Matthew G. Johnson **October 2019**

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 May, 2013

Dissertation: "Evolution of Mating Systems in *Sphagnum* peatmosses"

B.S. *with distinction*, Duke University, Durham, NC May 2006

Honors Thesis: "Genetic relationships within *Sphagnum cribrosum* Lind. "wave form" and "normal form" in southeastern North Carolina using three anonymous nuclear genes."

PROFESSIONAL APPOINTMENTS

Assistant Professor September 2017 to present
Biological Sciences
Texas Tech University

Director E.L. Reed Herbarium (TTC) September 2017 to present

Postdoctoral Research Associate June 2013 to August 2017
Plant Science and Conservation Research Center
Chicago Botanic Garden
Supervisor: Norman Wickett, Ph.D

PUBLICATIONS

Journal Articles (26 total, 10 first-author, h-index: 13)
Google Scholar Profile

1. 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, in press* doi:10.1016/j.tplants.2019.07.011

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 Physcomitrella, Physcomitridium and Aphanorrhegma. *J. Systematics and Evolution* 57(4): 404-417. doi:10.1111/jse.12516

3. 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

4. **M.G. Johnson†**, L. Pokorny†, S. Dodsworth†, L.R. Botigue, R.S. Cowan, A. Devault, W.L. Eiserhardt, N. Epitawalage, 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

5. 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:10.111/nph.15312

6. K. LaRiccia, **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

7. 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

8. 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

9. 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

10. 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.

11. 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 Sphagnome Project: Enabling Ecological and Evolutionary Insights through a Genus-Level Sequencing Project. *New Phytologist* 217 (1):16-25.

12. **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.

13. 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.

14. 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

15. **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.

16. **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

17. 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.

18. **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.

19. **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

20. **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

21. 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 warnstorfii* along geographic and pH gradients. *Ecology and Evolution*. 5(1) 229-242. doi:10.1002/ece3.1351

22. 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

23. 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

24. **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

25. A.J. Shaw, K.I. Flatberg, P. Szovenyi, M. Ricca, **M.G. Johnson**, H. Stenoein, 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

26. 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

27. 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*)

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

Intergeneric allopolyploidy in Funariaceae revealed through targeted sequencing
Plant and Animal Genomes XXVII, Polyploidy Session *January 2019*

Embracing the Conflict: Phylogenomics and the Diversifcation 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
Witchita 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*

Phylotransciptomic 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?

Teaching Experience

Instructor, Texas Tech University 2017 - present
Biology of Plants (BIOL 1401)
Non-majors course
Phylogenetics (BIOL 6304)
Graduate course

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
- Yanni Chen Texas Tech University Ph.D. Student 2018-
- Aman Pruthi, Texas Tech University M.S. Student 2019-
  Co-advisor: Zhixin Xie

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
- 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

- Claire Malley, Northwestern University — M.S. 2015
  Advisor: Norman Wickett
- Shariful Islam, Texas Tech University — Ph.D. Student 2018-2019
  Advisor: Cathy Wakeman
- Hendra Siaholo, Texas Tech University — Ph.D. Student 2019
  Advisor: Amanda Brown

Undergraduate Researchers

- Cassidy Coker, Honors College (URS) *Herbarium* — 2019-present
- Madeline Slimp, Honors College (URS) *Herbarium* — 2018- present
- Kristina Robinson *Herbarium* — 2018-present
- 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

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, Society for Herbarium Curators, Botanical Society of America (lifetime member)