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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	<b>Ph.D.</b> Duke University, Durham, NC	May, 2013
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Dissertation: “Evolution of Mating Systems in *Sphagnum* peatmosses”

	<b>B.S. with distinction</b> , Duke University, Durham, NC	May 2006
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Honors Thesis: “Genetic relationships within *Sphagnum cribrosum* Lind. “wave form” and “normal form” in southeastern North Carolina using three anonymous nuclear genes.”

PROFESSIONAL APPOINTMENTS	<b>Assistant Professor</b> Biological Sciences Texas Tech University	September 2017 to present
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	<b>Director</b> E.L. Reed Herbarium (TTC)	September 2017 to present
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	<b>Postdoctoral Research Associate</b> Plant Science and Conservation Research Center Chicago Botanic Garden Supervisor: Norman Wickett, Ph.D	June 2013 to August 2017
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PUBLICATIONS	<b>Journal Articles</b> (39 total, 11 first-author, 3 last-author) <a href="#">Google Scholar Profile</a>
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1. A.M. Duffy, M. Ricca, S. Robinson, B. Agüero, **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
2. 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
3. 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
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. 2022. *Systematic Botany* 46(3) 799-811. doi:10.1600/036364421X16312067913471

5. 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.
6. 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
7. 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
8. 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
9. E.M. Gardner, **M.G. Johnson**<sup>†</sup>, 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
10. 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
11. 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.
12. 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.
13. S. Dodsworth<sup>†</sup>, L. Pokorny<sup>†</sup>, **M.G. Johnson**<sup>†</sup>, 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
14. 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

15. Y. Liu<sup>†</sup>, **M.G. Johnson**<sup>†</sup>, 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
16. **M.G. Johnson**<sup>†</sup>, L. Pokorny<sup>†</sup>, S. Dodsworth<sup>†</sup>, 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
17. 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
18. K. LaRicca, **M.G. Johnson**, E.G. Gardner, D. Ragone, N. Zyrega, 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
19. 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
20. H.R. Kates<sup>†</sup>, **M.G. Johnson**<sup>†</sup>, 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
21. M.R. McKain<sup>†</sup>, **M.G. Johnson**<sup>†</sup>, S. Uribe-Convers<sup>†</sup>, D. Eaton<sup>†</sup>, and Y. Yang. 2018<sup>†</sup>. 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
22. 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.
23. 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. 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.
24. **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.

25. 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.
26. 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
27. **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.
28. **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
29. 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.
30. **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.
31. **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
32. **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
33. 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
34. 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
35. 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
36. **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
37. 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

38. 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
39. 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. 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*. *Annals of the Missouri Botanical Garden*. (in revision)
2. W. Freyman, **M.G. Johnson** and C.J. Rothfels. homologizer: Phylogenetic phasing of gene copies into polyploid subgenomes *Methods in Ecology and Evolution* in revision preprint doi:10.1101/2020.10.22.351486
3. B.J. Cooper, M.J. Moore, N.A. Douglas, W.L. Wagner, **M.G. Johnson**, R.P. Overton, 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*. *Systematic Biology*, in press, preprint doi:10.1101/2021.02.20.432097
4. 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

#### 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**

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 2022  
 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, 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, 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) *Non-majors course* Typical enrollment: 120-144  
 Phylogenetics (BIOL 6304) *Graduate course* Typical enrollment: 10-14  
 Evolution of Plants (BOT 3404) *Majors-level lab course* Typical enrollment: 16-20  
 Bioinformatics User Group Series (BIOL 4101-003)  
*Seminar course, co-instructor with Dr. Amanda Brown* Typical Enrollment: 10-15  
**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. Student 2019-2021
- 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

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

**Undergraduate Researchers**

- James Ogbeide, Independent Research 2021-present
- Sherese Price, Independent Research 2020-2021
- Anukriti Dey, Independent Research 2021-present
- Cassidy Coker, Honors College (URS) *Herbarium* 2019-2021
- Madeline Slimp, Honors College (URS) *Herbarium* 2018- 2021

	– Kristina Robinson <i>Herbarium</i>	2018-2019
	– Lauren Winfrey, Independent Research <i>Herbarium</i>	2018-2019
	– Zachary Bailey, Honors College (URS) <i>Herbarium</i>	2017-2019
	<b>Past Students Mentored</b>	
	– 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	<b>Departmental</b>	
	– <i>Director, E.L. Reed Herbarium</i>	2017-present
	– <i>Chair, Seminar Committee</i>	2019-present
	– <i>Member, Space Committee</i>	2018-present
	– <i>Elected Member, Initiatives Committee</i>	2020-present
	– <i>Search Committee Member, Quantitative Biologist</i>	2018
	<b>Professional</b>	
	– <i>Applications in Plant Sciences</i> , Guest Special Issue Editor: Angiosperms353	2020
	– <i>Technology Committee Member</i> , Botanical Society of America	2019-present
	– <i>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</i>	
	<b>Other Service</b>	
	<i>Freely available bioinformatics pipelines and programming tutorials</i>	
	<a href="http://github.com/mossmatters">http://github.com/mossmatters</a>	