
CONTACT INFORMATION	Biological Sciences 2901 Main Street Lubbock, TX 79409 806-834-5750 (office)	Texas Tech University matt.johnson@ttu.edu website: mossmatters.com
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EDUCATION	Ph.D. Duke University, Durham, NC Dissertation: “Evolution of Mating Systems in <i>Sphagnum</i> peatmosses”	May, 2013
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	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 2006
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PROFESSIONAL APPOINTMENTS	Assistant Professor Biological Sciences Texas Tech University	September 2017 to present
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	Director E.L. Reed Herbarium (TTC)	September 2017 to present
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	Postdoctoral Research Associate Plant Science and Conservation Research Center Chicago Botanic Garden Supervisor: Norman Wickett, Ph.D	June 2013 to August 2017
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PUBLICATIONS	Journal Articles (41 total, 12 first-author, 3 last-author) Google Scholar Profile
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1. 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*. 2022. *Annals of the Missouri Botanical Garden*. 107, doi:10.3417/2022735
2. A.M. Duffy, M. Ricca, S. Robinson, B. Aguero, **M.G. Johnson**, H. Stenoien, K.I. Flatburg, K. Hassel, and A.J. Shaw. 2022. Heterogeneous genetic structure in eastern North American peat mosses (*Sphagnum*). *Biological Journal of the Linnean Society*, blab175, doi:10.1093/biolinnean/blab175
3. 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. 2022. Differential gene expression associated with a floral scent polymorphism in the evening primrose *Oenothera harringtonii* (Onagraceae) *BMC Genomics* 23(124) doi:10.1186/s12864-022-08370-6
4. B.J. Cooper, M.J. Moore, N.A. Douglas, W.L. Wagner, **M.G. Johnson**, R.P. Overson, A.J. McDonnell, R.A. Levin, R.A. Raguso, H.F. Olvera, H. Ochoterena, J.B. Fant, K.A. Skogen, and N.J. Wickett. Target enrichment and extensive population sampling help untangle the recent, rapid radiation of *Oenothera* sect. *Calylophus*. 2022. *Systematic Biology*, syac032, doi:110.1093/sysbio/syac032

5. J.B. Beck, M.L. Markley, M.G. Zielke, J.R. Thomas, H.J. Hale, L.D. Williams, and **M.G. Johnson**. Is Palmer’s elm leaf goldenrod real? The Angiosperms353 kit provides within-species signal in *Solidago ulmifolia* s.l. 2022. *Systematic Botany* 46(4) 1107-1113 doi:10.1600/036364421X16370109698740
6. 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. 2022. *Systematic Botany* 46(3) 799-811. doi:10.1600/036364421X16312067913471
7. W.J. Baker, P. Bailey, V. Barber, A. Barker, S. Bellot, D. Bishop, L.R. Boutigue, G. Brewer, T. Carruthers, J.J. Clarkson, J. Cook, R.S. Cowan, S. Dodsworth, N. Epitawalage, D. Francoso, B. Gallego, **M.G. Johnson**, J.T. Kim, K. Leempoel, O. Maurin, C. McGinnie, L. Pokorny, S. Roy, M. Stone, E. Toledo, N.J. Wickett, A.R. Zuntini, W.L. Eiserhardt, P.J. Kersey, I.J. Leitch, and F. Forest. 2021. A Comprehensive Phylogenomic Platform for Exploring the Angiosperm Tree of Life. *Systematic Biology*. syab035, Published Online 13 May 2021. doi:10.1093/sysbio/syab035.
8. 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 *Ceratodon purpureus* genome uncovers structurally complex, gene rich sex chromosomes. 2021. *Science Advances* 7 (27), eabh2488. doi:10.1126/sciadv.abh2488
9. N. Patel, R. Medina, **M.G. Johnson**, and B. Goffinet. Karyotypic diversity and cryptic speciation: Have we vastly underestimated moss species diversity? 2021. *Bry. Div. Evol.* 043 (1): 150-165. doi:10.11646/bde.43.1.12
10. M. Slimp*, L.D. Williams, H. Hale, and **M.G. Johnson**. On the potential of Angiosperms353 for population genomics. 2021. *Applications in Plant Sciences* doi:10.1002/aps3.11419
11. 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 (*Artocarpus*, Moraceae). 2021 *Systematic Biology*, 70(3) 558-575. doi:10.1093/sysbio/syaa073
12. 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
13. 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.
14. 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.

15. 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
16. 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 *Aphanorrhagma*. *J. Systematics and Evolution* 57(4): 404-417. doi:10.1111/jse.12516
17. Y. Liu[†], **M.G. Johnson[†]**, C.J. Cox, R. Medina, N. Devos, A. Vanderpoorten, L. Hedenas, N. Bell, J.R. Shevock, B. Agüero, 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
18. **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
19. 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
20. K. LaRiccía, **M.G. Johnson**, E.G. Gardner, D. Ragone, N. Zyregá, 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
21. 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
22. H.R. Kates[†], **M.G. Johnson[†]**, E.G. Gardner, N. Zyregá, 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
23. 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
24. 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.
25. 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. Stenoien, 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. Benschoter, J. Chen, T.A. Oke, M.B. Nilsson, P. Ranjan, D. Jacobson, E.A. Lileskov, R.S. Clymo, and A.J. Shaw. 2018. The Sphagnome Project: Enabling Ecological and Evolutionary Insights through a Genus-Level Sequencing Project. *New Phytologist* 217 (1):16-25.
26. **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.
27. 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.
28. 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
29. **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.
30. **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
31. 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.
32. **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.
33. **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
34. **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
35. 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
36. 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
37. 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
38. **M.G. Johnson**, B. Shaw, P. Zhou, and A.J. Shaw. 2012. Genetic analysis of the peatmoss *Sphagnum cribrosum* indicates independent origins of an extreme infraspecific morphology shift. *Biological Journal of the Linnean Society*. 106(1):137-153. doi:10.1111/j.1095-8312.2012.01842.x
 39. A.J. Shaw, K.I. Flatberg, P. Szovenyi, M. Ricca, **M.G. Johnson**, H. Stenoëin, 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
 40. M. Ricca, P. Szovenyi, E. Tensch, **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
 41. 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. W. Freyman, **M.G. Johnson** and C.J. Rothfels. homologizer: Phylogenetic phasing of gene copies into polyploid subgenomes *Methods in Ecology and Evolution in press preprint* doi:10.1101/2020.10.22.351486
2. R.P. Overson, **M.G. Johnson**, L.L. Bechen, S.P. Kinosian, N.A. Douglas, J.B. Fant, P.C. Hoch, R.A. Levin, M.J. Moore, R.A. Raguso, W.L. Wagner, K.A. Skogen, and N.J. Wickett. A phylogeny of the evening primrose family (Onagraceae) using a target enrichment approach with 303 nuclear loci. *BMC Evolutionary Biology in revision*
3. N. Patel, R. Medina, L.D. Williams, O. Lemieux, B. Goffinet, and **M.G. Johnson** Frequent allopolyploidy with distant progenitors in the moss genera *Physcomitrium* and *Entosthodon* (Funariaceae) identified via subgenome phasing of targeted nuclear genes. *in revision*
4. Y. Chen, D. Schwilk, R. Cox, and **M.G. Johnson** Including Phylogenetic Conservatism of Shortgrass Prairie Restoration Desired Species Does Not Improve Species Germination Predictions. *in revision*, preprint: doi:10.1101/2022.07.12.499320
5. A.B. Osmanski, N.S. Paulat, J.M. Korstian, J.R. Grimshaw, M. Halsey, K.A.M. Sullivan, D.D. Moreno-Santillan, C. Crookshanks, J. Roberts, C.J. Garcia, L.M. Davalos, **M.G. Johnson**, L.D. Densmore, R.D. Stevens, Zoonomia Consortium, J. Rosen, J.M. Storer, R. Hubley, A.F.A. Smit, D.A. Ray. Insights into mammalian TE diversity via the curation of 200+ mammalian genome assemblies. *Science, in press*.

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* 2021 Jul;108(7):1059-1065. doi:10.1002/ajb2.1703

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* 2021 Jul; 9(7): 10.1002/aps3.11443 doi:10.1002/aps3.11443
3. E. Sorojsrisom and **M.G. Johnson** Putting specimens on the map: An introduction to georeferencing. QUBES. 2022 doi:10.25334/CBTJ-PV50

EXTERNAL
RESEARCH
GRANTS

Principal Investigator: Improving detection of plant contaminants in mixed samples with targeted sequencing of 353 nuclear protein coding genes *Broad Agency Agreement Center for Food Safety and Nutrition, US Food and Drug Administration..* 2022-2024. **Awarded Amount: \$400,765.** FSSWP19.

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.* 2018-2023. **Awarded Amount: \$417,685.** DEB-1753800

Subaward: Progress toward solving the silvery-thread moss issue in cool-season putting greens. *United States Golf Association.* 2019-2022. Total Awarded Amount: \$119,991. **TTU Sub-award: \$16,000.** 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.* 2019-2022. Total Awarded Amount: \$1,497,043. **TTU Sub-award: \$29,775.** Lead Principal Investigator: Peter Fritsch, Botanical Research Institute of Texas.

Subaward: 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.* DEB-1753673. Total awarded amount: \$128,732, **TTU Subaward: \$62,525.** Lead Principal Investigator: Kimberly Murphy, Augustana College.

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

What is a species? Cryptic biodiversity, polyploidy, and reproductive isolation in the cosmopolitan moss *Physcomitrium pyriforme*
Plant Evolution and Ecology Department, Oklahoma State University April 2022
Invited Seminar Speaker

New tools enable new questions: the expanding use of Angiosperms353 in flowering plant systematics and biodiversity studies
Korean Society of Plant Taxonomists August 2021
Invited Virtual Keynote Speaker

On the potential of Angiosperms353 for Population Genomics
Botanical Society of America July 2020
Invited Symposium Speaker: Angiosperms353: A new essential tool for plant systematics

Making sense of plant biodiversity using targeted DNA sequencing
Angelo State University Tri-Beta *October 2020*

Intergeneric allopolyploidy in Funariaceae revealed through targeted sequencing
Plant and Animal Genomes XXVII, Polyploidy Session *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, Anchorage, AK July 2022
Oral Paper: Expanding access to course based undergraduate research with digital natural history collections
- Botanical Society of America, Virtual Conference July 2021
Oral Paper: Damage in antique DNA from herbarium specimens: harmful rust or healthy patina?
- 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

Botanical Society of America, Anchorage, AK July 2022
Lightning Talk Developing a Restriction Digest Marker to Identify Cryptic Species within *Physcomitrium pyriforme*

Presented by: James Ogebeide, Undergraduate, Texas Tech University.

Oral Paper Herbaria uses in ecosystem health assessments: Impacts of land use and climate change on flora in the Guadalupe Mountains over 50 years

Presented by: Madison Bullock, Ph.D. Student, Texas Tech University

Oral Paper The Macroevolution of a Smoke-induced Seed Germination Trait

Presented by: Yanni Chen, Ph.D. Candidate, Texas Tech University

Oral Paper Phylogeography of the *Abronia fragrans* (Nyctaginaceae) species complex using Angiosperms353

Presented by: Sherese Price, M.S. Student, Texas Tech University

Botanical Society of America, Virtual Conference July 2021
Lightning Talk Development of genomic tools for *Bryum argenteum*: Genome assembly and annotation using long and short reads

Presented by: Aman Pruthi, M.S. Student, Texas Tech University.

Oral Paper Testing for cryptic species in *Physcomitrium pyriforme* using target capture sequencing of 800 nuclear genes

Presented by: Lindsay Williams, Ph.D. Student, Texas Tech University

Lightning Talk Reconstructing a phylogeny of sand verbenas (*Abronia*, *Tripterocalyx*) using Angiosperms353

Presented By: Sherese Price, Undergraduate Researcher, Texas Tech University

Oral Paper Conservation genomics of the ethnobotanically important argan tree.

Presented By: Madeline Slimp, Honors URS, Texas Tech University.

Oral Paper Differential gene expression of smoke induced seed germination of shortgrass prairie native species.

Presented By: Yanni Chen, Ph.D. Candidate, Texas Tech University.

Lightning Talk Comparison of machine learning and manual approaches for assessing morphology in herbarium specimens.

Presented By: Anukriti Dey, Undergraduate Researcher, Texas Tech University.

Oral Paper Correlation of plant traits along a fast-slow continuum using 50 year old herbarium specimens.

Presented By: Jose Villeda and Cassidy Coker, Honors URS, Texas Tech University

International Association of Bryologists, Virtual Conference June 2021
Poster Development of genomic tools for *Bryum argenteum*: Genome assembly and annotation using long and short reads

Presented by: Aman Pruthi, M.S. Student, Texas Tech University.

Oral Paper Testing for cryptic species in *Physcomitrium pyriforme* using target capture sequencing of 800 nuclear genes

Presented by: Lindsay Williams, Ph.D. Student, Texas Tech University

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>
Spring 2018, Spring 2019, Fall 2019, Spring 2021	Enrollment: 120-144
Phylogenetics (BIOL 6304)	<i>Graduate course</i>
Fall 2018, Fall 2020, Fall 2022	Enrollment: 10-14
Evolution of Plants (BOT 3404)	<i>Majors-level lab course</i>
Spring 2020, Spring 2022	Enrollment: 16-20
Bioinformatics User Group Series (BIOL 4101-003)	<i>Seminar Course</i>
<i>co-instructor with Dr. Amanda Brown</i>	
Spring 2019, Fall 2019, Spring 2020	Enrollment: 10-15
Use and Abuse of Evolutionary Theory (HONS 2406)	Enrollment: 12
<i>Honors first-year experience, co-instructor with Dr. Brian Giemza</i>	
Fall 2020	
Field Botany & Natural History Collections (BIOL 4301)	<i>Special topics course</i>
Fall 2021	Enrollment: 17

Co-instructor, Northwestern University 2013-2016
Field and Lab Methods in Plant Biology and Conservation (PSC 450)
Phylogenetics and Genomics Section
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: Current

- Yanni Chen, Texas Tech University Ph.D. Candidate 2018-
- Madison Bullock, Ph.D. Student Ph.D. Student 2021-
- Sherese Price, Ph.D. Student M.S. Student 2019-

Graduate Major Advisor: Past

- Lindsay Williams, Texas Tech University Ph.D. Student 2020-2021
 - Aman Pruthi, Texas Tech University M.S. 2019-2022
- Thesis Defended March 2022: Development of genomic tools for the moss *Bryum argenteum* and its comparative analysis with other published moss genomes.

Graduate Research Advisor

- Kira Buckowing, Texas Tech University M.S. 2021
Department: Biotechnology and Bioinformatics
- Katie Holt, Texas Tech University M.S. 2019
Department: Museum Science

Thesis and Dissertation Committees: Active

- Francisco Castellanos, Texas Tech University Ph.D. Student
Advisor: David Ray
- Diksha Gambir, Texas Tech University Ph.D. Student
Advisor: Matt Olson
- Sarah Vrla, Texas Tech University Ph.D. Student
Advisor: David Ray
- Daniela Arenasviveros, Texas Tech University Ph.D. Student
Advisor: Jorge Salazar-Bravo
- Shariful Islam, Texas Tech University Ph.D. Candidate
Advisor: Catherine Wakeman
- Austin Osmanski, Texas Tech University Ph.D. Student
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
- Mckinlee Salazar, Texas Tech University Ph.D. Student
Advisor: Amanda Brown
- Ari Rice, Texas Tech University Ph.D. Student
Advisor: Joseph Manthey
- Sachin Suresh, Texas Tech University Ph.D. Student
Advisor: Timothy Linksvayer

Thesis and Dissertation Committees: Past

- Jennifer Korstian, Texas Tech University Ph.D. 2022
Advisor: David Ray
- Simrandeep Singh, Texas Tech University M.S. 2021
Advisor: Amanda Brown

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

Undergraduate Researchers

- William Onyedionu, BAT-LSAMP Scholar 2022-present
- Courtney Miller, Honors College (URS) 2022-present
- Mara Hosaka, Independent Research 2022-present
- James Ogbeide, Independent Research 2021-present
- Sherese Price, Independent Research 2020-2021
- Anukriti Dey, Independent Research 2021
- 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 SERVICE

Departmental

- *Director, E.L. Reed Herbarium* 2017-present
- *Founding Member; Diversity, Equity and Inclusion Committee* 2020-present
- *Member; Student Assessment Committee* 2022-present
- *Chair; Seminar Committee* 2019-2022
- *Member; Space Committee* 2018-2020
- *Search Committee Member; Quantitative Biologist* 2018
- *Elected Member; Initiatives Committee* 2020-2022
- *Search Committee Member, Cell Biologist* 2022
- *Search Committee Member, Cell Biologist* 2023

Professional Service

- *Biological Collections in Ecology and Evolution Network,*
Facilitator for Course-based Undergraduate Research Experiences 2021-present
- *Applications in Plant Sciences,*
Guest Special Issue Editor: *Angiosperms353* 2020
- *Technology Committee Member,*
Botanical Society of America 2019-2022
- *Steering Committee Member,*
Texas and Oklahoma Regional Consortium of Herbaria 2022-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*

Professional Memberships

- Botanical Society of America
- American Bryological and Lichenological Society
- Society of Herbarium Curators

Other Service

Freely available bioinformatics pipelines and programming tutorials

<http://github.com/mossmatters>