Drew R. Schield, Ph.D.

Curriculum Vitae

Department of Ecology and Evolutionary Biology | University of Colorado, Boulder
1900 Pleasant Street, UCB 334
Boulder, CO 80309
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PROFESSIONAL POSITIONS

NSF Postdoctoral Research Fellow February 2020 – present
Research Advisor: Dr. Rebecca J. Safran
University of Colorado Boulder, Department of Ecology and Evolutionary Biology

Postdoctoral Research Fellow June 2018 – Jan 2020
Research Advisor: Dr. Todd A. Castoe
University of Texas at Arlington, Department of Biology

Graduate Research Assistant June 2017 – May 2018
University of Texas at Arlington, Arlington, TX
Project: *Systematics, introgression, and adaptation in Western Rattlesnakes: a model system for studying gene flow, selection, and speciation*

Enhanced Graduate Teaching Assistant August 2012 – June 2017
University of Texas at Arlington, Arlington, TX

EDUCATION

Doctor of Philosophy (Ph.D.) in Quantitative Biology May 2018
Dissertation title: *Rattlesnake genomics illustrate patterns of speciation, adaptation, and links between genome structure and function*
University of Texas at Arlington
Advisor: Dr. Todd A. Castoe

Bachelor's Degree (B.A.) in Biology May 2012
University of Minnesota Morris, Morris, MN
Advisor: Dr. Heather L. Waye

PUBLICATION AND CITATION STATISTICS

Publications: 43 (plus 4 manuscripts submitted or in review)
Total citations: Google Scholar = 995
H-index (h papers cited a minimum of h times): Google Scholar = 19
i10-index (papers cited a minimum of 10 times): Google Scholar = 23

PUBLICATIONS (PDFs available at https://drewschield.github.io/publications/)

Published Manuscripts (43)

1. **Schield, D.R.**, E.S.C. Scordato, C.C.R. Smith, J.K. Carter, S.I. Cherkaoui, S. Gombobaatar, S. Hajib, S. Hanane, A.K. Hund, K. Koyama, W. Liang, Y. Liu, N. Magri, A. Rubtsov, B. Sheta, S.P. Turbek, M.R. Wilkins, L. Yu, and R.J. Safran. Sex-linked genetic diversity and differentiation in a globally distributed avian species complex. *Accepted at* ***Molecular Ecology***.

2. Schortt, J.A., L.E. Timm, N.R. Hales, Z.L. Nikolakis, **D.R. Schield**, B.W. Perry, Y. Liu, B. Zhong, T.A. Castoe, E.J. Carlton, and D.D. Pollock. 2021. Population genomic analyses of schistosome parasites highlights critical challenges facing end-game elimination efforts. ***Scientific Reports*** 11:6884.

3. **Schield, D.R.**, B.W. Perry, Z.L. Nikolakis, S.P. Mackessy, and T.A. Castoe. 2021. Population genomic analyses confirm male-biased mutation rates in snakes. ***Journal of Heredity*** esab005.

4. **Schield, D.R.**, B.W. Perry, G.I.M. Pasquesi, R.W. Orton, Z.L. Nikolakis, A.K. Westfall, and T.A. Castoe. Applications of genomics and related technologies for studying reptile venoms. *In Press in* ***Handbook of Venom and Toxins of Reptiles, Second Edition***, S.P. Mackessy (Ed.), CRC Press, Boca Raton, FL.

5. Nikolakis, Z.L., N.R. Hales, B.W. Perry, **D.R. Schield**, L.E. Timm, Y. Liu, B. Zhong, K.J. Kechris, D.D. Pollock, E. Carlton, and T.A. Castoe. 2020. Patterns of transmission, relatedness, and genetic diversity inferred from whole genome sequencing of archival blood fluke miracidia (*Schistosoma japonicum*). ***PLoS Neglected Tropical Diseases*** 15:e0009020.

6. Perry, B.W., **D.R. Schield**, A.K. Westfall, S.P. Mackessy, and T.A. Castoe. 2020. Physiological demands and signaling mechanisms associated with snake venom production and storage illustrated by transcriptional analyses of venom glands. ***Scientific Reports*** 10:18083.

7. Perry, B.W., **D.R. Schield**, R.H. Adams, and T.A. Castoe. 2020. Microchromosomes exhibit distinct features of vertebrate chromosome structure and function with underappreciated ramifications for genome evolution. ***Molecular Biology and Evolution*** msaa253.

8. Pasquesi, G.I.M., B.W. Perry, R.P. Ruggiero, M.W. Vandewege, **D.R. Schield**, and T.A. Castoe. Vertebrate lineages exhibit diverse patterns of transposable element regulation and expression across tissues. 2020. ***Genome Biology and Evolution*** 12:506-521.

9. **Schield, D.R.**, G.I.M. Pasquesi, B.W. Perry, R.H. Adams, Z.L. Nikolakis, A.K. Westfall, R.W. Orton, J.M. Meik, S.P. Mackessy, and T.A. Castoe. 2020. Snake recombination landscapes are concentrated in functional regions despite PRDM9. ***Molecular Biology and Evolution*** 37:1272-1294.

10. Card, D.C., R.H. Adams, **D.R. Schield**, B.W. Perry, A.B. Corbin, G.I.M. Pasquesi, K. Row, J. Daza, W. Booth, C. Montgomery, S. Boback, and T.A. Castoe. 2019. Genomic basis of convergent island phenotypes in boa constrictors. ***Genome Biology and Evolution*** 11:3123-3143.

11. Watson, J.A., C.L. Spencer, **D.R. Schield**, B.O. Butler, L.L. Smith, O. Flores-Villela, J.A. Campbell, S.P. Mackessy, T.A. Castoe, and J.M. Meik. Geographic variation in morphology in the Mohave Rattlesnake (*Crotalus scutulatus* Kennicott 1861) (Serpentes: Viperidae): implications for species boundaries. ***Zootaxa*** 4683:129-143.

12. Perry, B.W, A.L. Andrew, A.H.M. Kamal, D.C. Card, **D.R. Schield**, G.I.M. Pasquesi, M. Pelligrino, S.P. Mackessy, S. Chowdhury, S.M. Secor, and T.A. Castoe. Multi-species comparisons of snakes suggest that insulin and stress response signaling modulate post-feeding intestinal regeneration. ***Proceedings of the Royal Society B*** 286:20190910.

13. **Schield, D.R.***, B.W. Perry*, R.H. Adams, D.C. Card, T. Jezkova, G.I.M. Pasquesi, Z.L. Nikolakis, K. Row, J.M. Meik, C.F. Smith, S.P. Mackessy, and T.A. Castoe. Allopatric divergence and secondary contact with gene flow – a recurring theme in rattlesnake speciation. ***Biological Journal of the Linnean Society*** 128:149-169. <u>*Joint primary authors.</u>

14. Adams, R.H., **D.R. Schield**, and T.A. Castoe. Recent advances in the inference of gene flow from population genomic data. ***Current Molecular Biology Reports*** 5:107-115. <u>Invited Article.</u>

15. **Schield, D.R.**, D.C. Card, N.R. Hales, B.W. Perry, G.I.M. Pasquesi, H. Blackmon, R.H. Adams, A.B. Corbin, C.F. Smith, B. Ramesh, J.P. Demuth, E. Betrán, M. Tollis, J.M. Meik, S.P. Mackessy, and T.A. Castoe. 2019. The origins and evolution of chromosomes, dosage compensation, and mechanisms underlying venom regulation in snakes. ***Genome Research*** 29:590-601.

16. Strickland, J.L., C.F. Smith, A.J. Mason, **D.R. Schield**, M. Borja, G. Casteñeda-Gaytán, C.L. Spencer, L.L. Smith, A. Trápaga, N.M. Bouzid, G. Campillo-García, O.A. Flores-Villela, D. Antonio-Rangel, S.P. Mackessy, T.A. Castoe, D.R. Rokyta, and C.L. Parkinson. Evidence for divergent patterns of local selection driving venom variation in Mojave Rattlesnakes (*Crotalus scutulatus*). ***Scientific Reports*** 8:17622.

17. Card, D.C., B.W. Perry, R.H. Adams, **D.R. Schield**, A.S. Young, A.L. Andrew, T. Jezkova, G.I.M. Pasquesi, N.R. Hales, M.R. Walsh, M.R. Rochford, F.J. Mazzotti, K.M. Hart, M.E. Hunter, and T.A. Castoe. 2018. Genomic adaptation of invasive Florida Burmese pythons to increased prey availability and thermal stress. ***Molecular Ecology*** 27:4744-4757.

18. Perry, B.W., **D.R. Schield**, and T.A. Castoe. Evolution: Plasticity versus selection, or plasticity and selection? ***Current Biology*** 28:R1104-R1106.

19. Perry, B.W., D.C. Card, J.W. McGlothlin, G.I.M. Pasquesi, R.H. Adams, **D.R. Schield**, N.R. Hales, A.B. Corbin, J.P. Demuth, F.G. Hoffman, M.W. Vandewege, R.K. Schott, N. Bhattacharyya, B.S.W. Chang, N.R. Casewell, G. Whiteley, J. Reyes-Velasco, S.P. Mackessy, K.B. Storey, K.K. Biggar, C.N. Passow, C. Kuo, S.E. McGaugh, A.M. Bronikowski, J. deKoning, S.V. Edwards, M.E. Pfrender, P. Minx, E.D. Brodie III, E.D. Brodie, Jr., W.C. Warren, and T.A. Castoe. Molecular adaptations for sensing and securing prey and insight into amniote genome diversity from the garter snake genome. ***Genome Biology and Evolution*** 10(8):2110-2129.

20. **Schield, D.R**, D.C. Card, R.H Adams, A.B. Corbin, T. Jezkova, N.R. Hales, J.M. Meik, C.L.

Spencer, L.L. Smith, G. Campillo Garcia, N.M. Bouzid, J.L. Strickland, R.W. Bryson Jr., C.L. Parkinson, O. Flores-Viella, S.P. Mackessy and T.A. Castoe. 2018. Cryptic genetic diversity, population structure, and gene flow in Mohave rattlesnakes (*Crotalus scutulatus*). ***Molecular Phylogenetics and Evolution*** 127:669-681.

21. Adams, R.H., **D.R. Schield**, D.C. Card, and Castoe, T.A. 2018. Assessing the impacts of positive selection on coalescent-based species tree estimation and species delimitation. ***Systematic Biology*** 67:1076-1090.

22. Pasquesi, G.I.M., R.H. Adams, D.C. Card, **D.R. Schield**, B.W. Perry, A.B. Corbin, J. Reyes-Velasco, R.P. Ruggiero, M.W. Vandewege, J.A. Shortt, and T.A. Castoe. Squamate reptiles challenge paradigms of genomic repeat element evolution set by birds and mammals. ***Nature Communications*** 9:2774.

23. Card, D.C, **D.R. Schield**, and T.A. Castoe. Plasticity and local adaptation explain lizard cold tolerance. ***Molecular Ecology*** 27:2173-2175.

24. Adams, R.H., **D.R. Schield**, D.C. Card, A.B. Corbin, and T.A. Castoe. 2017. ThetaMater: Bayesian estimation of population parameter θ from genomic data. ***Bioinformatics*** 34:1072-1073.

25. Gamble, T., T.A. Castoe, S.V. Nielsen, J.L. Banks, D.C. Card, **D.R. Schield**, G.W. Schuett, and W. Booth. 2017. The discovery of XY sex chromosomes in a boa and python. ***Current Biology*** 27:2148-2153.

26. Hales, N.R., **D.R. Schield**, A.L. Andrew, D.C. Card, M.R. Walsh, and T.A. Castoe. 2017. Contrasting gene expression programs underlie predator-induced phenotypic plasticity within and across-generations in *Daphnia*. ***Molecular Ecology*** 26:5003-5015.

27. **Schield, D.R.**, R.H. Adams, D.C. Card, B.W. Perry, G.I.M. Pasquesi, T. Jezkova, D.M. Portik, A.L. Andrew, C.L. Spencer, E.E. Sanchez, M.K. Fujita, S.P. Mackessy, and T.A. Castoe. Insight into the roles of selection in speciation from genomic patterns of divergence and introgression in secondary contact in venomous rattlesnakes. ***Ecology and Evolution*** 7:3951-3966.

28. Andrew, A.L.*, B. Perry*, D.C. Card, **D.R. Schield**, R.P. Ruggiero, S.E. McGaugh, A. Chowdhary, S.M. Secor T.A. Castoe. 2017. Growth and stress response mechanisms underlying post-feeding regenerative organ growth in the Burmese python. ***BMC Genomics*** 18:338. *Joint primary authors.

29. Shortt, J.A., D.C. Card, **D.R. Schield**, L. Yang, B. Zhong, **T.A. Castoe**, E.J. Carlton, and D.D. Pollock. 2017. Whole genome amplification and targeted genome sequencing in *Shistosoma japonicum* isolates. ***PLoS Neglected Tropical Diseases*** 11:e0005292.

30. Adams, R.H., **D.R. Schield**, D.C. Card, H. Blackmon, and T.A. Castoe. 2016. *GppFst*: Genomic posterior predictive simulations of FST and dXY for identifying outlier loci from population genomic data. ***Bioinformatics*** 33:1414-1415.

31. **Schield, D.R**, D.C. Card, J. Reyes-Velasco, A.L. Andrew, C.A. Modahl, S.M. Mackessy, D.D. Pollock, and T.A. Castoe. 2016. A role for genomics in rattlesnake research – current knowledge and future potential. In: ***Rattlesnakes of Arizona***, G.W. Schuett, L.W. Porras, and R.S. Reiserer (Eds.), Eco Books.

32. Card, D.C., **D.R Schield**, R.H. Adams, A.B. Corbin, B.W. Perry, A.L. Andrew, G.I.M. Pasquesi, E.N. Smith, T. Jezkova, S.M. Boback, W. Booth, and T.A. Castoe. 2016. Phylogeographic and population genetic analyses reveal multiple species of Boa and independent origins of insular dwarfism. ***Molecular Phylogenetics and Evolution*** 102:104-116.

33. Streicher, J.W., J.P. McEntee, L. Drzich, D.C. Card**, D.R. Schield**, U. Smart, C.L. Parkinson, T. Jezkova, E.N. Smith, and T.A. Castoe. 2016. Genetic surfing, not allopatric divergence, explains spatial sorting of mitochondrial haplotypes in highly venomous coralsnakes. ***Evolution*** 70:1435-1449. Cover Article.

34. Adams. R.H., H.G. Blackmon, J. Reyes-Velasco, **D.R. Schield**, D.C. Card, A.L. Andrew, N. Waynewood, and T.A. Castoe. 2016. Microsatellite landscape evolutionary dynamics across 450 million years of vertebrate genome evolution. ***Genome*** 59:295-310.

35. **Schield, D.R.**, M.F. Walsh, D.C. Card, A.L. Andrew, R.H. Adams, and T.A. Castoe. 2016. EpiRADseq: genome-wide analysis of shifts in DNA methylation using next-generation sequencing. ***Methods in Ecology and Evolution*** 7:60-69. Cover Article.

36. Andrew, A.L., D.C. Card, R.R. Ruggiero, **D.R. Schield**, R.H. Adams, D.D. Pollock, S.M. Secor, and T.A. Castoe. 2015. Rapid changes in gene expression direct rapid shifts in intestinal form and function in the Burmese python after feeding. ***Physiological Genomics*** 47 (5):147-157.

37. **Schield, D.R.**, D.C. Card, J. Reyes-Velasco, T. Jezkova, F.N. Proctor, C.L. Spencer, H.W. Herrmann, S.P. Mackessy, T.A. Castoe. 2014. Incipient speciation and biased gene flow between two lineages of the Western Diamondback Rattlesnake (*Crotalus atrox*). ***Molecular Phylogenetics and Evolution*** 83:213-223.

38. Jezkova, T., B.R. Riddle, D.C. Card, **D.R. Schield**, M.E. Eckstut, T.A. Castoe. 2014. Genetic consequences of post-glacial range expansion in two co-distributed rodents (genus *Dipodomys*) depend on ecology and genetic marker choice. ***Molecular Ecology*** 24:83-97.

39. Reyes-Velasco, J., D.C. Card, A.L. Andrew, K.J. Shaney, R.H. Adams, **D.R. Schield**, N. Casewell, S.P. Mackessy, and T.A. Castoe. 2014. Expression of venom gene homologs in diverse python tissues suggests a new model for the evolution of snake venom. ***Molecular Biology and Evolution*** 32:173-183.

40. Card, D.C., **D.R. Schield**, J. Reyes-Velasco, A.L. Andrew, R.P. Ruggiero, D.D. Pollock, D.F. Tomback, S.J. Oyler-McCance, M.K. Fujita, and T.A. Castoe. 2014. Two low coverage bird genomes and a comparison of reference-guided versus de novo genome assemblies. ***PLoSOne*** 9:e106649.

41. Shaney, K.J., D.C. Card, **D.R. Schield**, R.P. Ruggiero, D.D. Pollock, S.P. Mackessy, T.A. Castoe. *In Press*. Squamate reptile genomics and evolution. In: ***Handbook of Toxinology: Venom Genomics and Proteomics,*** P. Gopalakrishnakone (Ed.), Springer Reference Press, New York, NY.

42. Castoe. T.A., A.P.J. de Koning, K.T. Hall, D.C. Card, **D.R. Schield**, M.K. Fujita, R.P. Ruggiero, J.F. Degner, J.M. Daza, W. Gu, J. Reyes-Velasco, K.J. Shaney, J.M. Castoe, S.E. Fox, A.W. Poole, D. Polanco, J. Dobry, M.W. Vandewege, Q. Li, R. Schott, A. Kapusta, P. Minx, C. Feschotte, P. Uetz, D.A. Ray, F.G. Hoffmann, R. Bogden, E.N. Smith, B.S.W. Chang, F. Vonk, N.R. Casewell, C.V. Henkel, M.K. Richardson, S.P. Mackessy, A.M. Bronikowski, M. Yandell, W.C. Warren, S.M. Secor,

and D.D. Pollock. 2013. The Burmese Python genome reveals the molecular basis for extreme adaptation in snakes. ***Proceedings of the National Academy of Sciences, USA*** 110:20645-20650.

43. **Schield, D.R.** and H.L Waye. 2012. *Thamnophis radix*: tonic immobility. Natural History. ***Herpetological Review*** 43(2):352.

Manuscripts Submitted or In Review (4)

1. Turbek, S.P., **D.R. Schield**, E.S.C. Scordato, A. Contina, X. Da, Y. Liu, E. Pagani-Núñez, Q. Ren, C.C.R. Smith, C. Stricker, M. Wunder, D. Zonana, and R.J. Safran. A migratory divide spanning two continents is associated with genomic and ecological divergence. *In review at **Evolution***.

2. Farleigh, K., S.A. Vladimirova, C. Blair, J.T. Bracken, N. Koochekian, N. Finger, **D.R. Schield**, D.C. Card, J. Henault, A.D. Leaché, T.A. Castoe, and T. Jezkova. Interaction of selection and drift in shaping genomic variation across populations of the Desert Horned Lizard (*Phrynosoma platyrhinos*). *In review at **Molecular Ecology***.

3. Koochekian, N., A. Ascanio, K. Farleigh, D.C. Card, **D.R. Schield**, T.A. Castoe, and T. Jezkova. A chromosome-level genome assembly and annotation of the desert horned lizard, *Phrynosoma platyrhinos*, provides insight into chromosomal rearrangements among reptiles. *In review at **GigaScience***.

4. Westfall, A.K., B.W. Perry, A.H.M. Kamal, N.R. Hales, M. Sapkota, **D.R. Schield**, M.W. Pellegrino, S.M. Secor, S.M. Chowdhury, and T.A. Castoe. Stress response signaling modulates growth pathway outcomes to direct intestinal regenerative growth in snakes. *In review at **eLife***.

MEDIA COVERAGE

2019 – Press release on our work in ***Genome Research*** on the prairie rattlesnake genome covered by the **UTA College of Science Newsletter**.

2017 – Press coverage by **The Scientist** ("*Snake Sex Determination Dogma Overturned*"), **Reddit**, and others**,** of our recent paper (Gamble et al., 2017, *Current Biology*) that provides the first evidence that some snakes have an XY (i.e., mammal-like) sex determination system, despite decades of thought that all snakes have a ZW (i.e., bird-like) system. This paper was also featured by a commentary article in the same edition of the journal: Emerson, J.J. 2017. Evolution: A paradigm shift in snake sex chromosome genetics. ***Current Biology*** 27: R800-R803.

2017 – Three-page article profiling how research projects in the lab (including regenerative organ growth in snakes, and work on the role of adaptation in speciation) utilize supercomputing to analyze genomic data. Originally written and published by **Texas Advanced Computing Center** (TACC), and republished or expanded upon by numerous sources, including: **UTA**, **National Science Foundation** (NSF; published on main page), **National Geographic**, **EurekaAlert**, **Science Daily**, **Motherboard/Vice**, **R&D Magazine**, **International Business Times**.

2017 – Press coverage by **Biomedcentral (BMC) Series Blog – "*In the belly of the beast*"** of our recent paper in BMC Genomics describing the molecular mechanisms underlying organ regenerative growth in pythons (Andrew et al., 2017, *BMC Genomics*).

2015 – Press coverage by the American Society of Physiologists of our work on python intestinal regenerative growth (Andrew et al., 2015, *Physiological Genomics*), published in the quarterly **APS Newsletter**, and also covered by **UTA College of Science Newsletter**.

2015 – **UTA COS Mavwire** featured story on my research, and recent award of an NSF Doctoral Dissertation Improvement Grants.

2015 – Featured by **UTA Inquiry Magazine** for our work on snake genomics and physiological organ remodeling in snakes.

2014 – Popular press coverage of our work on the evolution of venom systems in snakes (Reyes-Velasco et al., 2015, *Molecular Biology and Evolution*) by **UTA** (official press release), **Science Daily**, **Nature World News**, **RedOrbit**, **Digital Journal, Science Codex, Science World Report, French Tribune, Planet Earth, Design and Trend**, and **Phys.Org**, as well as **UTA COS Mavwire**.

2013 – Five-page in-print editorial coverage of our work on snake genomics in: **Science** 342:1159-1167.

2013 – Radio interview discussing our research on the Burmese python on: **National Public Radio – Dallas KERA**.

2013 – Extensive editorial coverage of our work on the analysis and publication of the first snake genomes, by popular news media (only selected examples included): **NBC News, The Daily News, Huffington Post, Christian Science Monitor, ScienceNow, Denver News, New Scientist, American Free Press, EurekAlert, GenomeWeb, Headlines & Global News, RedOrbit, University Herald, Science Recorder, Nature World News, Mother Nature Network, ScienceDaily, LiveScience, International Business Times, Latino Post, Radio Canada, French Tribune, Tehran Times**, and **News Tonight Africa.**

PRESENTATIONS AND PUBLISHED ABSTRACTS (67)

2020 Mackessy S.P., C.F. Smith, A.J. Saviola, **D.R. Schield**, B.W.Perry, J. Parker, and T.A. Castoe. Complex interactions of biotic and abiotic factors shape venom phenotypes in the Western Rattlesnakes. Venom Week 2020 - North American Society of Toxinology. Gainesville, FL.

2020 Smith C.F., **D.R. Schield**, B.W. Perry, J. Parker, T.A. Castoe, and S.P. Mackessy. Evolutionary drivers of venom variation in the Prairie Rattlesnake (*Crotalus viridis viridis*). Venom Week 2020 - North American Society of Toxinology 2020. Gainesville, FL.

2019 **Schield, D.R.**, B.W. Perry, C.F. Smith, J.M. Meik, S.P. Mackessy, and T.A. Castoe. The origins and evolution of chromosomes and the recombination landscape in rattlesnake genomes. Biology of the Pitvipers 3. Rodeo, NM.

2019 Perry, B.W., **D.R. Schield**, D.C. Card, T. Jezkova, G.I.M. Pasquesi, J.M. Meik, C.F. Smith, S.P. Mackessy, and T.A. Castoe. And so we meet again: Allopatric divergence and secondary contact with gene flow is a recurring theme in rattlesnake evolution. Biology of the Pitvipers 3. Rodeo, NM.

2019 Castoe, T.A., **Schield, D.R.**, B.W. Perry, R.H. Adams, D.C. Card, N.R. Hales, Z.L. Nikolakis, R.W. Orton, G.I.M. Pasquesi, J.M. Meik, C.F. Smith, and S.P. Mackessy. Well assembled snake genomes: A foundation for understanding many things about snakes we wanted to know, and other things we didn't know we wanted to know. Biology of the Pitvipers 3. Rodeo, NM.

2019 Smith, C.F., **Schield, D.R.**, T.A. Castoe, J.M. Parker, and S.P. Mackessy. Snakes on a plain: Biochemical ecology of *Crotalus viridis* (prairie rattlesnake) in Colorado. Biology of the Pitvipers 3. Rodeo, NM.

2018 **Schield,D.R.**, N.R. Hales, D.C. Card, B.W. Perry, G.I.M. Pasquesi, R.H. Adams, H. Blackmon, J.M. Meik, S.P. Mackessy, and T.A. Castoe. Snake venom gene evolution is linked to unique structural and functional properties of snake genomes. Gordon Research Conference on Venom Evolution, Function, and Biomedical Applications. West Dover, VT.

2018 Castoe, T.A., **D.R. Schield**, N.R. Hales, D.C. Card, B.W. Perry, G.I.M. Pasquesi, R.H. Adams, J.M. Meik, and S.P. Mackessy. Genome scale perspectives on the mechanisms regulating snake venom gene specificity. Gordon Research Conference on Venom Evolution, Function, and Biomedical Applications. West Dover, VT.

2018 Smith, C.F., **D.R. Schield**, T.A. Castoe, J. Parker, and S.P. Mackessy. A genetic and venomic analysis of *C. v. viridis* x *C. o. concolor* hybrids in Western Colorado. Gordon Research Conference on Venom Evolution, Function, and Biomedical Applications. West Dover, VT.

2018 C.F. Smith, **D.R. Schield**, T.A. Castoe, J. Parker, S.P. Mackessy. Breaking the dichotomy: Type 3 venom expression in *C. v. viridis*/*C. o. concolor* natural hybrids. Venom Week VI. Texas A&M Kingsville, Kingsville, TX.

2018 **Schield, D.R.**, Card, D.C., R.H. Adams, **D.R. Schield**, G.I.M. Pasquesi, B.W. Perry, A.B. Corbin, K. Row, J.M. Daza, W. Booth, C.E. Montgomery, S.M. Boback, & T.A. Castoe. Genomic basis of adaptive island dwarfism in Boa constrictor snakes. Genetics Society of America – Population, Evolutionary, and Quantitative Genetics Meeting. Madison, WI.

2018 Card, D.C., R.H. Adams, **D.R. Schield**, G.I.M. Pasquesi, B.W. Perry, A.B. Corbin, K. Row, J.M. Daza, W. Booth, C.E. Montgomery, S.M. Boback, & T.A. Castoe. Genomic basis of adaptive island dwarfism in Boa constrictor snakes. Genetics Society of America – Population, Evolutionary, and Quantitative Genetics Meeting. Madison, WI.

2018 Hales, N.R., T.A. Castoe, M.R. Walsh, **D.R. Schield**, D.C. Card, and A.L. Andrew. Predator-induced transgenerational plasticity is mediated by underlying changes in gene expression and methylation. Genetics Society of America – Population, Evolutionary, and Quantitative Genetics Meeting. Madison, WI.

2018 Hales, N.R., **D.R. Schield**, D.C. Card, B.W. Perry, R.H. Adams, H. Blackmon, J.M. Meik, S.P. Mackessy, and T.A. Castoe. Hi-C and RNAseq analysis in the venom gland of a rattlesnake illustrate the unique structure and function of microchromosomes and coordinated interaction of chromatin and specific transcription factors in regulation of venom expression. Texas Genetics Society. College Station, TX.

2018 Corbin, A.B., **D.R. Schield**, D.C. Card, M. Moseley, A. Gluesenkamp, T.A. Castoe, and P.T. Chippindale. Genomic approaches provide insights into conservation of Texas cave and spring salamanders (Eurycea). North American Congress for Conservation Biology 2018. Toronto, ON, Canada.

2018 Perry, B.W., A.L. Andrew, A.H.M. Kamal, D.C. Card, **D.R. Schield**, G.I.M. Pasquesi, R.P. Ruggiero, S. Chowdhury, S.M. Secor, and T.A. Castoe. Transcriptional comparisons of intestinal regenerative growth in multiple snake species provide a new perspective on conserved vertebrate stress and growth pathways that may direct intestinal regeneration. 45th Annual Meeting of the Texas Genetics Society. College Station, TX.

2017 **Schield, D.R.**, D.C. Card, R.H. Adams, G.I.M. Pasquesi, B.W. Perry, N.R. Hales, A.L. Andrew, A.B. Corbin, S.P. Mackessy, and T.A. Castoe. Repeated patterns of adaptation along the speciation continuum: insight from studies of North American rattlesnakes. Joint Evolution Meetings 2017. Portland, OR.

2017 Adams, R.H., **D.R., Schield**, D.C. Card, and T.A. Castoe. Leveraging low coverage whole genome data to study selection, demography, and phylogeny. Joint Evolution Meetings 2017. Portland, OR.

2017 Hales, N.R., **D.R. Schield**, A.L. Andrew, D.C. Card, M.R. Walsh, and T.A. Castoe. Contacting gene expression programs correspond with predator-induced phenotypic plasticity within and across generations in *Daphnia*. Joint Evolution Meetings 2017. Portland, OR.

2017 Pasquesi, G.I.M., M.W. Vandewege, A.L. Andrew, B.W. Perry, **D.R. Schield**, N.R. Hales, A.B. Corbin, D.C. Card, R.H. Adams, and T.A. Castoe. Linking genomic transposable element evolution to germ-line expression in snakes. Joint Evolution Meetings 2017. Portland, OR.

2017 Andrew, A.L. B.W. Perry, D.C. Card, **D.R. Schield**, R.P. Ruggiero, S. McGaugh, A. Choudhary, S.M. Secor, and T.A. Castoe. Evolutionary variation in growth and stress responses underlying kidney regenerative growth from snakes to human organoids. Joint Evolution Meetings 2017. Portland, OR.

2017 Card, D.C., B.W. Perry, R.H. Adams, A.L. Andrew, **D.R. Schield**, A. Young, T. Jezkova, M. Rochford, F. Mazotti, K. Hart, M. Hunter, and T.A. Castoe. Genome-wide evidence of evolution and adaptation in the invasive Florida python population. Joint Evolution Meetings 2017. Portland, OR.

2017 Corbin, A.B. M. Moseley, G.I.M. Pasquesi, **D.R. Schield**, R.H. Adams, D.C. Card, T.A. Castoe, and P.T. Chippindale. Population genomics and genomic architecture of central Texas cave and spring salamanders (*Eurycea*). Joint Evolution Meetings 2017. Portland, OR.

2017 Perry, B.W., A.L. Andrew, D.C. Card, **D.R. Schield**, G.I.M. Pasquesi, A.H.K. Kamal, R. Ruggiero, S. Chowdhury, and T.A. Castoe. An evolutionary framework for dissecting and understanding regenerative intestine growth in snakes. Joint Evolution Meetings 2017. Portland, OR.

2016 **Schield, D.R.**, R.H. Adams, D.C. Card, B.W. Perry, T. Jezkova, A.L. Andrew, G.I.M. Pasquesi, S.P. Mackessy, and T.A. Castoe. Patterns of speciation and delimitation of populations, species, and genomic adaptations in widely-distributed North American rattlesnake lineages. Joint Evolution Meetings 2016. Austin, TX.

2016 Adams, R.H., **D.R. Schield**, D.C. Card, and T.A. Castoe. Friend or foe: investigating the impacts of positive selection on phylogenomic inferences. Joint Evolution Meetings 2016. Austin, TX.

2016 Pasquesi, G.I.M., R.H. Adams, D.C. Card, A.B. Corbin, **D.R. Schield**, and T.A. Castoe. Evolutionary dynamics of genomic repeat element landscapes across 200 million years of squamate evolution. Joint Evolution Meetings 2016. Austin, TX.

2016 Card, D.C., **D.R. Schield**, R.H. Adams, A.L. Andrew, B.W. Perry, F. Mazzotti, M.E. Hunter, K. Hart, and T.A. Castoe. Genome-wide evidence of evolution and adaptation in the invasive Florida python population. Joint Evolution Meetings 2016. Austin, TX.

2016 Jezkova, T., T.A. Castoe, D.C. Card, **D.R. Schield**, D. Elzinga, M. Leal, and J.A. Rodriguez-Robles. A peculiar case of hybridization with advantageous mtDNA introgression and lack of nuclear introgression in Caribbean anoles. Joint Evolution Meetings 2016. Austin, TX.

2016 Streicher, J.W., J.P. McEntee, L. Drzich, D.C. Card, **D.R. Schield**, U. Smart, C.L. Parkinson, T. Jezkova, E.N. Smith, and T.A. Castoe. Genetic surfing, not allopatric divergence, explains spatial sorting of mitochondrial haplotypes in venomous coralsnakes. Joint Evolution Meetings 2016. Austin, TX.

2016 Corbin, A.B., M. Moseley, **D.R. Schield**, G.I.M. Pasquesi, A. Gluesenkamp, T.A. Castoe, and P.T. Chippindale. Love under cover of darkness: population genomics of central Texas cave and spring salamanders (Plethodontidae: *Eurycea*). Joint Evolution Meetings 2016. Austin, TX.

2016 Hales, N.R., A.L. Andrew, D. Card, **D. Schield**, T. Castoe, M. Walsh. Transgenerational plasticity in *Daphnia ambigua*. Joint Evolution Meetings 2016. Austin, TX.

2016 Card, D.C., **D.R. Schield**, R.H. Adams, M. Hunter, K. Hart, and T.A. Castoe. Genome-wide evidence of evolution and adaptation in the invasive Florida python population. Annual Celebration of Excellence by Students (UTA-ACES), Arlington, TX.

2016 Castoe, T.A., Pasquesi, G.I.M., R.H. Adams, D.C. Card, and **D.R. Schield**. Sample sequencing 68 squamate genomes reveals extensive genomic repeat landscape dynamics. International Congress on Transposable Elements, Saint Malo, France.

2015 Reyes-Velasco J., D.C. Card, A.L. Andrew, K.J. Shaney, R.A. Adams, **D.R. Schield**, N.R. Casewell, S.P. Mackessy and T.A. Castoe. Expression of venom gene homologs in diverse python tissues: a new model for the evolution of snake venom and a re-assessment of transcriptome-based definition of venoms. International Society on Toxinology, 18th World Congress. Oxford, England.

2015 Card, D.C., **D.R. Schield**, R.A. Adams, W. Booth, S. Boback, and T.A. Castoe. Mitochondrial and nuclear SNP evidence for population genetic structure, independent island dwarfism, and genes putatively underlying dwarfism traits in Boa constrictor. Society for the Study of Amphibians and Reptiles Meeting. Lawrence, KS.

2015 Andrew, A.L., D.C. Card, R.P. Ruggiero, **D.R. Schield**, R.H. Adams, D.D. Pollock, S.M. Secor, and T.A. Castoe. Patterns of gene expression underlying extreme physiological remodeling in snakes. Society for the Study of Amphibians and Reptiles Meeting. Lawrence, KS.

2015 **Schield, D.R.**, G.M. Pasquesi, R.H. Adams, D.C. Card, and T.A. Castoe. Patterns of selection and introgression following isolation and secondary contact in a widely-distributed rattlesnake species (Crotalus atrox). Society for the Study of Amphibians and Reptiles Meeting. Lawrence, KS.

2015 Adams, R.H., D.C. Card, **D.R. Schield**, A.L. Andrew, N. Casewell, F. Vonk, and T.A. Castoe. Two blind snake genomes show promise for revealing the evolutionary origins of extreme adaptation in snakes. Society for the Study of Amphibians and Reptiles Meeting. Lawrence, KS.

2015 Card, D.C., **D.R. Schield**, K. Hart, M.E. Hunter, and T.A. Castoe. Evolution and putative adaptation in the invasive Florida Burmese python population inferred using genome-wide RADseq data. Society for Molecular Biology and Evolution Meeting. Vienna, Austria.

2015 **Schield, D.R**., M.R. Walsh, D.C. Card, A.L. Andrew, R.H. Adams, and T.A. Castoe. EpiRADseq: a novel technique for the examination of genome-wide epigenetic patterns. Annual Celebration of Excellence by Students (UTA-ACES), Arlington TX.

2015 Andrew, A.L, D.C. Card, R.P. Ruggiero, **D.R. Schield**, R.H. Adams, D.D. Pollock, S.M. Secor, E. La, and T.A. Castoe. Patterns of gene expression underlying extreme physiological remodeling in snakes. Annual Celebration of Excellence by Students (UTA-ACES), Arlington, TX.

2015 Adams, R.H, D.C. Card, J. Reyes-Velasco, **D.R. Schield**, A.L. Andrew, and T.A. Castoe. Sample sequencing 46 squamate reptiles reveals extensive evolutionary dynamics of genomic repeat landscapes. Annual Celebration of Excellence by Students (UTA-ACES), Arlington, TX.

2015 Card, D.C., **D.R. Schield**, R.H. Adams, W. Booth, S.M. Boback, and T.A. Castoe. Genomic basis of adaptive island dwarfism in Boa constrictor. Annual Celebration of Excellence by Students (UTA-ACES), Arlington, TX.

2014 **Schield, D.R.**, D.C. Card, S.P. Mackessy, and T.A. Castoe. Delineation of populations, species, and genomic adaptations across a widely distributed venomous snake species complex. Ecological Genomics Symposium. Kansas City, MO.

2014 Card, D.C., **D.R. Schield**, M.E. Hunter, K.M. Hart, & T.A. Castoe. Evolution and putative adaptation in the Florida python population inferred using genome-wide RADseq data. Ecological Genomics Symposium. Kansas City, MO.

2014 Castoe, T.A., A.P. J. de Koning, D.C. Card, **D.R. Schield**, J. Reyes-Velasco, A. Andrew, and R. Adams and D.D. Pollock. Snake genomes reveal insight into the evolution of extreme adaptive phenotypes in vertebrates. Ecological Genomics Symposium. Kansas City, MO.

2014 **Schield, D.R.**, D.C Card, J. Reyes-Velasco, C.L. Spencer, T. Jezkova, and T.A. Castoe. Using genome-wide single nucleotide polymorphisms to estimate patterns of gene flow and population structure in Crotalus atrox. Joint Evolution Meetings 2014. Raleigh, NC.

2014 Card, D.C, **D.R. Schield**, M. Hunter, and T.A. Castoe. Genome-wide evidence of evolution and adaptation in the invasive Florida python population. Joint Evolution Meetings 2014. Raleigh, NC.

2014 Andrew, A.L., D.C. Card, **D.R. Schield**, E. La, S.M. Secor, T.A. Castoe. Patterns of gene expression underlying the extreme physiological remodeling of the Burmese Python Intestine upon feeding. Joint Evolution Meetings 2014. Raleigh, NC.

2014 Adams, R., D.C. Card, **D.R. Schield**, J. Reyes-Velasco, and T.A. Castoe. Sample sequencing of 40 squamate reptile genomes reveals extensive evolutionary dynamics of genomic repeat element landscapes. Joint Evolution Meetings 2014. Raleigh, NC.

2014 Reyes-Velasco, J., K.J. Shaney, D.C Card, **D.R. Schield**, A. Andrew, C. Modal, N. Casewell, S.P. Mackessy and T.A. Castoe. Expression of venom homologs in the python suggest a model for venom gene recruitment and question the definition of a venom toxin. Joint Evolution Meetings 2014. Raleigh, NC.

2014 Castoe, T.A., A.P. J. de Koning, D.C. Card, **D.R. Schield**, J. Reyes-Velasco, A. Andrew, and R. Adams and D.D. Pollock. Snake genomes provide insight into the molecular evolutionary origins of a phenotypically distinct vertebrate clade. Joint Evolution Meetings 2014. Raleigh, NC.

2014 **Schield, D.R.**, D.C Card, J. Reyes-Velasco, F.N. Proctor, T. Jezkova, C.L. Spencer, H-W. Herrmann, S.P. Mackessy and T.A. Castoe. Using genome-wide single nucleotide polymorphisms to estimate patterns of gene flow and population structure in *Crotalus atrox*. *Biology of the Pitvipers 2*, Tulsa, OK.

2014 Reyes-Velasco, J, K.J. Shaney, D.C Card, **D.R. Schield**, A. Andrew, C. Modal, N. Casewell, S.P. Mackessy and T.A. Castoe. Leveraging the Burmese python genome to investigate the origin and evolution of snake venom gene families and to understand what a reasonable definition of 'a venom' might be. *Biology of the Pitvipers 2*, Tulsa, OK.

2014 Card. D.C., **D.R. Schield**, J. Reyes-Velasco, R.H. Adams, S.P. Mackessy and T.A. Castoe. The genome of the Prairie Rattlesnake (*Crotalus viridis viridis*). *Biology of the Pitvipers 2*, Tulsa, OK.

2014 **Schield, D.R.**, D.C Card, J. Reyes-Velasco, C.L. Spencer and T.A. Castoe. Using genome-wide single nucleotide polymorphisms to estimate patterns of gene flow and population structure in *Crotalus atrox*. *Annual Celebration of Excellence by Students (UTA-ACES)*, Arlington, TX.

2014 Card, D.C, **D.R. Schield**, M. Hunter, and T.A. Castoe. Genome-wide evidence of evolution in the invasive Florida python population. *Annual Celebration of Excellence by Students (UTA-ACES)*, Arlington, TX.

2014 Andrew, A.L., D.C. Card, **D.R. Schield**, E. La, S.M. Secor, T.A. Castoe. Differential gene expression underlying the extreme physiological remodeling of the Burmese Python Intestine upon feeding. *Annual Celebration of Excellence by Students (UTA-ACES)*, Arlington, TX.

2014 Hales, N., **D.R. Schield**, J. Reyes-Velasco, C.L. Spencer and T.A. Castoe. Phylogeography of the Mojave rattlesnake (*Crotalus scutulatus*) in the U.S. and Mexico. *Annual Celebration of Excellence by Students (UTA-ACES)*, Arlington, TX.

2013 **Schield, D.R.**, Proctor, F.N., Shaney, K.J., Reyes-Velasco, J., Card, D.C., Mackessy, S.P., T.A. Castoe. Investigating gene flow, population genetics, and failed speciation in Western Diamondback Rattlesnakes (*Crotalus atrox*). *Joint Evolution Meetings*, Snowbird, UT.

2013 Card, D.C., Proctor, F.N., Shaney, K.J., **Schield, D.R.**, Booth, W., Boback, S.M., T.A. Castoe. Evolution and population genomics of the *Boa constrictor*, and comparison between island and mainland population pairs. *Joint Evolution Meetings,* Snowbird, UT.

2013 Shaney, K.J., **Schield, D.R.**, Reyes-Velasco, J., Card, D.C., Mackessy, S.P., T.A. Castoe. Gene expression in Burmese Pythons sheds light on the evolution of venom gene families. *Joint Evolution Meetings*, Snowbird, UT.

2013 Riddle, B. R., Jezkova, T., **Schield, D.R.**, Card, D.C., T.A. Castoe. Genetic consequences of a range expansion in two congeneric rodents (genus *Dipodomys*). *American Society of Mammologists 93rd Annual Meeting,* Philidelphia, PA.

2013 **Schield, D.R.**, D.C. Card, K.J. Shaney, Q. Li, M. Yandell, S.P. Mackessy, T.A. Castoe. Differential expansion of select gene families in squamate genomes. *Mechanisms of Protein Evolution II*. Denver, CO.

2013 Card, D.C., K.J. Shaney, **D.R. Schield**, Q. Li, M. Yandell, D. Pollock, & T.A. Castoe. Evolutionary dynamics of protein domains across snake and lizard genomes. *Mechanisms of Protein Evolution II*. Denver, CO.

2012 **Schield, D.R.** and D.J. Baun. Habituation of anti-predator behavior and development of positive feeding response to an otherwise negative stimulus in *Ambystoma tigrinum*. *University of Minnesota Morris Undergraduate Research Symposium*. Morris, MN.

INVITED LECTURES

2020 *The role of the Z chromosome in barn swallow speciation*. Speciation and Introgression Discussion Group, University of California Berkeley, Berkeley, CA.

2019 *The origins and evolution of chromosomes and the recombination landscape in snake genomes*. Department of Biology Seminar, Miami University, Oxford, OH.

2019 *Snake genomes illustrate links between genome structure, function, and evolution*. Biology Department Graduate Recruitment Seminar, University of Texas at Arlington, Arlington, TX.

2018 *The molecular biology of translation*. Genetics (BIOL 3315). University of Texas at Arlington. Arlington, TX.

2017 *Repeated patterns of adaptation across the species continuum in North American rattlesnakes*. University of Minnesota. St. Paul, MN.

2015 *Fundamentals of epigenetics: function, mechanisms, and development*. Genomics (BIOL 3317/5335). University of Texas at Arlington. Arlington, TX.

2014 *Fundamentals of epigenetics: function, mechanisms, and development*. Genomics (BIOL 3317/5335). University of Texas at Arlington. Arlington, TX.

GRANTS AND AWARDS

2019 (2/2020 – 2/2022) NSF – Division of Biological Infrastructure – Postdoctoral Research Fellowships in Biology, Research Using Biological Collections Program: *The evolution of mate-choice traits and genomic architecture of speciation in swallows (genus* Hirundo*)*; Drew Schield, PI (**$138,000**).

2019 Charlie Painter Award in Herpetology – Chiricahua Desert Museum – Project Title: *The genomic consequences of hybridization between divergent rattlesnake species (*Crotalus viridis *and* Crotalus scutulatus*)* (**$1,000**).
2017 Outstanding Graduate Research Award – University of Texas at Arlington Department of Biology (**$500**).
2015 Travel award for Society for the Study of Amphibians and Reptiles meeting – Phi Sigma Biological Sciences Honor Society (**$750**).
2015 Research Grant – Phi Sigma Biological Honor Society (**$5,000**).
2015 NSF – Division of Environmental Biology – Systematics Panel: Doctoral Dissertation Improvement Grant: DISSERTATION RESEARCH: *Delineation of populations, species, and genomic adaptations across a widely distributed venomous snake species complex*; Todd Castoe as Co-PI (**$19,695**).
2014 Travel award for Joint Evolution Meetings – Phi Sigma Biological Sciences Honor Society (**$750**).
2014 Sponsored membership – AAAS (2 years).
2013 Research Grant – Phi Sigma Biological Sciences Honor Society (**$1250**).
2013 Travel award for Joint Evolution Meetings – Phi Sigma Biological Sciences Honor Society (**$750**)
2013 Travel Award – Evolution meeting, Snowbird, UT (**$500**).
2013 Travel Award – Mechanisms of Protein Evolution II meeting, Denver, CO (**$500**).
2012 Enhanced Graduate Teaching Fellowship – UTA (**~$24,000**/year, 5 years).
2012 Jay Y. Roshal Award – University of Minnesota Morris (**$500**).
2011 Undergraduate Research Opportunity Program – University of Minnesota Morris (**$1,700**).
2010 Morris Student Administrative Fellowship – University of Minnesota Morris (**$500**/semester, 5 semesters).

STUDENT ADVISING AND TRAINING

As a Ph.D. student and postdoctoral fellow in the laboratory of Dr. Castoe at the University of Texas at Arlington, I assisted Dr. Castoe in mentoring six undergraduate researchers, **Frances Proctor**, **Zachary Rodrigues**, **Nicole Hales**, **Nour Louzon**, **Ola Moussa**, and **Kristopher Row**, in semi-independent research projects. I have trained these students in molecular laboratory techniques, including next-generation library construction and sequencing, and advised them in developing computational approaches to analyze data. Several of these students have presented at academic conferences and co-authored peer-reviewed publications, and five of these students have since pursued graduate degrees in biology and related fields. As a postdoctoral researcher, I have also mentored to Ph.D. students **Zachary Nikolakis** and **Richard Orton** in population genetic theory, genomic data generation, and analysis. As a postdoctoral fellow in the laboratory of Dr. Rebecca Safran, I have mentored Ph.D. student **Javan Carter** in topics related to phylogenomic and population genomic analyses and population genetic theory.

TEACHING EXPERIENCE

Graduate Teaching Assistant Fall 2012 – Summer 2017
University of Texas at Arlington, Arlington, TX
Laboratory instructor for semester long undergraduate course **Ecology and Evolution** (BIOL1442).
Tutor Fall 2014 – Summer 2017
University of Texas at Arlington, Arlington, TX
Supplementary instruction to students in the undergraduate **Genetics** course

PROFESSIONAL SOCIETIES

Society for the Study of Evolution – member (2013 – present)
American Society of Naturalists – member (2020 – present)
American Genetics Association – member (2020 – present)
Society of Systematic Biologists – member (2014 – present)
Snake Genomics Consortium – member (2013 – present)
Society for the Study of Amphibians and Reptiles – member (2011 – present)
American Academy of Arts & Sciences – member (2014-2016)

SERVICE

Vice President – Phi Sigma Biological Honor Society, Beta Phi Chapter (Fall 2013 – Summer 2015)
Graduate Mentor – University of Texas at Arlington I-ENGAGE Program – Summer 2014
Graduate student volunteer – *Joint Evolution Meetings 2013,* Snowbird, UT
Session moderator – *Joint Evolution Meetings 2014*, Raleigh, NC
Ad hoc manuscript reviewer – ***Ecology Letters***, ***Systematic Biology***, ***Evolution***, ***Molecular Ecology***, ***Briefings in Bioinformatics, Philosophical Translations of the Royal Society B: Biological Sciences, Heredity***, ***Genome Biology and Evolution***, ***Molecular Phylogenetics and Evolution***, ***PLOS One***, ***Scientific Reports***, ***Genomics***, ***Ecology and Evolution, Toxicon***, ***Journal of Herpetology***, ***Phyllomedusa, and Conservation Genetics***

PROFESSIONAL REFERENCES

Rebecca J. Safran, Ph.D. [Postdoctoral advisor]
Associate Professor – Department of Ecology and Evolutionary Biology
University of Colorado Boulder
Boulder, CO 80309
Office: 303-735-1495
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Todd A. Castoe, Ph.D. [Ph.D./postdoctoral advisor]
Associate Professor – Department of Biology
University of Texas at Arlington
Arlington, TX 76019
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Stephen P. Mackessy, Ph.D. [Collaborator]
Professor - Dept. of Biological Sciences
University of Northern Colorado
Greeley, CO 80639
Office: 970-351-2429
Email: Stephen.mackessy@unco.edu