

Stephen A. Smith

University of Michigan
2071A Kraus Natural Science Building
830 North University
Ann Arbor, MI 48109-1048

Phone: 734.764.7923
eebsmith@umich.edu
<http://blackrim.org>

Education

Ph.D. Evolutionary Biology, Yale University, Major Advisor: Michael Donoghue, 2008

M.S. Evolutionary Biology, Yale University, 2005

B.A. Liberal Arts, Sarah Lawrence College, 2003

Professional Experience

Assistant Professor 2012–
University of Michigan Ann Arbor, MI
Department of Ecology and Evolutionary Biology and Department of Computational Medicine and Bioinformatics

Assistant Curator - Biodiversity Informatics 2015–
University of Michigan Ann Arbor, MI
University of Michigan Herbarium and University of Michigan Museum of Zoology

iPlant Postdoctoral Researcher 2010–2011
Casey Dunn & Alexandros Stamatakis Brown University
Developing tools for constructing large phylogenetic datasets, comparative analyses, and examining the utility of new sequencing technologies for phylogenetics.

NESCent Postdoctoral Fellow 2008–2010
NESCent Duke University
National Evolutionary Synthesis Center postdoctoral fellow examining the evolution of angiosperms with comparative analyses and large datasets.

Teaching Experience

Instructor – Evolution (University of Michigan, EEB 390) 2012-2016

Instructor – Phylogenetic Methods and Theory (University of Michigan, EEB 491) 2013, 2015, 2017

Instructor – Evolution and Ideology (University of Michigan, EEB 800) 2016

Instructor – Programming Primer (University of Michigan, EEB 800) 2014

Instructor – Computational Molecular Evolution (Sanger/Wellcome Trust Cambridge) 2013-2016

Instructor – High school teachers workshop on Genes and Genomes at University of Michigan 2014

Instructor – Bodega Bay Workshop in Applied Phylogenetics, Spring 2009

Instructor – NESCent Computational Phyloinformatics Course: Java Component, Summer 2007

Lecturer – MB&B 230 Rainforest Expedition and Laboratory: Phyloinformatics Workshop, Yale University, Yale University, Spring 2007 and Summer 2008

Teaching Assistant – Plant Diversity and Evolution, Yale University, 2004-2007

Publications

(*lab members in italics*), 48 publications, 31 h-index, >6596 total citations

in review and submitted

Smith, S. A., M. J. Moore, S. F. Brockington, and Y. Yang. Disparity, Diversity, and Duplications in Caryophyllales. *New Phytologist*.

Yang, Y., M. J. Moore, S. F. Brockington, J. Mikenas, and **S. A. Smith**. Improved transcriptome sampling pinpoints widespread paleopolyploidy events in Caryophyllales *New Phytologist*.

Yang, Y., M. J. Moore, S. F. Brockington, A. Timoneda-Monfort, T. Feng, H. E. Marx, *Joseph F. Walker*, and **S. A. Smith**. An efficient field and laboratory workflow for plant phylotranscriptomic projects. *Molecular Methods*.

Walker, J., Y. Yang, M. Moore, S. F. Brockington, and **S. A. Smith**. Conflict among carnivores: whole transcriptomes unable to resolve the carnivorous clade of Caryophyllales. *Molecular Biology and Evolution*.

Brown, J., *J. Walker*, and **S. A. Smith**. phyx: Phylogenetic tools for Unix. *Bioinformatics*.

2016

Smith, S. A. and *J. B. Pease*. 2016. Heterogeneous molecular processes among the causes of how sequence similarity scores can fail to recapitulate phylogeny. *Briefings in Bioinformatics*.

OMeara, B. C., S. D. Smith, W. S. Armbruster, L. D. Harder, C. R. Hardy, L. C. Hileman, Larry Hufford, Amy Litt, Susana Magallan, **S. A. Smith**, P. F. Stevens, C. B. Fenster, P. K. Diggle. 2016. Non-equilibrium dynamics and floral trait interactions shape extant angiosperm diversity. *Proc Roy Soc B*

2015

*Hinchliff, C.*¹, **S. A. Smith**^{1,2}, J. Allman, G. Burleigh, R. Chaudhary, L. Cognill, K. Crandall, J. Deng, B. Drew, R. Gazis, K. Gude, D. Hibbett, L. Katz, D. Laughinghouse IV, E. McTavish, C. Owen, R. Ree, J. Rees, D. Soltis, and K. Cranston². 2015. Synthesis of phylogeny and taxonomy into a comprehensive tree of life *PNAS* ¹co-first author, ²corresponding authors

Smith, S. A., Y. Yang, *J. Brown*, and M. Moore. 2015. Analysis of phylogenomic datasets reveals conflict, concordance, and gene duplications with examples from animals and plants. *BMC Evolutionary Biology*

Yang, Y., M. Moore, S. Brockington, D. Soltis, G. Wong, E. Carpenter, Y. Zhang, L. Chen, Z. Yan, Y. Xie, R. Sage, S. Covshoff, J. Hibberd, M. Nelson, and **S. A. Smith**. 2015. Dissecting molecular evolution in the highly diverse plant clade Caryophyllales using transcriptome sequencing. *Molecular Biology and Evolution*

Brockington S.F., Y. Yang, F. Gandia-Herrero, S. Covshoff, J.M. Hibberd, R.F. Sage, G.K.-S. Wong, M.J. Moore and **S.A. Smith**. 2015. Lineage specific gene radiations underly the evolution of novel betalain pigmentation in Caryophyllales. *New Phytologist*.

McTavish, E. J., *C. E. Hinchliff*, J. F. Allman, *J. W. Brown*, K. A. Cranston, M. T. Holder, J. A. Rees, and **S. A. Smith**. 2015. Phylesystem: a git-based data store for community curated

phylogenetic estimates. *Bioinformatics*.

2014

Smith, S. A. and A. Stamatakis. 2014. Inferring and Postprocessing Huge Phylogenies. in Biological Knowledge Discovery Handbook: Preprocessing, Mining and Post-processing of Biological Data. Wiley, NY.

Yang, Y. and **S. A. Smith**. 2014. Orthology Inference in Nonmodel Organisms Using Transcriptomes and Low-Coverage Genomes: Improving Accuracy and Matrix Occupancy for Phylogenomics. *Molecule Biology and Evolution*. 31: 3081-3092. doi: 10.1093/molbev/msu245

Hinchliff, C. and **S. A. Smith**. 2014. Some Limitations of Public Sequence Data for Phylogenetic Inference (in Plants). *PLoS One*. doi: 10.1371/journal.pone.0098986.

Izquierdo-Carrasco, F., J. Cazes, **S. A. Smith**, and A. Stamatakis. 2014. PUmPER: phylogenies updated perpetually. *Bioinformatics*. doi: 10.1093/bioinformatics/btu053

Cornwell, W. K., M. Westoby, D. S. Falster, R. G. FitzJohn, B. C. O'Meara, M. W. Pennell, D. J. McGlinn, J. M. Eastman, A. T. Moles, P. B. Reich, D. C. Tank, I. J. Wright, Lonnie Aarssen, J. M. Beaulieu, R. M. Kooyman, M. R. Leishman, E. T. Miller, U. Niinemets, J. Oleksyn, A. Ordóñez, D. L. Royer, **S. A. Smith**, P. F. Stevens, L. Warman, P. Wilf, and A. E. Zanne. 2014. Functional distinctiveness of major plant lineages. *Journal of Ecology*. 102: 345-356

Drew, B. T., B. R. Ruhfel, **S. A. Smith**, M. J. Moore, B. G. Briggs, M. A. Gitzendanner, P. S. Soltis, and D. E. Soltis. 2014. Another look at the root of angiosperms reveals a familiar tale. *Systematic Biology*. doi: 10.1093/sysbio/syt108

2013

Smith, S. A., J. Brown, and C. Hinchliff. 2013. Analyzing and Synthesizing Phylogenies Using Tree Alignment Graphs. *PLoS Computational Biology*. doi: 10.1371/journal.pcbi.1003223

Yang, Y. and **S. A. Smith**. 2013. Optimizing de novo assembly of short-read RNA-seq data for phylogenomics. *BMC Genomics*. doi:10.1186/1471-2164-14-328

Zanne, A. Z. D. C. Tank, W. K. Cornwell, J. M. Eastman, **S. A. Smith**, R. G. FitzJohn, D. J. McGlinn, B. C. O'Meara, A. T. Moles, P. B. Reich, D. L. Royer, D. E. Soltis, P. F. Stevens, Mark Westoby, I. J. Wright, Lonnie Aarssen, R. I. Bertin, Andre Calaminus, R. Govaerts, F. Hemmings, M. R. Leishman, Jacek Oleksyn, P. S. Soltis, N. G. Swenson, L. Warman, J. M. Beaulieu. 2013. Three keys to the radiation of angiosperm into freezing environments. *Nature*. doi:10.1038/nature12872

Ryan, J., P. Pang, C. Schitzler, A. Nguyen, R. Moreland, D. Simmons, B. Koch, W. Francis, P. Havlak, NISC Comparative Sequence Program, **S. A. Smith**, N. Putnam, S. Haddock, C. Dunn, T. Wolfsberg, J. Mullikin, M. Martindale, A. Baxevannis. 2013. The genome of the Ctenophore *Mnemiopsis leidyi* and its implications for cell type evolution. *Science* 342: doi: 10.1126/science.1242592

Rabosky, D. L., F. Santini, J. Eastman, **S. A. Smith**, B. Sidlauskas, J. Chang, M. E. Alfaro. 2013. Rates of speciation and morphological evolution are correlated across the largest vertebrate radiation. *Nature Communications*. 4: 1958.

2012

Smith, S. A. and B. O'Meara. 2012. treePL: Divergence time estimation using penalized likelihood for large phylogenies. *Bioinformatics*. doi: 10.1093/bioinformatics/bts492.

Stamatakis, A., A. Aberer, C. Goll, **S. A. Smith**, S. Berger, and F. Izquierdo-Carrasco. 2012. Raxml-light: a tool for computing terabyte phylogenies. *Bioinformatics*, 28(15):20642066. doi: 10.1093/bioinformatics/bts309.

Grass Phylogeny Working Group II. 2012. New grass phylogeny resolves deep evolutionary relationships and discovers C4 origins. *New Phytologist*. 193: 304-312.

2011

Izquierdo-Carrasco F, **S. A. Smith**, A. Stamatakis. 2011. Algorithms, Data Structures, and Numerics for Likelihood-based Phylogenetic Inference of Huge Trees. *BMC Bioinformatics*. 12(1):470.

Smith, S. A., N. G. Wilson, F. E. Goetz, C. Feehery, S. C. S. Andrade, G. W. Rouse, G. Giribet, C. W. Dunn. 2011. Resolving the evolutionary relationships of molluscs with phylogenomic tools. *Nature*. doi:10.1038/nature10526.

Siebert, S., M. Robinson, S. Tintori, F. Goetz, R. Helm, **S. A. Smith**, N. Shaner, S. Haddock, C. Dunn. 2011. Differential Gene Expression in the Siphonophore *Nanomia bijuga* (Cnidaria) Assessed with Multiple Next-Generation Sequencing Workflows. *PLoS ONE*. e22953. doi:10.1371/journal.pone.0022953

Soltis, D. E., **S. A. Smith**, N. Cellinese, K. J. Wurdack, D. C. Tank, S. F. Brockington, N. F. Refulio-Rodriguez, J. B. Walker, M. J. Moore, B. S. Carlswald, C. D. Bell, M. Latvis, S. Crawley, C. Black, D. Diouf, Z. Xi, C. A. Rushworth, M. A. Gitzendanner, K. J. Sytsma, Y. Qiu, K. W. Hilu, C. C. Davis, M. J. Sanderson, R. S. Beaman, R. G. Olmstead, W. S. Judd, M. J. Donoghue & P. S. Soltis. 2011. Angiosperm phylogeny: 17 genes, 640 taxa. *American J. of Botany*. **98**, 704-730.

Smith, S. A., J. Beaulieu, A. Stamatakis, & M. J. Donoghue. 2011. Understanding angiosperm diversification using large and small phylogenies. *American J. of Botany*. 98: 404-414.

2010

Goldberg, E. E., J. R. Kohn, R. Lande, K. A. Robertson, **S. A. Smith** & B. Iqic. 2010. Species Selection Maintains Self-Incompatibility. *Science*. 328: 587-591.

Smith, S. A. & M. J. Donoghue. 2010. Informing large-scale biogeography with niche models in *Lonicera* (Caprifoliaceae, Dipsacales) subgenus *Caprifolium*. *Systematic Biology*. 590: 322-341.

Edwards, E., C. P. Osborne, C. A. E. Stromberg, **S. A. Smith** & C4 Grasses Consortium. 2010. The Evolutionary Origins of C4 Grasslands. *Science*. 328: 587-591.

Smith, S. A., J. Beaulieu & M. J. Donoghue. 2010. An uncorrelated relaxed-clock analysis suggests an earlier origin for flowering plants. *PNAS*. 107: 5897-5902.

Beaulieu, J. M., **S. A. Smith** & I. J. Leitch. 2010. On the tempo of genome size evolution in angiosperms *Journal of Botany*. doi:10.1155/2010/989152.

Bendiksby, M., T. Schumacher, G. Gussarova, J. Nais, K. Mat-Salleh, N. Sofiyanti, D. Madulid, S. A. Smith & T. Barkman. 2010. Elucidating the evolutionary history of the Southeast Asian, holoparasitic, giant-flowered Rafflesiaceae: Pliocene vicariance, morphological convergence and character displacement. *Molecular Phylogenetics and Evolution*. 57: 620-633.

Edwards, E. & **S. A. Smith**. 2010. Phylogenetic analyses reveal the shady history of C4 grasses. *PNAS*. 107: 2532-2538.

2009

Smith, S. A. & J. Beaulieu. 2009. Life history influences rates of climatic niche evolution in flowering plants. *Proc Roy Soc B*. DOI: 10.1098/rspb.2009.1176. 276: 4345-4352. (*USAToday article*)

Smith, S. A. & B. C. O'Meara. 2009. Morphogenera, monophyly, and macroevolution. *PNAS*. 106: E97-E98. (*in response to Jablonski & Finarelli, 2009*)

Smith, S. A., J. Beaulieu & M. J. Donoghue. 2009. Mega-phylogenies for comparative biology: an alternative to supertree and supermatrix approaches. *BMC Evol Bio*. 9: 37. (*NYTimes article*)

Smith, S. A. 2009. Taking into account phylogenetic and divergence-time uncertainty in a parametric biogeographic analysis of the Northern Hemisphere plant clade Caprifolieae. *Journal of Biogeography*. DOI: 10.1111/j.1365-2699.2009.02160.x.

Cellinese, N., **S. A. Smith**, E. J. Edwards, S. T. Kim, R. C. Haberle, M. Avramakis & M. J. Donoghue. 2009. Historical biogeography of the endemic Campanulaceae of Crete. *Journal of Biogeography*. 36: 1253-1269.

Evans, M. E., **S. A. Smith**, R. E. Flynn & M. J. Donoghue. 2009. Climate, niche evolution, and diversification of the "bird-cage" evening primroses (*Oenothera*, sections *Anogra* and *Kleinia*). *American Naturalist*. 173: 225-240.

2008

Smith, S. A. & M. J. Donoghue. 2008. Rates of molecular evolution are linked to life history in flowering plants *Science*. 322: 86-89.

Smith, S. A. & C. Dunn. 2008. Phyutility: a phyloinformatics utility for trees, alignments, and molecular data. *Bioinformatics* 24: 715-716.

Ree, R. H. & **S. A. Smith**. 2008. Maximum-likelihood Inference of Geographic Range Evolution by Dispersal, Local Extinction, and Cladogenesis. *Systematic Biology* 57: 400-414.

Dunn, C. W., A. Hejnol, D. Q. Matus, K. Pang, W. E. Browne, **S. A. Smith**, et al. 2008. Broad taxon sampling improves resolution of the Animal Tree of Life in phylogenomic analyses. *Nature* 452: 745-749.

Smith, S. A. et al. 2008. Bioactive Endophytes Warrant Intensified Exploration and Conservation. *PLoS ONE* 3(8): e3052. (*product of Phyloinformatics Workshop*)

2007-older

Roulston, T. H., **S. A. Smith** & A. L. Brewster. 2007. Comparison of Pan Trap and Intensive Net Sampling Techniques for Documenting a Bee (Hymenoptera: Apiformes) Fauna. *Journal Kansas Entomological Society*. (product of REU)

Moore, B. R., **S. A. Smith** & M. J. Donoghue. 2006. Increasing Data Transparency and Estimating Phylogenetic Uncertainty in Supertrees: Approaches Using Nonparametric Bootstrapping. *Systematic Biology* 55: 662-676.

Donoghue, M. J. & **S. A. Smith**. 2004. Patterns in the assembly of temperate forests around the Northern Hemisphere. *Philosophical Transactions of the Royal Society: Biological Sciences*. 359: 1633-1644.

Invited Presentations

S. A. Smith¹. 2016. Next generation sequencing, transcriptomics, and phylogenetics: a case study with the Caryophyllales. Madison, WI. International Conference on Quantitative Genetics.

S. A. Smith. 2016. Investigating macroevolution using transcriptomes: a story with cacti, carnations, and carnivores. University of California, Davis, CA.

Yang, Y., M. Moore, S. Brockington, and **S. A. Smith**. 2015. Phylotranscriptomics of the Caryophyllales: paleopolyploidy, gene tree discordance and evolution of genes associated with adaptive changes. Symposium on plant transcriptomics. Botany Conference, Edmonton, Canada.

Smith, S. A.*, J. Brown, C. Hinchliff, and Ya Yang 2014. Invited speaker for Symposium on Phylogenetic comparative methods in plant sciences. Botany Conference (Snowbird, UT)

Knowles, L.*, S. A. Smith, and L. Kubatko. 2014. Phylogenomics and Next-generation Inferences: the Future of Phylogenetics in an Era of Big Data. Presidential Address for the Society for Systematic Biology. Evolution Conference (Raleigh, NC)

Smith, S. A.* 2014. Invited speaker for Biology Department (Clark University, Massachusetts).

Smith, S. A.* 2014. Invited speaker for Biology Department (Wake Forest, Wake Forest, North Carolina).

Smith, S. A.* 2013. Invited speaker for Neo4j graph database company.

Smith, S. A.* 2013. Invited speaker for Biology Department (University of Arizona, Tuscon, Arizona).

Smith, S. A.* 2013. Invited speaker for iBEST (University of Idaho, Moscow, Idaho).

Smith, S. A.* 2013. Invited speaker for Biology Department (University of Florida, Gainseville, Florida).

Smith, S. A.* 2013. Invited speaker for Genetics, Bioinformatics, and Computational Biology Department (Virginia Tech, Blacksburg, Virginia).

Smith, S. A.* 2012. Invited speaker for Biology Department (Oberlin College, Ohio).

¹presenter *

- Smith, S. A.*** 2012. Invited speaker for Seventh Annual Organismal Biology Day at the Smithsonian (Smithsonian Institute, Washington, D. C.).
- Smith, S. A.*** 2012. Invited speaker for Seventh Annual Organismal Biology Day at College Park (University of Maryland, College Park).
- Smith, S. A.*** 2011. Invited speaker for LIFE SCIENCES COLLOQUIUM (Smith College, Northampton, Massachusetts).
- Smith, S. A.*** 2011. Invited speaker for Biology 2011 (University of Zurich, Zurich, Switzerland).
- Smith, S. A.*** 2011. Large scale phylogenetics and the exploration of evolutionary patterns. Invited speaker for the Dept. Plant Biology (MSU, Lansing, MI)
- Smith, S. A.*** 2010. The challenges of large scale biogeographic analyses: examples in angiosperms. (SSB Symposium: The Future of Historical biogeography: Conceptual and methodological challenges, Evolution 2010, Portland, OR).
- Smith, S. A.*** 2009. Large-scale angiosperm phylogenies uncover broad evolutionary patterns. (A. Watson Armour Research Seminar Series, Field Museum, Chicago, IL).
- Smith, S. A.*** 2009. Large-scale angiosperm phylogenies uncover broad evolutionary patterns. (Seminar Series, North Carolina State University, Raleigh, NC).
- Smith, S. A.***, J. Beaulieu & M. J. Donoghue. 2009. Large-scale phylogenies uncover large-scale evolutionary patterns. (BSA Past-President's Symposium, Snowbird, UT).
- Smith, S. A.*** 2009. Mega-phylogeny: an alternative to supertree and supermatrix approaches. (Symposium on Advances in Tree Reconstruction from Complex Data Matrices, Evolution 2009, Moscow, ID)
- Smith, S. A.*** 2007. A novel method for estimating the rate of evolution of niches: an example from desert evening primroses (*Oenothera*, Sections *Anogra* and *Kleinia*). (Museum National d'Histoire Naturelle, Paris).
- Ree, R. H.* & **S. A. Smith**. 2007. Stochastic models of geographic range evolution and likelihood-based inference of ancestral ranges. *Origin and Evolution of Biota in Mediterranean Climate Zones*, (Zurich, Switzerland).
- Donoghue, M.J.*, **S. A. Smith**, S. Carlson, & B. Moore. 2007. Phylogenetic Biogeography: Past, Present, and Future. *Origin and Evolution of Biota in Mediterranean Climate Zones*, (Zurich, Switzerland).
- Ree, R. H.*, M. J. Donoghue, B. R. Moore & **S. A. Smith**. 2005. Likelihood-based inference of historical biogeography. *52nd Annual Systematics Symposium*, (Missouri Botanical Garden).
- Smith, S. A.***, R. H. Ree, M. J. Donoghue & B. R. Moore. 2005. Computer Demonstration: Likelihood-based inference of historical biogeography. *52nd Annual Systematics Symposium*, (Missouri Botanical Garden).
- Smith, S. A.*** 2004. New methods for Biogeography. *Sarah Lawrence College Science Seminar*, (Sarah Lawrence College, NY).
- Donoghue, M.J.*, **S. A. Smith**, R. C. Winkworth, & R. Ree. 2004. Assembly of temperate

deciduous forests of the Northern Hemisphere. *Plant phylogeny and the origin of major biomes*, Royal Society Scientific Discussion Meeting, (London, UK).

Contributed Presentations

- Knowles, L. L., H. Huang, J. Sukumaran, **S. A. Smith**. 2016. Interrogating transcriptomes to characterize the different causes of gene tree discord in empirical data. Evolution Conference, Austin, TX.
- Walker, J., Yang, Y., and S. A. Smith*. 2016. Influence of gene family evolution on phylogenomic analyses. Evolution Conference, Austin, TX.
- Yang, Y., M. J. Moore, S. F. Brockington, and S. A. Smith*. 2016. Functional and spatial heterogeneity of gene family evolution in non-model species: three strategies using the plant group Caryophyllales as an example. Evolution Conference, Austin, TX.
- Walker, J., Y. Yang, M. Moore, S. Brockington, and S. A. Smith*. 2016. Gene family evolution in the carnivorous clade of Caryophyllales. Botany Conference, Savannah, GA.
- Diggle, P. K., B. C. O'Meara, S. D. Smith, S. Armbruster, L. Harder, C. Hardy, L. C. Hileman, L. Hufford, A. Litt, **S. A. Smith**, P. Stevens, S. Magallon, and C. Fenster 2016. Non-equilibrium dynamics and floral trait interactions shape extant angiosperm diversity. Botany Conference, Savannah, GA.
- Pease, J. C. Dick, D. Haak, M. Hahn, L. Moyle, M. Silman, S. A. Smith*. 2016. Phylogenomics of rapid speciation and adaptation in Andean-Amazonian plant species. Botany Conference, Savannah, GA.
- Smith, Stephen; Moore, Michael; Yang, Ya; Pease, James; Walker, Joseph, 28 Transcriptome analyses for non-model plants: phylogenomics and more. Botany Conference, Savannah, GA.
- Sun, Miao; Germain-Aubrey, Charlotte; Gitzendanner, Matthew; Smith, Stephen; Soltis, Pamela S.; Chen, Zhiduan; Soltis, Douglas. 2016. Wrestling with the Rosids I: progress and challenges for phylogenetics of a large, hyper-diverse angiosperm clade. Botany Conference, Savannah, GA.
- Soltis, Douglas E; Sun, Miao; Germain-Aubrey, Charlotte; Smith, Stephen; Soltis, Pamela S.; Chen, Zhiduan; Folk, Ryan; Guralnick, Robert. 2016. Wrestling with the rosids II: too big to nail—challenges in conducting comprehensive analyses in the angiosperms. Botany Conference, Savannah, GA.
- Yang, Y., M. J. Moore, S. F. Brockington, and **S. A. Smith**. 2016. Functional and spatial heterogeneity of gene family evolution in non-model species: three strategies using the plant group Caryophyllales as an example. Botany Conference, Savannah, GA.
- Gazis, R., **S. A. Smith**, K. Cranston, *J. Brown*, J. Rees, and D. Hibbett. 2015. Fungi in the Open Tree of Life. Botany Conference, Edmonton, Canada.
- Smith, S. A.**, *C. Parins-Fukuchi*, and C. Dick. 2014. Biogeographic, molecular evolution, and diversification patterns in Neotropical plants. American Geophysical Union, San Francisco, CA
- Yang, Y. and S. A. Smith*. 2014. Using transcriptomes for functional phylogenomic studies: promises and pitfalls. Evolution Conference, Raleigh, NC.
- O'Meara, B., S. Smith, W. Ambruster, L. Harder, C. Hardy, L. Hileman, L. Hufford, A. Litt, S. Magallon, **S. A. Smith**, P. Stevens, C. Fenster, and C. Diggle. 2014. Non equilibrium dynam-

- ics lead to long-term persistence of ancestral floral forms in modern angiosperms. Evolution Conference, Raleigh, NC.
- Ryan, J., C. Schnitzler, E. Maxwell, K. Pang, W. Francis, **S. A. Smith**, T. Wolfsberg, J. Mulikin, S. Haddock, C. Dunn, M. Martindale, and A. Baxevanis. 2014. The genome of ctenophore *Mnemiopsis leidyi*: bringing resolution to the phylogenetic position of the ctenophores. Evolution Conference, Raleigh, NC.
- Hinchliff, C.*, D. Soltis, B. Drew, and **S. A. Smith**. 2014. Evolutionary patterns and processes of epiphytism in vascular plants. Botany Conference, Snowbird, UT
- Moore, M., V. Mandala, N. Douglas, *Y. Yang*, G. Stull, S. Brockington, **S. A. Smith**, P. Soltis, and D. Soltis. 2014. From cacti to carnivores: Clarifying the backbone relationships of Caryophyllales using NGS data. Botany Conference, Snowbird, UT
- Brockington, S., *Y. Yang*, M. Moore, and **S. A. Smith**. 2014. From cacti to carnivores: using transcriptomics to explore the evolution of the highly diverse and globally distributed Caryophyllales. Botany Conference, Snowbird, UT
- Drew, B., *C. Hinchliff*, **S. A. Smith**, and D. Soltis. 2014. Green plants and the open tree of life. Botany Conference, Snowbird, UT
- Yang, Y.*, M. Moore, S. Brockington, and **S. A. Smith**. 2014. Using transcriptomes for functional phylogenomic studies: an example from the Caryophyllales. Botany Conference, Snowbird, UT
- Yang, Y.*, M.J. Moore, and **S. A. Smith**. 2013. Dissecting heterogeneity in rates of molecular evolution in Caryophyllales using RNA-seq data. Society for Molecular Biology and Evolution, Chicago, IL.
- Smith, S. A.**, *J. W. Brown*, and *C. Hinchliff*. 2013. Analyzing and synthesizing the tree of life with graphs. Evolution, Snowbird, UT.
- Beaulieu, J.* , **S. A. Smith** & M. J. Donoghue. 2009. (Moscow, ID) Angiosperm Radiations Aren't Where We Thought They Were, But They're Close.
- Smith, S. A.***, M. Evans, R. Flynn & M. J. Donoghue. 2007. (Chicago, IL) Rates of climatic niche evolution in *Oenothera* sect. *Anogra* and *Kleinia* (Onagraceae).
- Cellinese, N.* , **S. A. Smith**, E. Edwards, S. Kim, & M. J. Donoghue. 2007. (Chicago, IL) Dating the Campanulaceae: implications for the biogeography of Cretan campanulas.
- Ree, R. H.* & **S. A. Smith**. 2007. (Chicago, IL) Likelihood models for inferring the evolution of geographic ranges on phylogenetic trees.
- Ree, R. H.* & **S. A. Smith**. 2007. (Christchurch, NZ) Maximum-likelihood inference of geographic range evolution.
- Smith, S. A.*** 2005. (Austin, TX) Likelihood methods for inference of geographic ranges.
- Smith, S. A.***, M. J. Donoghue, R. Beaman. 2004. (Snowbird, UT) Comparison of predictive distribution modeling in a *Viburnum* species complex from Mexico and Central America. (poster)

Current Scientific Software

treemachine – Software for synthesizing phylogenies with millions of tips. (in collaboration with OpenTreeOfLife) - github.com/OpenTreeofLife/treemachine

taxomachine – Software for combining taxonomies from different sources. (in collaboration with OpenTreeOfLife) - github.com/OpenTreeofLife/taxomachine

treePL – Divergence time estimation for large phylogenies (in collaboration with Brian O’Meara) - github.com/blackrim/treePL

lagrange – Biogeographic likelihood reconstruction and stochastic mapping (in collaboration with Richard Ree) - code.google.com/p/lagrange

PHLAWD – (pronounced flawd) allows for the creation of large (mega) phylogenies using NCBI databases - code.google.com/p/phlawd

phyutility – Phylogenetic utilities and analyses - code.google.com/p/phyutility (over 1600 users)

Funding

Total funding awarded to date: \$2,754,915

NSF ABI (2015-2018, #1458466, \$294,514) – *Co PI* – Connecting resources to enable large-scale biodiversity analyses.

NSF DEB (2014-2017, #1354048, \$590,000) – *PI* – From Cacti to Carnivores, Transcriptomics of Caryophyllales

NSF FESD (2015-2018, #1338694 \$672,000) – *Co PI* – The Dynamics of Mountains, Landscapes and Climate in the Distribution and Generation of Biodiversity of the Amazon/Andean Forest

NSF AVATOL (2013-2017, #1207915, \$1,198,401) – *Co PI* – Assembling, Visualizing, and Analyzing the Tree of Life (2012-2017)

University of Michigan (2015, 30,000) – *Co PI* –

Other Funded Activities

iPlant Collaborative – *Member* Assembling the Tree of Life to Enable the Plant Sciences

NESCent – *Co PI* for Working group on Phylogenetics and biogeographic evolution of C4 grasses (with Erika Edwards)

CIPRES – *Graduate Student* Cyberinfrastructure for Phylogenetic Research

NESCent – *Member* Evolution of C4 grasses catalysis meeting

NESCent – *Collaborator* Floral Evolution Working Group

NESCent – *Member* Northern Hemisphere Phytogeography Working Group

NESCent – *Member* Developing an Integrative Algorithmic Method for Historical Biogeography

Tree of Life – *Member* Angiosperms

Service

Workshop Organizer – Transcriptome analyses for non-model plants: phylogenomics and more, Botany 2016

Workshop Organizer – Phylogenomics and non-model organisms, Evolution 2015

Mentor – Google Summer of Code, student Chanda Phelan, 2013

Mentor – Google Summer of Code, student Nick Matzke, 2009

Reviewer – Science, PLoS Biology, BMC Evolutionary Biology, National Science Foundation (NSF), Systematic Biology, Molecular Phylogenetics and Evolution, Molecular Biology and Evolution, Systematic Botany, Functional Ecology, New Phytologist, and Bioinformatics.

Panelist – National Science Foundation (NSF)

Advisory – National Science Foundation (NSF)

Organizer – Bayesian Invasion, Bayesian Phylogenetics Conference (with B. Moore), 2006

Honors and Awards

Scientist to Watch, "The Botanist Hacker" in the magazine *The Scientist* March, 2010 *link to article*

John Spangler Nicholas prize for outstanding doctoral candidate at Yale University, 2009

NSF Postdoctoral Research Fellowship in Biology, 2008 (declined; accepted NESCent fellowship)

The Edward Cogan Prize for Mathematics and Science, Sarah Lawrence College, 2003

Young Botanist of the Year, Certificate of Special Achievement, Botanical Society of America, 2003

NSF REU Fellowship, Univ. of VA, 2002

Collaborations

Graduate Advisors and Postdoctoral Sponsors

Graduate advisor: Michael J. Donoghue (Yale)

Postdoctoral sponsors: Casey Dunn (Brown); Todd Vision (Univ of NC)

Lab personnel

Postdoctoral researchers: Joseph Brown (AVATOL funded), Ning Wang (AVATOL and DEB funded), Oscar (NSF funded), Greg Stull (NSF funded) former: James Pease (NSF FESD funded, currently Asst. Professor at Wake Forest), Ya Yang (NSF DEB funded, currently Asst. Prof. at University of Minnesota), Cody Hinchliff (AVATOL funded, currently researcher at University of Idaho)

Graduate students: Joseph Walker, Lijun Zhao, Drew Larson

Undergraduate students: Jordan Shore, Sonia Ahluwalia, Nolan Kavanagh, Rahul Vyas, Julia Olivieri (Oberlin College)

Professional Societies

Society for the Study of Evolution

Society of Systematic Biologists

American Society of Plant Taxonomists

References

Dr. Michael Donoghue (PhD advisor)
G. Evelyn Hutchinson Professor
Department of Ecology and Evolutionary Biology
Yale University
P.O. Box 208118
New Haven, CT 06520-8118
203.432.3753
michael.donoghue@yale.edu

Dr. Doug Soltis
Distinguished Professor
Department of Biology
University of Florida
Gainesville, FL 32611
352.273.1963
dsoltis@ufl.edu

Dr. Casey Dunn (former Postdoc advisor)
Assistant Professor

Department Ecology and Evolutionary Biology
Brown University
Providence, RI 02912
401.863.6275
casey_dunn@brown.edu

Dr. Alexandros Stamatakis (former Postdoc advisor)
Assistant Professor
Department of Computer Science
Technische Universität München
D-85748 Garching b. München
+49 162 8541515 (Mobile)
+49 89 28919434 (Office)
stamatak@cs.tum.edu

Dr. Todd Vision (former Postdoc advisor)
Assistant Professor
Department of Biology
University of North Carolina at Chapel Hill
Chapel Hill, NC 27599
919.843.4507
tjv@email.unc.edu