

STEPHEN R. KELLER

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EXPERTISE

Research in my lab addresses the ecological and evolutionary responses of organisms to environmental change. My students and I integrate approaches from ecological genetics and genomics to address the genetic diversity and evolutionary history of populations, and in turn how this history shapes the response to novel selection pressures exerted by environmental change. Our primary focus is on (1) climate adaptation in forest trees, and (2) the evolution of invasiveness in introduced plants, in both cases investigating how the spatial or temporal dynamics of shifting ranges affects genomic diversity and the evolution of functional traits. An additional area of our research (3) integrates genetic perspectives on biodiversity conservation, in collaboration with colleagues working on a variety of plant, animal, and microbial systems.

EDUCATION

2008 Ph.D. Biology, University of Virginia, Advisor: Dr. Douglas Taylor
2002 M.S. Biology, University of Alaska Fairbanks, Advisor: Dr. Kent Schwaegerle
1997 B.S. Ecology, Juniata College

APPOINTMENTS

2019- Associate Professor, Department of Plant Biology, University of Vermont
2014-2019 Assistant Professor, Department of Plant Biology, University of Vermont
2011-2014 Assistant Professor, University of Maryland Center for Environmental Science
2009-2011 Postdoctoral Associate, Department of Plant Biology, University of Minnesota
2008-2009 Postdoctoral Research Associate, Department of Biology, University of Virginia

PUBLICATIONS (TOTAL CITATIONS: 2183; H-INDEX 20)

IN REVIEW:

Chhatre, V. E., Fetter, K. C., Gougherty, A. V., Fitzpatrick, M. C., Soolanayakanahally, R. Y., Zalusky, R. S., & **S.R. Keller**. Climatic niche predicts the landscape structure of locally adaptive standing genetic variation (in revision for *Communications Biology*).

Fetter, K. C., Nelson, D. M., & **S.R. Keller**. Trade-offs and selection conflicts in hybrid poplars indicate the stomatal ratio as an important trait regulating disease resistance. (in revision for *Evolution*).

Fitzpatrick, M.C., V. Chhatre, R. Soolanayakanahally, and **S.R. Keller**. Experimental support for genomic prediction of climate maladaptation using the machine learning approach *Gradient Forests*. (in revision for *Molecular Ecology Resources*).

2020

Gougherty, A.V., **S.R. Keller**, V.E. Chhatre, and M.C. Fitzpatrick. 2020. Future climate change promotes novel gene-climate associations in balsam poplar (*Populus balsamifera* L.), a forest tree species. *Nature Climate Change* (in press).

Thibault, E., R. Soolanayakanahally, **S.R. Keller**. 2020. Counter-gradient latitudinal clines in bud flush phenology reflect genetic variation in chilling requirements in balsam poplar, *Populus balsamifera* L. (Salicaceae). *American Journal of Botany* (in press).

Capblancq, T., M.C. Fitzpatrick, R.A. Bay, M. Exposito-Alonso, and **S.R. Keller**. 2020. Genomic prediction of (mal)adaptation across current and future climatic landscapes. *Annual Review of Ecology, Evolution, and Systematics* Vol. 51.

Capblancq, T., D.M. Nelson, J.R. Butnor, S. DeYoung, M.C. Fitzpatrick, E. Thibault, H. Munson, and **S.R. Keller**. 2020. Whole exome sequencing reveals a long-term decline in effective population size of red spruce (*Picea rubens*). *Evolutionary Applications*, 13(9).

Lapierre, S., R.H. Hilderbrand, **S.R. Keller**, R. Trott, and A.E. Santoro. 2020. Headwater stream microbial diversity and function across gradients of agricultural and urban land use. *Applied and Environmental Microbiology* 86(11).

Hilderbrand, R.H., **S.R. Keller**, S.M. Lapierre, A.E. Santoro, J. Cessna, and R. Trott. 2020. Microbial communities can predict the ecological condition of headwater streams. *PLoS One* 15: e0236932.

Gougherty, A.V. V.E. Chhatre, **S.R. Keller**, and M.C. Fitzpatrick. 2020 Contemporary range position predicts the range-wide pattern of genetic diversity in balsam poplar (*Populus balsamifera* L.). *Journal of Biogeography* 47: 1246-1257.

Sun, Y., J. Ding, E. Siemann, and **S.R. Keller**. 2020. Biocontrol of invasive weeds under climate change: progress, challenges, and management implications. *Current Opinion in Insect Sciences* 38: 72-78.

Verrico, B.M., J. Weiland, T. Perkins, B. Beckage, and **S.R. Keller**. 2020. Long-term monitoring reveals forest community change driven by atmospheric sulfate pollution and contemporary climate change. *Diversity and Distributions* 26: 270-283.

2019

Fetter, K.C., S. Eberhardt, R.S. Barclay, S. Wing, and **S.R. Keller**. 2019. StomataCounter: a deep learning method applied to automatic stomatal identification and counting. *New Phytologist* 223:1671-1681.

Lachmuth, S., J. Molofsky, L. Milbrath, J. Suda, and **S.R. Keller**. 2019. Associations between genomic ancestry, genome size and capitula morphology in the invasive meadow knapweed hybrid complex (*Centaurea × moncktonii* C.E. Britton) in eastern North America: associations between genomic ancestry, genome size and capitula morphology. *AoBPlants* 11: plz055.

Butnor, J.R., B.M. Verrico, K.J. Johnsen, C.A. Mayer, V. Vankus, and **S.R. Keller**. 2019. Phenotypic variation in climate-associated traits of red spruce (*Picea rubens* Sarg.) along elevation gradients in the southern Appalachian Mountains. *Castanea* 84: 128-143.

Schrieber, K., S. Wolf, C. Wypior, D. Hohlig, **S.R. Keller**, I. Hensen, and S. Lachmuth. 2019. Enemy release mitigates inbreeding depression in native and invasive *Silene latifolia* populations: experimental insight into the role of inbreeding × environment interactions in invasion success. *Ecology and Evolution* 9: 3564-3576.

Hoogland, J.L., R. Trott, and **S.R. Keller**. 2019. Polyandry and polygyny in a social rodent: an integrative perspective based on social organization, copulations, and genetics. *Frontiers in Ecology and Evolution* 7: 3.

2018

Gougherty, A.V., **S.R. Keller**, A. Kruger, C.D. Stylinski, A.J. Elmore, and M.C. Fitzpatrick. 2018. Estimating tree phenology from high frequency tree movement data. *Agricultural and Forest Meteorology* 263:217-224.

Chhatre, V.E., L.M. Evans, S.P. DiFazio, and **S.R. Keller**. 2018. Adaptive introgression and maintenance of a trispecies hybrid complex in range-edge populations of *Populus*. *Molecular Ecology*. <https://doi.org/10.1111/mec.14820>

Fitzpatrick, M.C., **S.R. Keller**, and K.E. Lotterhos. 2018. Comment on “Genomic signals of selection predict climate-driven population declines in a migratory bird”. *Science* 361, eaat7279 (2018). doi:10.1007/s10584-012-0396-6.

Butnor, J.R., B.M. Verrico, V. Vankus, and **S.R. Keller**. 2018. Ethanol exposure can inhibit red spruce (*Picea rubens* Sarg.) germination. *Seed Science and Technology*. 46: 259-265.

2017

Keller, S.R., V.E. Chhatre, and M.C. Fitzpatrick. 2017. Influence of range position on locally adaptive gene-environment associations in *Populus* flowering time genes. *Journal of Heredity*, 109:47-58.

Palacio-Lopez, K., **S.R. Keller**, J.M. Molofsky. 2017. Genomic admixture between locally adapted populations of *Arabidopsis thaliana* (Mouse ear cress): Evidence of optimal genetic outcrossing distance. *Journal of Heredity*. 109:38-46.

Keller, S.R., R. Hilderbrand, M.K. Shank, and M. Potapova. 2017. Environmental DNA genetic monitoring of the nuisance freshwater diatom, *Didymosphenia geminata*, in eastern North American streams. *Diversity and Distributions*, 23:381-393.

Colautti, R.I., J.M. Alexander*, K.M. Dlugosch*, **S.R. Keller***, and S.E. Sultan*. 2017. Invasions and extinctions: through the looking glass of evolutionary ecology. *Philosophical Transactions of the Royal Society B*, 372(1712):20160031. **These authors contributed equally to this work.*

2016

Sebasky, M. **S.R. Keller**, and D.R. Taylor. 2016. Investigating past range dynamics for a weed of cultivation, *Silene vulgaris*. *Ecology and Evolution*, 6:4800-4811.

Pylant, C.L., D.M. Nelson, M.C. Fitzpatrick, J.E. Gates, and **S.R. Keller**. 2016. Geographic origins and population genetics of bats killed at wind-energy facilities. *Ecological Applications*, 26:1381. doi:10.1890/15-0541.

Kazyak, D.C., R.H. Hilderbrand, T.L. King, **S.R. Keller**, and V.E. Chhatre. 2016. Hiding in plain sight: a case for cryptic metapopulations in brook trout. *PLoS ONE* 11(1): e0146295. doi:10.1371/journal.pone.0146295.

2015

Fitzpatrick, M.C. and **S.R. Keller**. 2015. Ecological genomics meets community-level modeling of biodiversity: Mapping the genomic landscape of current and future environmental adaptation. *Ecology Letters* 18:1-16.

Kazyak, D.C., R.H. Hilderbrand, **S.R. Keller**, M.C. Colaw, A.E. Holloway, R.P. Morgan III, and T.L. King. 2015. Spatial structure of morphological and neutral genetic variation in Brook Trout *Salvelinus fontinalis*. *Trans. Amer. Fisheries Soc.* 144:480-490.

2014

Pylant, C.L., D.M. Nelson, and **S.R. Keller**. 2014. Stable hydrogen isotopes record the summering grounds of eastern red bats (*Lasiurus borealis*). *Peer J* 10.7717/peerj.629.

Molofsky, J., **S.R. Keller**, S. Lavergne, M. Kaproth, and M. Eppinga. 2014. Human-aided admixture may fuel ecosystem transformation during biological invasions: theoretical and experimental evidence. *Ecology and Evolution* 4: 899-910.

Keller, S.R., P. D. Fields, A. E. Berardi, and D. R. Taylor. 2014. Recent admixture generates heterozygosity-fitness correlations during the range expansion of an invading species. *Journal of Evolutionary Biology* 27:616-627.

2013

Keller, S.R., R. Trott, C. Pylant, and D. Nelson. 2013. Genome-wide microsatellite marker development from next-generation sequencing of two non-model bat species impacted by wind turbine mortality: *Lasiurus borealis* and *L. cinereus* (Vespertilionidae). *Molecular Ecology Resources*. 14:435-436.

Olson, M.S., N. Levens, R. Soolanayakanahally, R. Guy, W. Schroeder, **S.R. Keller**, and P. Tiffin. 2013. The adaptive potential of the dominant boreal forest tree *Populus balsamifera* L. to phenology requirements in a warmer global climate. *Mol. Ecol.* 22:1214-1230.

2012

S. R. Keller, K. J. Gilbert, P. D. Fields, and D. R. Taylor. 2012. Bayesian inference of a complex invasion history revealed by nuclear and chloroplast genetic diversity in the colonizing plant, *Silene latifolia*. *Mol. Ecol.* 21:4721-4734.

S. R. Keller, N. Levens, M.S. Olson, and P. Tiffin. 2012. Local adaptation in the flowering time genetic network of balsam poplar, *Populus balsamifera* L. *Mol. Biol. Evol.* 29:3143-3152.

2011

Sloan, D.B., **S.R. Keller**, A.E. Berardi, B.J. Sanderson, J.F. Karpovich, and D.R. Taylor. 2011. *De novo* transcriptome assembly and polymorphism detection in the flowering plant *Silene vulgaris* (Caryophyllaceae). *Mol. Ecol. Res.* 12:333-343.

S. R. Keller, N. Levensen, P. K. Ingvarsson, M. S. Olson, and P. Tiffin. 2011. Local selection across a latitudinal gradient shapes nucleotide diversity in balsam poplar, *Populus balsamifera* L. *Genetics* doi: 10.1534/geneticsd.111.128041.

S. R. Keller, R. Soolanayakanahally, R. Guy, S. Silim, M. Olson, and P. Tiffin. 2011. Climate-driven local adaptation in ecophysiology and phenology in balsam poplar, *Populus balsamifera* L. (Salicaceae). *American Journal of Botany* 98:99-108.

Jenkins, C.E. and **S.R. Keller**. 2011. A phylogenetic comparative study of preadaptation for invasiveness in the flowering plant genus *Silene* (Caryophyllaceae). *Biological Invasions* 13:1471-1486.

2010 and earlier

S. R. Keller and D.R. Taylor. 2010. Genomic admixture increases fitness during a biological invasion. *Journal of Evolutionary Biology* 23:1720-1731.

S. R. Keller, M.S. Olson, S. Silim, W. Schroeder, and P. Tiffin. 2010. Genomic diversity, population structure and migration following rapid range expansion in the Balsam Poplar, *Populus balsamifera*. *Molecular Ecology*, 19:1212-1226.

P.D. Fields, **Keller, S.R.**, Ingvarsson, P.K., Pederson, A., and D.R. Taylor. 2010. Isolation and characterization of polymorphic microsatellite loci in the white campion, *Silene latifolia* (Caryophyllaceae). *Molecular Ecology Resources* 10:232-238.

S.R. Keller, Sowell, D.R., Neiman, M., Wolfe, L.M., and D.R. Taylor. 2009. Adaptation and colonization history affect the evolution of clines in two introduced species. *New Phytologist*, 183:678-690.

S.R. Keller and D.R. Taylor. 2008. History, chance, and adaptation during biological invasion: separating stochastic phenotypic evolution from response to selection. *Ecology Letters*, 11: 852-866.

Sloan, D.B., C.M. Barr, M.S. Olson, **S.R. Keller**, and D.R. Taylor. 2008. Evolutionary rate variation at multiple levels of biological organization in plant mitochondrial DNA. *Molecular Biology and Evolution*, 25:243-246.

Etterson, J.R., **S.R. Keller**, and L.F. Galloway. 2007. Epistatic and cytonuclear interactions govern outbreeding depression in the autotetraploid *Campanulastrum americanum*. *Evolution*, 61:2671-2683.

Barr, C.M., **S.R. Keller**, P.K. Ingvarsson, D.B. Sloan, and D.R. Taylor. 2007. Variation in mutation rate and polymorphism among mitochondrial genes of *Silene vulgaris*.

Molecular Biology and Evolution, 24:1783-1791.

Taylor, D.R. and **S.R. Keller**. 2007. Historical range expansion determines the phylogenetic diversity introduced during contemporary species invasion. *Evolution*, 61:334-345.

Keller, S.R. and K.E. Schwaegerle. 2006. Maternal sex and mate relatedness affect offspring quality in the gynodioecious *Silene acaulis*. *Journal of Evolutionary Biology*, 19:1128-1138.

BOOK CHAPTERS:

Fetter, K.C., P. Gugger, and **S.R. Keller**. 2017. Landscape genomics in angiosperm trees: model systems at the foundations and forefront of the field. *Comparative and Evolutionary Genomics of Angiosperm Trees*, Andrew Groover and Quentin Cronk, eds. Springer, ISBN 978-3-319-49329-9. doi: 10.1007/7397_2016_19

Jaramillo-Correa, J.P., J. Prunier, A. Vazquez-Lobo, **S.R. Keller**, A. Moreno-Letelier. 2015. Molecular signatures of adaptation and selection in forest trees. *Advances in Botanical Research*, Vol. 74, 265-306.

REPORTS:

Keller, S.R. 2017. A genetic assessment of the population health and connectivity of a keystone species in high elevation Appalachian forest ecosystems: red spruce (*Picea rubens* Sarg.). Final report to the West Virginia Department of Natural Resources.

Kopeny, M., Grady, J., Matthews, W., **Keller, S.R.**, and Lynch, A. 2008. Conservation Status of the Spotted Form of the Margined Madtom *Noturus insignis* in the Dan River: A Genetic, Morphological and Distributional Investigation. Final Report to Virginia Department of Game and Inland Fisheries.

GRANTS AND FELLOWSHIPS (TOTAL AWARDED: \$9.66M; TOTAL AS PI: \$3.07M) _____

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| 2020-2023 | USDA-HATCH: "Genomic and demographic insights into red spruce responses to climate in northeastern forests"; \$45,000; (PI). |
| 2019-2023 | National Science Foundation Plant Genome Research Program: "RESEARCH-PGR: Genomic architecture of porous species boundaries: implications for climatic adaptation and hybrid breeding" \$2,500,000; (Co-PI) |
| 2019-2021 | Vermont Agency of Agriculture, Food, & Markets and USDA-AMS: "A survey of heirloom and feral hops for resistance to fungal and insect pests" \$20,000; (Co-PI) |

- 2018-2021 National Science Foundation DEB: "SG: Linking above and belowground interactions in highbush blueberry." \$199,528; (Senior Personnel)
- 2017-2020 National Science Foundation DEB: "COLLABORATIVE: Evolutionary responses to climate change at range limits: adaptation, migration and population size at the core, margin, and trailing edge" \$1,209,604 (\$699,960 to UVM); (PI)
- 2017-2022 NSF Division of Graduate Education: "National Research Traineeship: Quantitative & Evolutionary STEM Training (QuEST): An integrative training program for versatile STEM professionals to solve environmental and global health problems" \$2,999,999; (Co-PI).
- 2017-2019 USDA Forest Service Cooperative Agreement: "Seedling propagation for red spruce genealogical study" \$13,008; (PI)
- 2015-2020 USDA-HATCH: "Genomic analysis of climate change responses in northeastern red spruce forests"; \$100,000; (PI).
- 2014-2020 USDA Cooperative Agreement: "Understanding the Role of Population Genetic Structure and Population Dynamics in the Invasion of Knapweeds (Centaurea spp.)"; \$233,298 (including cost-share); (Co-PI)
- 2014-2019 National Science Foundation IOS: "LTREB: Impacts of polyandry over the lifetime of a social mammal"; \$498,695; (Co-PI)
- 2013-2017 National Science Foundation Plant Genome Research Program: "Combining Genomics, Remote Sensing, and Geospatial Modeling to Understand Adaptation to Growing Season Length in Balsam Poplar"; \$1,495,713; (PI)
- 2015-2017 National Science Foundation Plant Genome Research Program: "Supplement to: Combining genomics, remote sensing, and geospatial modeling to understand adaptation to growing season length in balsam poplar" \$24,948; (PI)
- 2013-2015 Maryland Sea Grant: "From genes to ecosystems: integrating measures of aquatic biodiversity and ecosystem health within urbanizing Bay watersheds"; \$146,560; (PI)
- 2013-2015 Mid-Atlantic Panel on Aquatic Invasive Species: "Environmental DNA Monitoring of the Invasive Freshwater Diatom, *Didymosphenia germinata*, in Mid-Atlantic Waters"; \$13,500; (PI)
- 2013-2015 West Virginia Department of Natural Resources: "A genetic assessment of the population health and connectivity of a keystone species in high elevation Appalachian forest ecosystems: red spruce (*Picea rubens* Sarg.)"; \$10,643; (PI)

- 2013-2015 Maryland Department of Natural Resources: "How representative are wind-turbine killed red bats of the broader population in Maryland? An isotopic and genetic assessment"; \$40,000; (Co-PI)
- 2012-2013 Chesapeake Bay Trust: "Citizens Restoring American Chestnut (CRAC)"; \$14,993; (Co-PI)
- 2012-2013 Maryland Department of Natural Resources: "Continuing Isotopic and Genetic Investigations of the Impacts of Wind-Turbine Mortality on Bat Populations in the Central Appalachians", \$40,000; (Co-PI)
- 2011-2013 Maryland Department of Natural Resources: "A preliminary isotopic and genetic investigation of the impacts of wind-turbine mortality on bat populations in the central Appalachians", \$40,000; (Co-PI)
- 2011-2012 MPGI Illumina Sequencing Grant: "Comparative evolutionary analysis of mutation rate variability and strength of selection in *Populus*"; \$4000; (PI)
- 2006-2007 National Science Foundation: "DISSERTATION: Separating Stochastic Events From Adaptive Evolution During A Biological Invasion"; \$8,356; (PI)

FELLOWSHIPS AND AWARDS

- 2016 Nominated for the UVM Graduate Student Senate Excellence in Teaching Award
- 2008 Fleming Award for outstanding doctoral dissertation, Department of Biology, University of Virginia.
- 2007 Nominated for the Seven Society Graduate Fellowship for Superb Teaching, University of Virginia.
- 2006-2007 University of Virginia Graduate School of Arts and Sciences Dissertation Year Fellowship; \$22,440.
- 2006 Graduate Teaching Assistant Award for excellence in undergraduate instruction, Graduate School of Arts and Sciences, University of Virginia.
- 2004 Kepner Award for excellence in teaching biology, Department of Biology, University of Virginia.
- 2002-2005 University of Virginia Presidential Fellowship, \$72,000.

TEACHING

COURSES TAUGHT AS PRIMARY INSTRUCTOR:

- *BCOR101: Genetics*; 3 credits; Fall 2016, 2017, 2018, 2019, 2020; University of Vermont
- *PBIO/BIO381: Ecological Genomics*; 4 credits; Fall 2015, Spring 2017, 2018, 2020; University of Vermont
- *PBIO292: Independent Study in Quantitative Genetics*; 1 credit; Spring 2017; University of Vermont
- *MEES608R: Analysis of Messy Data*; 1 credit; Spring 2013; University of Maryland Center for Environmental Science.
- *MEES608R: Mixed effects models in R*; 1 credit; Fall 2012; University of Maryland Center for Environmental Science.
- *BIOL403: Experimental and Investigative Evolution*; 3 credits; Fall 2007; Department of Biology, University of Virginia.

POSTDOCTORAL FELLOW MENTORING:

Vikram Chhatre (2013-2016), Thibaut Capblancq (2019-present)

GRADUATE STUDENT MENTORING:

Cortney Pylant (M.Sc., 2011-2014), Karl Fetter (Ph.D., 2014-2019), Brittany Verrico (Ph.D, 2015-present), Zoe Portlas (Ph.D., 2018-present), Anoob Prakash (Ph.D., 2018-present), Baxter Worthing (Ph.D., 2018-present).

GRADUATE THESIS COMMITTEES:

Kattia Palacio-Lopez (PhD, 2014-2017), Andy Gougherty (PhD, 2015-2020), Jordan Harris (PhD, 2015-2016); Federico Lopez (PhD, 2016), April Garrett (MS, 2016-2020), Emily Mikucki (PhD, 2016-2020), Lisa Chamberland (PhD, 2016-2020), Muhammad Kala (PhD, 2016-2018), Lauren Ashlock (PhD, 2017-present), Aayudh Das (PhD, 2017-present), Melanie Kazenel (PhD, 2017-2018), Michael Mariani (PhD, 2017-present), Peter Clark (PhD, 2018-present), Jess Wilke (PhD, 2020-present), Raquel Lima (PhD, 2020-present), .

UNDERGRADUATE STUDENT MENTORING:

Rachel Prunier (2003), Allen Gunn (2003-4), Jennifer Howenstine (2003-4), Charles Farnum (2004-5), Tara Poole (2006-7), Christina Jenkins (2006-7), Constance Armanda Roco (2008-2009), Alice Vislova (2009-2010), Callistus Ditah (2009-2010), Britta Herzan (2010), Katy Limpert (2013), Madie Hassett (2014-2015), Molly Estabrook (2014-2015), Maddi Sorrentino (2015-2016), Christine Nolan (2016-2017), Ethan Thibault (2016-2018), Jamie Waterman (2016-2018), Jeremy Weiland (2017-2018), Eva Murray (2017), Tianna Lee (2018), Helena Munson (2018-2020), Corey Davis (2018), Laura Schelling (2018-2019), Sacha Yanulavich (2018), Katie Beardsley (2019-present), Will Seligmann (2019-present), Noah Kaufman (2019-present).

INVITED SYMPOSIA TALKS AND SEMINARS

SYMPOSIA KEYNOTE AND PLENARY LECTURES:

- 2018 EEdays 2018: "Predicting Outcomes of Species Interactions. Linking ecology and evolution with demography and spread", invited keynote speaker (University of Fribourg, Switzerland)
- 2017 POPBIO2017: "Population Biology in a Changing World", invited keynote speaker (Martin Luther University, Germany)
- 2016 American Genetic Association President's Symposium: "Local adaptation: from phenotype to genotype to fitness"; invited plenary speaker (Asilomar, CA)
- 2015 20th Penn State Plant Biology Symposium: "Plant Stress-Omics in a Changing Climate"; invited plenary speaker (The Pennsylvania State University, PA)

INVITED SEMINARS:

- 2021 Workshop: "The Evolution of Species Ranges", invited speaker (University of Gothenburg's Tjärnö Marine Biological Laboratory)
- 2020 Central Appalachian Spruce Restoration Initiative
- 2019 University of California Davis Plant Biology Graduate Group
- 2017 Penn State University; Amherst College
- 2016 Harvard University Arnold Arboretum; Buffalo State University; Castleton State University
- 2015 National Science Foundation Plant Genome Research Program PI Meeting ("Approaches to Broader Impacts"); University of Vermont (RESNR, Biology)
- 2014 Virginia Commonwealth University; University of Vermont (Plant Biology)
- 2013 West Virginia University; UMCES Institute of Marine and Environmental Technology; UMCES Chesapeake Bay Biological Laboratory; National Park Service Center for Urban Ecology
- 2012 University of Virginia; Franklin and Marshall College; Maryland Native Plant Society
- 2011 Central Appalachian Spruce Restoration Initiative; UMCES Horn Point Laboratory

- 2010 Haverford College; Rhodes College; University of Maryland Center for Environmental Science; University of Virginia; Williams College; St. Olaf College;
- 2009 University of Wisconsin-Green Bay; University of Minnesota; Carleton College; Washington and Lee University

CONFERENCE PRESENTATIONS

- 2018 Chhatre, V.E., K.C. Fetter, A.G. Gougherty, M.C. Fitzpatrick, and **S.R. Keller**. “*Is standing genetic variation for local adaptation concentrated in rear edge populations? A test of range limit theory in Populus balsamifera.*” Second Joint Conference on Evolutionary Biology, Montpellier, France.
- S.R. Keller**, V.E. Chhatre, and M.C. Fitzpatrick. *Genomic prediction and phenotypic validation of climate change maladaptation in Populus balsamifera.* Second Joint Conference on Evolutionary Biology, Montpellier, France.
- 2017 Fetter, K.C. and **S.R. Keller**. “Natural hybridization in poplars reveals new genomic architectures of disease resistance” *Society for the Study of Evolution*
- Verrico, B.M. and **S.R. Keller**. “Microgeographic analysis of gene flow across an elevational gradient in northeastern red spruce forests” *Society for the Study of Evolution*
- Gougherty, A., Chhatre, V.E., **Keller, S.R.**, and Fitzpatrick, M.C. (Aug 2017) “Integrating genetic information and spatial modeling to estimate migration speeds through past and future climates” *Ecological Society of America*.
- 2016 Gougherty, A., Chhatre, V.E., **Keller S.R.**, and M.C. Fitzpatrick. “How did past climate change and current range patterns shape genetic patterns of balsam poplar (*Populus balsamifera*)” *Ecological Society of America*
- Verrico, B.M. and **S.R. Keller**. “Microgeographic analysis of local adaptation and gene flow across an elevational gradient in northeastern red spruce forests” *American Genetic Association President’s Symposium*.
- Fitzpatrick MC, **S.R. Keller**, and V.E. Chhatre. “Incorporating climate adaptation into biogeographical models of species responses to climate change.” *International Biogeography Society*
- Keller, S.R.**, Molofsky, J., Palacio-Lopez, K., Suda, J., and L. Milbraith. “Genome size and invasiveness traits in the hybrid meadow knapweed complex (*Centaurea x. moncktonii*) in eastern North America. *NEBIOTA*

- 2015 Fetter, K.C., Chhatre, V.E., and **S.R. Keller**. "Selection scans identify genomic regions associated with adaptation to environment in *Populus balsamifera* (L.)" *Ecological Genomics Symposium*
- Fetter, K.C., Chhatre, V.E., and **S.R. Keller**. "Local adaptation to environment is observed from genome-wide SNP data in *Populus balsamifera* (L.)" 35th *New Phytologist Symposium: The genomes of forest trees: new frontiers of forest biology*
- Chhatre, V.E., Fitzpatrick, M.C., and **S.R. Keller**. "Detecting local selection in spatially heterogeneous environments: clues from simulations and empirical data from a widespread boreal tree, *Populus balsamifera*", 35th *New Phytologist Symposium: The genomes of forest trees: new frontiers of forest biology*
- Chhatre, V.E., Fitzpatrick, M.C., and **S.R. Keller**. "Understanding Climate Adaptation through Genome-Wide Patterns of Differentiation and Local Selection in *Populus balsamifera*. How Important Are Peripheral Populations?" *Plant and Animal Genome Conference XXIII*
- Keller, S.R.**, Chhatre, V.E., and Fitzpatrick, M.C. "Adaptive gene-environment associations in *Populus* flowering time genes: new insights from the southern range edge of balsam poplar. *Plant and Animal Genome Conference XXIII*
- 2014 Stylinski, C.D., **Keller, S.R.**, Elmore, A.J., Fitzpatrick, M.C. "Scientists and volunteers partner to explore poplar phenology and vulnerability to climate change" *Ecological Society of America*
- Fitzpatrick, M.C. and **S.R. Keller**. "Using community-level modeling to understand and map current and future spatial patterns of adaptive genetic variation" *Ecological Society of America*
- Pylant, C., Nelson, D.M., and **Keller, S.R.** "Stable isotope and genetic tools for investigating the impacts of wind-turbine mortality on Lasiurine tree bats" *Wind Wildlife Research Meeting X*
- 2013 Fitzpatrick, M.C. and **S.R. Keller**. "Spatial analysis and predictive mapping of adaptive genetic variation using novel modeling approaches." *International Biogeography Society*
- Pylant, C.L., D.M. Nelson, **S.R. Keller**, M.C. Fitzpatrick, and J.E. Gates. "Assessing regional sources of bat mortality at wind turbine sites using stable isotopes and population genetics", *Ecological Society of America*
- Sebasky, M.E., **S.R. Keller**, B.K. Blackman, and D.R. Taylor. "Testing the sensitivity of

- species distribution models”, *Ecological Society of America*
- Crimmins, T.M., A.J. Elmore, A. Huete, **S.R. Keller**, E. Levetin, J. Luvall, O. Myers, C. Stylinski, P.K. Van de Water, and A. Vukovic. “Research-driven campaigns engage *Nature’s Notebook* participants in scientific data collection”, *Ecological Society of America*
- 2011 Gilbert, K.J., **S.R. Keller**, P.D. Fields, and D.R. Taylor. “Inferred invasion history of *Silene latifolia* into North America utilizing population genetic data and approximate Bayesian computation”, *European Society for Evolutionary Biology*
- 2010 **Keller S.R.**, N. Levsen, M. Olson, and P. Tiffin. “The scale of adaptation in poplar phenological genes: species-wide sweeps versus local selection”, *Society for the Study of Evolution. Portland Oregon.*
- Vislova, A., **S.R. Keller**, and P. Tiffin. “The role of hybridization between *Silene vulgaris* and *Silene csereii* in invasion and range expansion”, *Society for the Study of Evolution. Portland Oregon*
- 2009 **Keller, S.R.**, N. Levsen, M. Olson, S. Salim, W. Schroeder, and P. Tiffin “Population genomics of post-glacial range expansion in *Populus balsamifera* and diversity in candidate genes for phenological adaptation”, *Ecological Genomics Symposium. Kansas City, Missouri.*
- 2008 **Keller S.R.** and D.R. Taylor. “The postglacial history of *Silene vulgaris*: population structure and cytonuclear disequilibria in the native and introduced ranges”, *Society for the Study of Evolution. Minneapolis, Minnesota.*
- 2007 **Keller S.R.** and D.R. Taylor. “Separating stochastic events from adaptive evolution during the process of species invasion”, *Society for the Study of Evolution. Christchurch, New Zealand.*
- Jenkins, C.E. and **S.R. Keller**. “A phylogenetic comparative analysis of invasiveness in the flowering plant genus *Silene* (Caryophyllaceae)”, *National Conference on Undergraduate Research. Dominican University of California, San Rafael, CA.*
- Poole, T.B. and **S. R. Keller**. “Escaping enemies during invasion: genes or just luck?”, *National Conference on Undergraduate Research. Dominican University of California, San Rafael, CA.*
- 2006 D.R. Taylor, **S.R. Keller**, D.R. Sowell, M.B. Neiman & L.M. Wolfe. “Geneological history, chance and adaptation in two invasive plant species”, *An evolutionary perspective of biological invasions. University of Fribourg, Switzerland.*
- 2004 **Keller, S.R.** “Offspring quality in a long-lived gynodioecious plant: inbreeding, outbreeding, and maternal sex effects”, *Society for the Study of Evolution. Fort*

SERVICE

ASSOCIATE EDITOR:

- Biological Invasions (2011-2019)
- American Journal of Botany (2017-present)

PEER REVIEWS: *(I review approximately 10 manuscripts per year)*

American Journal of Botany, Annals of Botany, Axios, Biological Invasions, Biology Letters, Conservation Genetics, Current Biology, Ecology, Ecology Letters, eLife, Evolution, Evolutionary Applications, Functional Ecology, Genetica, Heredity, International Journal of Plant Science, Journal of Applied Ecology, Journal of Biogeography, Journal of Ecology, Journal of Evolutionary Biology, Molecular Ecology, Nature Ecology and Evolution, New Phytologist, Oecologia, PLoS Pathogens, PLoS One, Proceedings of the National Academy of Sciences USA, Trees -- Structure and Function, The Plant Cell, Tree Genetics and Genomes, Trends in Ecology and Evolution.

PROPOSAL PANELIST:

NSF Plant Genome Research Program, NSF Division of Environmental Biology, California Conservation Genomics Project

AD-HOC PROPOSAL REVIEWS:

Swiss National Science Foundation, Army Corps of Engineers, Grant Agency of the Academy of Sciences of the Czech Republic, NSF Plant Genome Research Program, NSF Division of Environmental Biology.

EXTERNAL ADVISORY BOARD MEMBER:

Consortium for Plant Invasion Genomics (2020-present)

EXTERNAL PH.D. EXAMINER:

Dr. David Macaya-Sanz, Universidad de Valladolid, Spain.

UNIVERSITY OF VERMONT SERVICE COMMITTEES:

- CALS Equity, Diversity, and inclusion committee (2020-present)
- QuEST Leadership Team (2017-present).
- Faculty Senate Research Scholarship and Creative Arts Committee (2018-2020)
- Crop Geneticist Faculty Search Committee (2016-2017)
- Plant Biology Graduate Admissions Committee (2014-2018)

UNIVERSITY OF MARYLAND SERVICE COMMITTEES:

- Ecological Genetics Faculty Search Committee (2013)
- Seminar Chair (Spring 2013)
- Faculty Retreat Committee (2012)

- Safety Committee (2011-present)
- Facilities Master Plan Committee (Fall 2011)

PUBLIC SCIENCE OUTREACH:

- “PopClock” citizen science phenology monitoring project (co-coordinator)
- “Stream Microbial Diversity” citizen science project (co-coordinator)
- Keynote Speaker at the Home Ground Annual Banquet (2013)
- Richard A. Johnson Environmental Education Award Keynote Address (2013)
- Citizens Restoring American Chestnuts (multiple presentations during Spring and Fall 2013)
- Volunteer at the Annual Meeting of the National Association of Biology Teachers (2010).