

Stephen A. Smith

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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) 2012-2017
Instructor – Phylogenetic Methods and Theory (University of Michigan, EEB 491) 2013, 2015, 2017
Instructor – Science, Reason, and Nonsense (University of Michigan) 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) 2013-2017
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*), 58 publications, 33 h-index, >7838 total citations

In revision, in review, submitted

- ⊕ **Smith, S. A.**, J. F. Walker, and J. Brown. *In revision*. So many genes, so little time: rate variation in phylogenomic datasets. *Methods in Ecology and Evolutionary Biology* <https://doi.org/10.1101/114975>
- ⊕ Walker, J.¹, J. W. Brown, and **S. A. Smith**. *In revision*. Site and gene-wise likelihoods unmask influential outliers in phylogenomic analyses. *Systematic Biology* <https://doi.org/10.1101/115774>

Published and accepted

- ⊕ **Smith, S. A.** and J. W. Brown. *accepted*. Constructing a comprehensive seed plant phylogeny. *American Journal of Botany*
- ⊕ Pease J.B., J. W. Brown, J. F. Walker, C. E. Hinchliff, **S. A. Smith**. *in press*. Quartet Sampling distinguishes lack of support from conflicting support in the plant tree of life. *American Journal of Botany*
- ⊕ Fleischmann, A., J. Schlauer, T. Givnish, and **S. A. Smith**. *In press*. Evolution of carnivory in angiosperms. Chapter 3. *in forthcoming book on Carnivory in angiosperms*.
- ⊕ Lopez-Nieves, S., Y. Yang, T. Feng, **S. A. Smith**, S. F. Brockington, and H. A. Maeda. *In press*. Relaxation of Tyrosine Pathway Regulation Underlies the Evolution of Betalain Pigmentation in Caryophyllales. *New Phytologist*
- ⊕ Brown, J. W., N. Wang, and **S. A. Smith**. 2017. The development of scientific consensus: analyzing conflict and concordance among Avian phylogenies. *Molecular Phylogenetics and Evolution* <https://doi.org/10.1101/123034>
- ⊕ Brown, J. W. and **S. A. Smith**. 2017. The Past Sure Is Tense: On Interpreting Phylogenetic Divergence Time Estimates. *Systematic Biology* <https://doi.org/10.1101/113720>
- ⊕ Walker, J., Y. Yang, M. Moore, S. F. Brockington, and **S. A. Smith**. 2017. Conflict among carnivores: whole transcriptomes unable to resolve the carnivorous clade of Caryophyllales. *American Journal of Botany*. <https://doi.org/10.1101/115741>
- ⊕ **Smith, S. A.**, M. J. Moore, S. F. Brockington, and Y. Yang. 2017. Disparity, Diversity, and Duplications in Caryophyllales. *New Phytologist*. <https://doi.org/10.1101/132878>
- ⊕ Yang, Y., M. J. Moore, S. F. Brockington, J. Mikenas, and **S. A. Smith**. 2017. Improved transcriptome sampling pinpoints widespread paleopolyploidy events in Caryophyllales *New Phytologist*. <https://doi.org/10.1101/143529>
- ⊕ Brown, J., J. Walker, and **S. A. Smith**. 2017. phyx: Phylogenetic tools for Unix. *Bioinformatics*. <https://doi.org/10.1093/bioinformatics/btx063>
- ⊕ Yang, Y., M. J. Moore, S. F. Brockington, A. Timoneda-Monfort, T. Feng, H. E. Marx, Joseph F. Walker, and **S. A. Smith**. 2017. An efficient field and laboratory workflow for plant phylotranscriptomic projects. *Applications in Plant Sciences*. <https://doi.org/10.1101/079582>
- ⊕ **Smith, S. A.**, J. B. Pease. 2016. Heterogeneous molecular processes among the causes of how sequence similarity scores can fail to recapitulate phylogeny. *Briefings in Bioinformatics*. 18: 451-457. <https://doi.org/10.1093/bib/bbw034>
- ⊕ O'Meara, B. C., S. D. Smith, W. S. Armbruster, L. D. Harder, C. R. Hardy, L. C. Hileman, Larry Hufford, Amy Litt, Susana Magalln, **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 London:B* <https://doi.org/10.1098/rspb.2015.2304>

- ⊕ *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. <https://doi.org/10.1073/pnas.1423041112>
- ⊕ **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* <https://doi.org/10.1186/s12862-015-0423-0>
- ⊕ *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* <https://doi.org/10.1093/molbev/msv081>
- ⊕ 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*. <https://dx.doi.org/10.1111%2Fnph.13441>
- ⊕ 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*. <https://dx.doi.org/10.1093%2Fbioinformatics%2Fbtv276>
- ⊕ Zapata, F., F. E. Goetz, **S. A. Smith**, M. Howison, S. Siebert, S. Church, S. Sanders, C. Ames, C. McFadden, S. France, M. Daly, A. Collins, S. Haddock, C. Dunn, and P. Cartwright. 2015. Phylogenomic Analyses Support Traditional Relationships within Cnidaria. *PLOS One* <https://doi.org/10.1371/journal.pone.0139068>
- ⊕ **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. <https://dx.doi.org/10.1093%2Fmolbev%2Fmsu245>
- ⊕ *Hinchliff, C. and S. A. Smith.* 2014. Some Limitations of Public Sequence Data for Phylogenetic Inference (in Plants). *PLoS One*. <https://doi.org/10.1371/journal.pone.0098986>
- ⊕ Izquierdo-Carrasco, F., J. Cazes, **S. A. Smith**, and A. Stamatakis. 2014. PUMPER: phylogenies updated perpetually. *Bioinformatics*. <https://doi.org/10.1093/bioinformatics/btu053>
- ⊕ Cornwell, W. K., M. Westoby, D. S. Falster, R. G. FitzJohn, B. C. O'Meara, M. W. Pennell, D. J. McGlenn, 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. Ordonez, 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*. <https://doi.org/10.1093/sysbio/syt108>
- ⊕ **Smith, S. A.**, *J. Brown,* and *C. Hinchliff.* 2013. Analyzing and Synthesizing Phylogenies Using Tree Alignment Graphs. *PLoS Computational Biology*. <https://doi.org/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*. <https://doi.org/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. McGlenn, 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*. <https://doi.org/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: <https://doi.org/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.
- ⊕ **Smith, S. A.** and B. O'Meara. 2012. treePL: Divergence time estimation using penalized likelihood for large phylogenies. *Bioinformatics*. <https://doi.org/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. <https://doi.org/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.
- ⊕ 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*. <https://doi.org/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. <https://doi.org/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.
- ⊕ Goldberg, E. E., J. R. Kohn, R. Lande, K. A. Robertson, **S. A. Smith** & B. Igic. 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*. 59: 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.
- ⊕ **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 Caprifoliaceae. *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.
- ⊕ **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*)
- ⊕ 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. Smith**¹. 2017. Next generation phylogenetics: How computational methods and new data are changing evolutionary biology. University of Oregon, Eugene, OR.
- ⊕ **S. A. Smith**. 2017. Phylogenetics, computational genomics, and the origin of biodiversity. University of Maryland, College Park, MD.
- ⊕ **S. A. Smith**. 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).
- ⊕ **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, Portand, OR).
- ⊕ **Smith, S. A.*** 2009. Large-scale angiosperm phylogenies uncover broad evolutionary patterns. (A. Watson Armour Research Seminar Series, Field Museum, Chicago, IL).

¹presenter *

- ⊕ **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, S. A.**, M. Moore, Y. Yang, J. Pease, J. Walker. 2016. Transcriptome analyses for non-model plants: phylogenomics and more. Botany Conference, Savannah, GA.

- ⊕ Sun, M., C. Germain-Aubrey, M. Gitzendanner, **S. A. Smith**, P. Soltis, Z. Chen, D. Soltis. 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 dynamics 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
- ⊕ *phyx* – Phylogenetic utilities and analyses - <https://github.com/FePhyFoFum/phyx>
- ⊕ *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, \$15,000) – *Co PI* – Transcriptomics of non-model organisms.

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

- ⊕ *Associate Editor* – Systematic Biology journal, Society for Systematic Biology
- ⊕ *Guest Editor* – American Journal of Botany, Tree of Life issue 2017
- ⊕ *Panelist* – National Science Foundation (NSF)
- ⊕ *Advisory* – National Science Foundation (NSF)
- ⊕ *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, 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.
- ⊕ *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

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