

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”	May, 2013
	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
PROFESSIONAL APPOINTMENTS	Assistant Professor Biological Sciences Texas Tech University	September 2017 to present
	Director E.L. Reed Herbarium (TTC)	September 2017 to present
	Postdoctoral Research Associate Plant Science and Conservation Research Center Chicago Botanic Garden Supervisor: Norman Wickett, Ph.D	June 2013 to August 2017
PUBLICATIONS	Journal Articles (25 total, 10 first-author, h-index: 12) Google Scholar Profile	
	<ol style="list-style-type: none"> 1. 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. <i>Nature Communications</i> 10, Article number: 1485. doi:10.1038/s41467-019-09454-w 2. 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. <i>Systematic Biology</i> Published online 10 December 2018. doi:10.1093/sysbio/syy086 3. 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 <i>Euphorbia balsamifera</i>. <i>New Phytologist</i> 220:636-650. doi:10.1111/nph.15312 4. 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 (<i>Artocarpus</i> spp.). <i>American Journal of Botany</i> 105(5): 915-926. doi:10.1002/ajb2.1095 	

5. 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
6. 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
7. 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
8. 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.
9. 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. Stenoiien, 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.
10. **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.
11. 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.
12. 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
13. **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.
14. **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
15. 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.

16. **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.
17. **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
18. **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
19. 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
20. 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
21. 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
22. **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
23. 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
24. 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
25. 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)*
2. 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 <i>Physcomitrella</i> , <i>Physcomitridium</i> and <i>Aphanorrhegma</i> . <i>J. Systematics and Evolution in review</i>
EXTERNAL RESEARCH GRANTS	<p>Principal Investigator: Collaborative Research: Diversity of <i>Physcomitrium pyriforme</i> in North America and Europe: significance of autoployploidy within a phylogenomic and experimental framework. <i>National Science Foundation Division of Environmental Biology</i>. 2018-2021. Awarded Amount: \$417,685. DEB-1753800</p> <p>Subaward: Progress toward solving the silvery-thread moss issue in cool-season putting greens. <i>United States Golf Association</i>. 2019-2021. Total Awarded Amount: \$119,991. Sub-award: \$12,000. Lead Principal Investigator: Lloyd Stark, University of Nevada Los Vegas. Collaborator: Zane Raudenbush, Ohio State University.</p>
AWARDS AND FELLOWSHIPS	<p>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.</p> <p>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</p>
PRESENTATIONS	<p>Invited Seminars</p> <p>Embracing the Conflict: Phylogenomics and the Diversification of Mosses <i>American Bryological and Lichenological Society Annual Meeting</i> August 2018 Invited Keynote Speaker</p> <p>Including herbarium specimens in targeted sequencing projects: data analysis challenges and solutions. <i>Botanical Society of America</i> July 2018 Invited Colloquium Speaker: Herbaria in the Genomics Age</p> <p>One Set of Markers to Rule them All: Advances in Targeted Sequencing for Phylogenetics from Populations to Phyla <i>Wichita State University</i> April 2018</p> <p>Phylogenomic insights into the radiation of bryophytes. <i>Utah State University</i> October 2017</p> <p>Phylotranscriptomic analysis reveals widespread gene duplication associated with the radiation of pleurocarpous mosses <i>XIX International Botanical Congress, Shenzhen, China</i> July 2017</p> <p>Building a better tree and using it wisely: Phylogenomic approaches in non-model organisms <i>Chicago Plant Science Symposium, Field Museum</i> April 2017</p> <p>Building a better tree and using it wisely: Phylogenomic approaches in non-model organisms <i>University of Connecticut Biology Forum</i> March 2017</p> <p>Targeted Exon Sequencing in Non-Model Organisms: Best Practices for Probe Design and Data Analysis with HybPiper <i>PAG XXV, MycroArray Session</i> January 2017</p> <p>Introns, Paralogs, and Ditching the Bootstrap: Targeted Sequencing with HybPiper <i>University of Florida PopBio Seminar Series</i> September 2016</p>

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

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?*

TEACHING EXPERIENCE	Instructor , Texas Tech University	2017 - present
	Biology of Plants (BIOL 1401)	
	<i>Non-majors course</i>	
	Phylogenetics (BIOL 6304)	
	<i>Graduate course</i>	
	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	
	Guest Lectures	
MENTORING AND ADVISING	“Introduction to Phylogenetics”	January 2014, 2015, and 2016
	<i>Functional Genomics</i> (BIOL 378, Northwestern University)	
	Norman Wickett, Instructor	
	“Species Trees: Methods and Considerations”	November 2012
	<i>Systematic Biology</i> (BIO 556L, Duke University)	
	David Swofford and Francois Lutzoni, Instructors	
	“Introduction to R”	October 2012
	<i>Practical Bioinformatics</i> (BIO 313, Duke University)	
	Carrie Olson-Manning, Instructor	
	Teaching Assistant , Duke University Biology Department	
	BIO 212L Microbiology	Spring 2009, Fall 2012, Spring 2013
	BIO 26L Organismal Diversity	Summer 2010
	Major Advisor	
	– Yanni Chen, Texas Tech University	Ph.D. Student 2018-
	Thesis Committees: Active	
	– Austin Osmanski, Texas Tech University	Ph.D. Student
	Advisor: David Ray	
	– Jennifer Korstian, Texas Tech University	Ph.D. Candidate
	Advisor: David Ray	
	– Shariful Islam, Texas Tech University	Ph.D. Student
	Advisor: Cathy Wakeman	
	– Hendra Siaholo, Texas Tech University	Ph.D. Student
	Advisor: Amanda Brown	
	– Nan Hu, Texas Tech University	Ph.D. Student
	Advisor: Matt Olson	
	– Minghao Guo, Texas Tech University	Ph.D. Student
	Advisor: Matt Olson	
	– Colby Witherup, Northwestern University	Ph.D. Candidate
	Advisor: Norman Wickett	
	Thesis Committees: Past	
	– Claire Malley, Northwestern University	M.S. 2015
	Advisor: Norman Wickett	
	Undergraduate Researchers	
	– Zachary Bailey, Honors College (URS) <i>Herbarium</i>	2017-present
	– Madeline Slimp, Honors College (URS) <i>Herbarium</i>	2018- present
	– Lauren Winfrey, Independent Research <i>Herbarium</i>	2018-present
	– Kristina Robinson <i>Herbarium</i>	2018-present
	– Stephanie Moreno <i>Bioinformatics</i>	2018
	– David Hernandez-Martinez, Independent Research <i>Herbarium</i>	2018
	– Bruce Archer, Independent Research <i>Bioinformatics</i>	2018

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****Reviewer**

- *Annals of Botany, American Journal of Botany, Biological Journal of the Linnaean Society, The Bryologist, Heredity, International Journal of Plant Sciences, Molecular Phylogenetics and Evolution, Organismal Diversity and Evolution, Taxon, Botanical Journal of the Linnean Society, Analytical Biochemistry, PeerJ.*

Memberships

- American Bryological and Lichenological Society, American Society of Naturalists, Botanical Society of America (lifetime member)