio State University.

Subaward: Digitization TCN: Collaborative: American Crossroads: Digitizing the Vascular Flora of the South-Central United States. *National Science Foundation*. 2019-2021. Total Awarded Amount: \$1,497,043. Sub-award: \$29,775. Lead Principal Investigator: Peter Fritsch, Botanical Research Institute of Texas.

AWARDS AND FELLOWSHIPS

Harold Sanford Perry Prize (\$5,500)	May 2013
– Annual departmental cash award for the best dissertation in Plant Sciences.	
– Students are nominated and selected by Duke Biology faculty.	
Duke Biology Department Grant-in-Aid of Research (\$500)	June 2012
E. Bayard Halsted Scholarship (\$19,836)	August 2010
Sigma Xi Grant-in-Aid of Research (\$1,000)	December 2009

PRESENTATIONS

Invited Seminars

On the potential of Angiosperms353 for Population Genomics	
<i>Botanical Society of America</i>	July 2020
Invited Symposium Speaker: Angiosperms353: A new essential tool for plant systematics	
Making sense of plant biodiversity using targeted DNA sequencing	
<i>Angelo State University Tri-Beta</i>	October 2020
Intergeneric allopolyploidy in Funariaceae revealed through targeted sequencing	
<i>Plant and Animal Genomes XXVII, Polyploidy Session</i>	January 2019

Embracing the Conflict: Phylogenomics and the Diversification of Mosses
American Bryological and Lichenological Society Annual Meeting August 2018
Invited Keynote Speaker

Including herbarium specimens in targeted sequencing projects: data analysis challenges and solutions.
Botanical Society of America July 2018
Invited Colloquium Speaker: Herbaria in the Genomics Age

One Set of Markers to Rule them All: Advances in Targeted Sequencing for Phylogenetics from Populations to Phyla
Wichita State University April 2018

Phylogenomic insights into the radiation of bryophytes.
Utah State University October 2017

Phylotranscriptomic analysis reveals widespread gene duplication associated with the radiation of pleurocarpous mosses
XIX International Botanical Congress, Shenzhen, China July 2017

Building a better tree and using it wisely: Phylogenomic approaches in non-model organisms
Chicago Plant Science Symposium, Field Museum April 2017

Building a better tree and using it wisely: Phylogenomic approaches in non-model organisms
University of Connecticut Biology Forum March 2017

Targeted Exon Sequencing in Non-Model Organisms: Best Practices for Probe Design and Data Analysis with HybPiper
PAG XXV, MycroArray Session January 2017

Introns, Paralogs, and Ditching the Bootstrap: Targeted Sequencing with HybPiper
University of Florida PopBio Seminar Series September 2016

Phylotranscriptomic insights into the radiation of mosses
2nd International Symp. on Pleurocarpous Mosses. Bonn, Germany June 2016

Evolution of niche preferences in *Sphagnum*
New Phytologist Sphagnum genomics meeting, invited participant April 2016

Ecological genomics in peatlands: the rise of *Sphagnum* as a model system
University of Chicago Darwin's Weekly Seminar Series February 2016

Reconstructing the ancestral gene set of bryophytes from comparative transcriptomes
PAG XXIV, Non-Seed Plant Section, San Diego, CA January 2016

Another abominable mystery: using phylogenomics to explore the radiation of mosses
University of Wisconsin Biology Colloquium March 2015

Scaling evolution from genomes to ecosystem in peatmosses (*Sphagnum*)
NESCent Catalysis Meeting, invited participant October 2014

What can phylogenetics teach us about peatland ecology?
Symposium: The evolution and ecology of aquatic bryophytes.
American Bryological and Lichenological Society Botany Conference, July 2014

Scientific Meetings

- Botanical Society of America, Tuscon, AZ July 2019
Oral Paper: Phylogenomic delineation of Physcomitrium based on targeted sequencing rejects the retention of Physcomitrella and other genera
Oral Paper: A phylogenomic approach to decode contentious relationships across all angiosperm families
- Texas Plant Conservation Conference, Fort Worth, TX September 2018
Lightning Talk: The Genetic Time Machine: Investigating the Response to Climate Change and Land Management Via a 50-Year-Old Herbarium Collection from Guadalupe Mountains National Park
- International Moss (iMOSS), Tampa, FL June 2018
Oral Paper: Intergeneric allopolyploidy in Funariaceae revealed through targeted sequencing
- Botanical Society of America, Savannah, GA July 2016
Colloquium Presentation: A re-evaluation of ancient horizontal transfer in bryophytes using comparative transcriptome data.
- Botanical Society of America, Edmonton, AB July 2015
Oral Paper: Phylotranscriptomic insights into the radiation of pleurocarpous mosses.
- Botanical Society of America, Boise, ID July 2014
Oral Paper: Constructing phylogenetic datasets with bait-capture data without a genome: strategies and challenges.
- Botanical Society of America, New Orleans, LA July 2013
Oral Paper: The relationship between mating patterns, sexual condition, and microhabitat preference in *Sphagnum*
- American Society of Human Genetics, San Francisco, CA November 2012
Poster: Comparison of phylogenetic and haplotype methods for the study of genotype-phenotype association in genome-wide studies.
- Botanical Society of America, Columbus, OH July 2012
Poster: Evolution of microhabitat preference in *Sphagnum*
- Evolution Meeting, Norman, OK June 2011
Oral Paper: Fitness and fecundity variance in a natural *Sphagnum* population: potential for sexual selection?

Co-authored Presentations by Mentees

- Texas Plant Conservation Conference August 2020
Oral Paper Towards a Genetic Database of Texas Flora Via Targeted Sequencing of 353 Genes
Presented by: Haley Hale, Technician III, Texas Tech University
- Botanical Society of America, Virtual Conference July 2020
Oral Paper Herbaria as botanical snapshots: 50 years of land use and climate change impacts on genetics and physiology in the Guadalupe Mountains
Presented by: Madeline Slimp, Honors URS, Texas Tech University
Oral paper Implementing undergraduate research in an upper-level botany lab using target capture sequencing of herbarium specimens

Presented by: Haley Hale, Technician III, Texas Tech University
Lightning Talk Characterization of the Fungal Microbiome in 50-year-old plant herbarium specimens
 Presented by: Cassidy Coker, Honors URS, Texas Tech University
Lightning Talk Methods to delimit speciation and determine population parameters of the moss *Physcomitrium pyriforme* using target capture sequencing.
 Presented by: Lindsay Williams, Ph.D. Student, Texas Tech University
Lightning Talk: Development of genomic tools for *Bryum argenteum*: applications in small RNA and population genetics
 Presented by: Aman Pruthi, Master's student, Texas Tech University
Lightning Talk: Phylogenomics and Habitat restoration: detecting the effects of gene duplication and diversification of KAI2 on seed germination
 Presented by: Yanni Chen, Ph.D. Student, Texas Tech University
Lightning Talk: Expanded phylotranscriptomic sampling reveals gene family expansion in pleurocarpous mosses
 Presented by: Kira Buckowing, Master's Student, Texas Tech University

Botanical Society of America, Tuscon, AZ July 2019
Poster Conservation genomics of plant populations in Guadalupe Mountains National Park using herbarium specimens.
 Presented by: Madeline Slimp, Honors URS, Texas Tech University
Poster The effect of life-history strategies on stomatal characteristics using herbarium specimens from Guadalupe Mountains National Park.
 Presented by: Zachary Bailey, Honors URS, Texas Tech University
Oral Paper Phylogenetic information in seed morphology and seed germination for shortgrass prairie species.
 Presented by: Yanni Chen, Ph.D. Student, Texas Tech University
Oral Paper Developing a cost-effective workflow for targeted sequencing of herbarium specimens using Angiosperms353.
 Presented by: Haley Hale, Technician III, Texas Tech University

TEACHING EXPERIENCE	Professor , Texas Tech University	2017 - present
	Biology of Plants (BIOL 1401)	<i>Non-majors course</i> Typical enrollment: 120-144
	Phylogenetics (BIOL 6304)	<i>Graduate course</i> Typical enrollment: 8-10
	Evolution of Plants (BOT 3404)	<i>Majors-level lab course</i> Typical enrollment: 16-20
	Bioinformatics User Group Series (BIOL 4101-003)	
	<i>Seminar course, co-instructor with Dr. Amanda Brown</i>	Typical Enrollment: 10-15
	Co-instructor , Northwestern University	2013-2016
	Field and Lab Methods in Plant Biology and Conservation (PSC 450)	
	<i>Phylogenetics and Genomics Section</i>	
	Nyree Zerega, Course Coordinator	
	Teaching Assistant , Duke University Biology Department	
	BIO 212L Microbiology	Spring 2009, Fall 2012, Spring 2013
	BIO 26L Organismal Diversity	Summer 2010
MENTORING AND ADVISING	Graduate Major Advisor	
	– Yanni Chen, Texas Tech University	Ph.D. Student 2018-
	– Aman Pruthi, Texas Tech University	M.S. Student 2019-
	Co-advisor: Zhixin Xie	
	– Lindsay Williams, Texas Tech University	Ph.D. Student 2020-

Graduate Research Advisor

- Kira Buckowing, Texas Tech University M.S. Student 2019-
Department: Biotechnology and Bioinformatics
- Katie Holt, Texas Tech University M.S. 2019
Department: Museum Science

Thesis Committees: Active

- Francisco Castellanos, Texas Tech University M.S. Student
Advisor: David Ray
- Diksha Gambir, Texas Tech University Ph.D. Student
Advisor: Matt Olson
- Sarah Vrla, Texas Tech University Ph.D. Student
Advisor: Robert Bradley
- Daniela Arenasviveros, Texas Tech University Ph.D. Student
Advisor: Jorge Salazar-Bravo
- Shariful Islam, Texas Tech University Ph.D. Candidate
Advisor: Catherine Wakeman
- Morgan Long, Texas Tech University M.S. Student
Advisor: Dylan Schwilk
- Austin Osmanski, Texas Tech University Ph.D. Student
Advisor: David Ray
- Jennifer Korstian, Texas Tech University Ph.D. Candidate
Advisor: David Ray
- Nan Hu, Texas Tech University Ph.D. Student
Advisor: Matt Olson
- Shiva Aghdam, Texas Tech University Ph.D. Student
Advisor: Amanda Brown
- Minghao Guo, Texas Tech University Ph.D. Student
Advisor: Matt Olson
- Colby Witherup, Northwestern University Ph.D. Candidate
Advisor: Norman Wickett

Thesis Committees: Past

- Kelly McMillen, Texas Tech University M.S. 2021
Advisor: Natasja VanGestel
- Simrandeep Singh, Texas Tech University M.S. 2021 Advisor: Amanda Brown
- Claire Malley, Northwestern University M.S. 2015
Advisor: Norman Wickett

Undergraduate Researchers

- Sherese Price, Independent Research 2020-present
- Anukriti Dey, Independent Research 2021-present
- Cassidy Coker, Honors College (URS) *Herbarium* 2019-2021
- Madeline Slimp, Honors College (URS) *Herbarium* 2018- 2021
- Kristina Robinson *Herbarium* 2018-2019
- Lauren Winfrey, Independent Research *Herbarium* 2018-2019
- Zachary Bailey, Honors College (URS) *Herbarium* 2017-2019

Past Students Mentored

- Elliot Gardner, Northwestern University Ph.D. 2017
- Marissa Ashner, Illinois Institute of Technology REU 2016
- Lindsey Bechen, Amherst College REU 2015
- Kristen Laricchia, Northwestern University M.S. 2014

**PROFESSIONAL
AFFILIATIONS****Departmental**

- *Director, E.L. Reed Herbarium* 2017-present
- *Chair, Seminar Committee* 2019-present
- *Member, Space Committee* 2018-present
- *Elected Member, Initiatives Committee* 2020-present

- *Search Committee Member, Quantitative Biologist* 2018

Professional

- *Applications in Plant Sciences*, Guest Special Issue Editor: Angiosperms353 2020
- *Technology Committee Member*, Botanical Society of America 2019-present
- *Reviewer: Analytical Biochemistry, American Journal of Botany, Applications in Plant Sciences, Botanical Journal of the Linnean Society, Ecology and Evolution, Frontiers in Plant Science, Molecular Biology and Evolution, Molecular Phylogenetics and Evolution, New Phytologist, Perspectives in Plant Ecology Evolution and Systematics, Restoration Ecology, Reviews in Plant Science, PeerJ, Bioinformatics*

Other Service

Freely available bioinformatics pipelines and programming tutorials

<http://github.com/mossmatters>