

DAREN C. CARD, PH.D.
Curriculum Vitae

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PROFESSIONAL SYNOPSIS

- Broadly trained evolutionary geneticist interested in the generation and maintenance of biodiversity
- Expertise in studying the genomic basis of adaptation and convergent evolution in non-model vertebrates
- Integrative skillset merging field biology, genomics, bioinformatics, and developmental biology
- Author of 43 peer-reviewed publications, with 9 as first author

EDUCATION

- 2018 Ph.D. in Quantitative Biology, University of Texas, Arlington (UTA), Arlington, TX
 Faculty Mentor: Dr. Todd A. Castoe
 Thesis: Using snake genomes to illuminate the patterns and mechanisms of rapid adaptation
 Funding: NSF Doctoral Dissertation Improvement Grant
- 2011 B.S. in Conservation Biology, SUNY College of Environmental Science and Forestry (ESF),
 Syracuse, NY

PROFESSIONAL POSITIONS

- 2022– Postdoctoral Fellow, Department of Organismic & Evolutionary Biology
 and Museum of Comparative Zoology, Harvard University, Cambridge, MA
 Faculty Mentor: Dr. Scott V. Edwards
- 2018–22 NSF Postdoctoral Research Fellow, Department of Organismic & Evolutionary Biology
 and Museum of Comparative Zoology, Harvard University, Cambridge, MA
 Faculty Mentor: Dr. Scott V. Edwards
 Project: Evolutionary genomics of parallel limb and digit reduction in *Lerista* skinks
 Funding: NSF Postdoctoral Research Fellowship in Biology

FELLOWSHIPS & AWARDS

National Fellowships

- | | | |
|------|---|-------------------------------------|
| 2018 | NSF Postdoctoral Research Fellowship in Biology | \$216,000 salary; \$60,000 research |
| 2013 | NSF Graduate Research Fellowship | Honorable Mention |

Research Grants

- | | | |
|------|---|----------|
| 2015 | NSF Doctoral Dissertation Improvement Grant (Co-PI) | \$19,695 |
| 2014 | Philosophical Society Lewis & Clark Fund for Exploration and Field Research | \$5,000 |
| 2013 | Study of Evolution Rosemary Grant Award 2013 | \$2,250 |

2013–16 Three UTA Phi Sigma & Graduate Student Senate Awards \$14,250 total

Academic Awards

2018 UTA Office of Graduate Studies Dissertation Fellowship \$6,700
 2017 William L. & Martha Hughes Scholarship \$2,000
 2016 UTA ACES Conference Awards \$500
 2015 UTA College of Science Dean's Excellence Scholarship \$5,000
 2012–18 Enhanced Graduate Teaching Assistantship (salary & tuition) \$150,000 total

Travel Awards

2015 Full travel support for the NESCent Hackathon on Population Genetics in R \$1,800
 2012– Various travel awards from UTA Phi Sigma, UTA Graduate Studies, and \$11,000
 others to attend meetings: Joint Evolution Meetings, GSA PEQG, SMCBE, *et al.*

PUBLICATIONS

Citation Statistics

Publications: 43 peer-reviewed; 3 perspectives/book chapters; 1 articles in review/revision
Total citations: Google Scholar = 1,953, CrossRef = 1,454
Mean/Median citations per publication: Google Scholar = 43.4/32, CrossRef = 36.4/28.5
i10-index (papers cited a minimum of 10 times): Google Scholar = 37 CrossRef = 32
H-index (h papers cited a minimum of h times): Google Scholar = 27, CrossRef = 25

Google Scholar Profile: <http://scholar.google.com/citations?user=umOwsMAAAAJ>

PDFs available for personal use at <http://www.darencard.net/publications>

* Authors who are/were undergraduate students mentored by the lab

† Authors contributed equally

Selected

43. **Card, D.C.**, W.B. Jennings, & S.V. Edwards. **2023**. Genome evolution and the future of phylogenomics of non-avian reptiles. *Animals* 13(3): 471. doi: [10.3390/ani13030471](https://doi.org/10.3390/ani13030471).
42. **Card, D.C.**, A.G. Van Camp*, T. Santonastaso, M.I. Jensen-Seaman, N.M. Anthony, & S.V. Edwards. **2022**. Structure and evolution of the squamate major histocompatibility complex as revealed by two *Anolis* lizard genomes. *Frontiers in Genetics* 13: 979746. doi: [10.3389/fgene.2022.979746](https://doi.org/10.3389/fgene.2022.979746).
41. **Card, D.C.**, F.J. Vonk, S. Smalbrugge, N.R. Casewell, W. Wüster, T.A. Castoe, G.W. Schuett, & W. Booth. **2021**. Genome-wide data implicate terminal fusion automixis in King Cobra facultative parthenogenesis. *Scientific Reports* 11(7271). doi: [10.1038/s41598-021-86373-1](https://doi.org/10.1038/s41598-021-86373-1).
40. **Card, D.C.**, B. Shapiro, G. Giribet, C. Moritz, & S.V. Edwards. **2021**. Museum Genomics. *Annual Review of Genetics* 55(1): 633-659. doi: [10.1146/annurev-genet-071719-020506](https://doi.org/10.1146/annurev-genet-071719-020506).
39. **Card, D.C.**, R.H. Adams, D.R. Schield, B.W. Perry, A.B. Corbin, G.I.M. Pasquesi, K. Row*, J.M. Daza, W. Booth, C.E. Montgomery, S.M. Boback, & T.A. Castoe. **2019**. Genomic basis of convergent island phenotypes in boa constrictors. *Genome Biology & Evolution* 11(11): 3123-3143. doi: [10.1093/gbe/evz226](https://doi.org/10.1093/gbe/evz226).

38. **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, & T.A. Castoe. **2018**. Novel ecological and climatic conditions drive rapid adaptation in invasive Florida Burmese pythons. *Molecular Ecology* 27(23): 4744-4757. doi: [10.1111/mec.14885](https://doi.org/10.1111/mec.14885). (Top 10% of downloaded papers in 12 months following publication)
37. 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. Hoffmann, M.W. Vandeweghe, R. 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.-H. Kuo, S.E. McGaugh, A.M. Bronikowski, J. de Koning, S.V. Edwards, M.E. Pfreder, P. Minx, E.D. Brodie III, E.D. Brodie Jr., W.C. Warren, & T.A. Castoe. **2018**. Molecular adaptations for sensing and securing prey, and insights into amniote diversity, from the garter snake genome. *Genome Biology & Evolution* 10(8): 2110-2129. doi: [10.1093/gbe/evy157](https://doi.org/10.1093/gbe/evy157).
36. **Card, D.C.**, D.R. Schield, R.H. Adams, A.B. Corbin, A.L. Andrew, G.I.M. Pasquesi, B. Perry, T. Jezkova, S.M. Boback, W. Booth, & T.A. Castoe. **2016**. Phylogeographic and population genetic analyses reveal multiple species of *Boa* and independent origins of insular dwarfism. *Molecular Phylogenetics & Evolution* 102: 104-116. doi: [10.1016/j.ympev.2016.05.034](https://doi.org/10.1016/j.ympev.2016.05.034).
35. **Card, D.C.**, D.R. Schield, J. Reyes-Velasco, A.L. Andrew, M.K. Fujita, S.J. Oyler-McCance, J.A. Fike, D.F. Tomback, R.P. Ruggiero, & T.A. Castoe. **2014**. Two new low-coverage bird genome references and a comparison of reference-guided versus *de novo* assembly content and utility. *PLOS ONE* 9(9): e106649. doi: [10.1371/journal.pone.0106649](https://doi.org/10.1371/journal.pone.0106649).

Additional Peer Reviewed

34. Schield, D.R., B.W. Perry, **D.C. Card**, G.I.M. Pasquesi, A.K. Westfall, S.P. Mackessy, & T.A. Castoe. **2022**. The rattlesnake W chromosome: A GC-rich retroelement refugium with retained gene function across ancient evolutionary strata. *Genome Biology & Evolution* 14(9): evac116. doi: [10.1093/gbe/evac116](https://doi.org/10.1093/gbe/evac116).
33. Koochekian, N., Ascanio, A., Farleigh, K., **D.C. Card**, D.R. Schield, T.A. Castoe, & T. Jezkova. **2022**. A chromosome-level genome assembly and annotation of the Desert Horned Lizard, *Phrynosoma platyrhinos*, provides insight into chromosomal rearrangements among reptiles. *GigaScience* 11: giab098. doi: [10.1093/gigascience/giab098](https://doi.org/10.1093/gigascience/giab098).
32. Farleigh, K., S.A. Vladimirova, C. Blair, J.T. Bracken, N. Koochekian, D.R. Schield, **D.C. Card**, N. Finger, J. Henault, A.D. Leaché, T.A. Castoe, & T. Jezkova. **2021**. The effects of climate and demographic history in shaping genomic variation across populations of the Desert Horned Lizard (*Phrynosoma platyrhinos*). *Molecular Ecology* 30(18): 4481-4496. doi: [10.1111/mec.16070](https://doi.org/10.1111/mec.16070).
31. Kazi, M.I., B.W. Perry, **D.C. Card**, R.D. Schargel, H.B. Ali, V.C. Obuekwe, M. Sapkota, K.N. Kang, M.W. Pellegrino, D.E. Greenberg, T.A. Castoe, & J.M. Boll. **2020**. Discovery and characterization of New Delhi metallo-β-lactamase-1 inhibitor peptides that potentiate meropenem-dependent killing of carbapenem-resistant *Enterobacteriaceae*. *Journal of Antimicrobial Chemotherapy* 75(10): 2843-2851. doi: [10.1093/jac/dkaa242](https://doi.org/10.1093/jac/dkaa242). (Designed bioinformatics analysis pipeline.)
30. Lamichhaney, S., **D.C. Card**, P. Grayson, J.F.R. Tonini, G.A. Bravo, K. Näpflin, F. Termignoni-Garcia, C. Torres, J.A. Clarke, F. Burbrink, T.B. Sackton, & S.V. Edwards. **2019**. Integrating natural history-derived phenomic data and comparative genomics as core tools to study evolutionary convergence. *Philosophical Transactions of the Royal Society B* 374(1777). doi: [10.1098/rstb.2018.0248](https://doi.org/10.1098/rstb.2018.0248).

29. Casewell, N.R., D. Petras, **D.C. Card**, V. Suranse, A.M. Mychajliw, D. Richards, I. Koludarov, L.-O. Albulescu, J. Slagboom, B.-F. Hempel, N.M. Ngum, R.J. Kennerley, J.L. Brocca, G. Whiteley, R.A. Harrison, F.M.S. Bolton, J. Debono, F.J. Vonk, J. Alföldi, J. Johnson, E. Karlsson, K. Lindblad-Toh, I. Mellor, R.D. Süßmuth, B.G. Fry, S. Kuruppu, W.C. Hodgson, J. Kool, T.A. Castoe, I. Barnes, K. Sunagar, E.A.B. Undheim, & S.T. Turvey. **2019**. Solenodon genome reveals convergent evolution of venom in eulipotyphlan mammals. *Proceedings of the National Academy of Sciences USA* 116(51): 25745-25755. doi: [10.1073/pnas.1906117116](https://doi.org/10.1073/pnas.1906117116). (Annotated genome repeats and genes.)
28. 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, & T.A. Castoe. **2019**. Allopatric divergence and secondary contact with gene flow – a recurring theme in rattlesnake speciation. *Biological Journal of the Linnean Society* 128(1):149-169. doi: [10.1093/biolinnean/blz077](https://doi.org/10.1093/biolinnean/blz077).
27. Perry, B.W., A.L. Andrew, A.H.M. Kamal, **D.C. Card**, D.R. Schield, G.I.M. Pasquesi, M. Pellegrino, S.P. Mackessy, S. Chowdhury, S.M. Secor, & T.A. Castoe. **2019**. Multi-species comparisons of snakes suggest that insulin and stress response signaling modulate post-feeding intestinal regeneration. *Proceedings of the Royal Society B* 286(1906). doi: [10.1098/rspb.2019.0910](https://doi.org/10.1098/rspb.2019.0910).
26. 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, & T.A. Castoe. **2019** The origins and evolution of chromosomes, dosage compensation, and mechanisms underlying venom regulation in snakes. *Genome Research* 29: 590-601. doi: [10.1101/gr.240952.118](https://doi.org/10.1101/gr.240952.118).
25. Pinto, B.J., **D.C. Card**, T.A. Castoe, R.E. Diaz, S.V. Nielsen, P.A. Trainor, & T. Gamble. **2019**. The transcriptome of the Veiled Chameleon (*Chamaeleo calyptrotus*): a resource for studying the evolution and development of vertebrates. *Developmental Dynamics* 248(8): 702-708. doi: [10.1002/dvdy.20](https://doi.org/10.1002/dvdy.20).
24. Pasquesi, G.I.M., R.H. Adams, **D.C. Card**, D.R. Schield, A.B. Corbin, B.W. Perry, J. Reyes-Velasco, R.P. Ruggiero, M.W. Vandewege, J.A. Shortt, & T.A. Castoe. **2018**. Evolutionary dynamics of genomic repeat element landscapes in squamate reptiles. *Nature Communications* 9: 2774. doi: [10.1038/s41467-018-05279-1](https://doi.org/10.1038/s41467-018-05279-1).
23. 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. C. Garcia, N.M. Bouzid, J.L. Strickland, C.L. Parkinson, O. Flores-Villela, S.P. Mackessy, & T.A. Castoe. **2018**. Cryptic genetic diversity, population structure, and gene flow dynamics in the highly venomous Mohave rattlesnake (*Crotalus scutulatus*). *Molecular Phylogenetics & Evolution* 127: 669-681. doi: [10.1016/j.ympev.2018.06.013](https://doi.org/10.1016/j.ympev.2018.06.013).
22. Adams, R.H., D.R. Schield, **D.C. Card**, & T.A. Castoe. **2018**. Assessing the impacts of positive selection on coalescent-based species tree estimation and delineation. *Systematic Biology* 67(6): 1076-1090. doi: [10.1093/sysbio/syy034](https://doi.org/10.1093/sysbio/syy034).
21. Schott, R.K., A. Van Nynatten, **D.C. Card**, T.A. Castoe, & B. Chang. **2018**. Shifts in selective pressures on snake phototransduction genes associated with photoreceptor transmutation and dim-light ancestry. *Molecular Biology & Evolution* 35(6): 1376-1389. doi: [10.1093/molbev/msy025](https://doi.org/10.1093/molbev/msy025).
20. Adams, R.H., D.R. Schield, **D.C. Card**, A.B. Corbin, & T.A. Castoe. **2017**. ThetaMater: Bayesian estimation of population size parameter θ from genomic data. *Bioinformatics* 34(6): 1072-1073. doi: [10.1093/bioinformatics/btx733](https://doi.org/10.1093/bioinformatics/btx733).
19. Hales, N.R., D.R. Schield, A.L. Andrew, **D.C. Card**, M.R. Walsh, & T.A. Castoe. **2017**. Contrasting gene expression programs underlie predator-induced phenotypic plasticity within the across generations in *Daphnia*. *Molecular Ecology* 26(19): 5003-5015. doi:[10.1111/mec.14213](https://doi.org/10.1111/mec.14213).

18. Gamble, T., T.A. Castoe, S.V. Nielsen, J.L. Banks, **D.C. Card**, D.R. Schield, G.W. Schuett, & W. Booth. **2017**. The discovery of XY sex chromosomes in a *Boa* and *Python*. *Current Biology* 27(14): 2148-2153. doi:[10.1016/j.cub.2017.06.010](https://doi.org/10.1016/j.cub.2017.06.010).
17. Lotterhos, K., **D.C. Card**, S. Schaal, L. Wang, C. Collins, & R. Verity. **2017**. Composite measures of selection can improve the signal-to-noise ratio in genome scans. *Methods in Ecology and Evolution* 8(6): 717-727. doi:[10.1111/2041-210X.12774](https://doi.org/10.1111/2041-210X.12774).
16. Schield, D.R., R.H. Adams, **D.C. Card**, B.W. Perry, T. Jezkova, A.L. Andrew, G.I.M. Pasquesi, C.L. Spencer, E.E. Sanchez, S.P. Mackessy, & T.A. Castoe. **2017**. Genomic patterns of divergence and admixture in a widely distributed rattlesnake provide insight into speciation with gene flow. *Ecology and Evolution* 7(11): 3951-3966. doi:[10.1002/ece3.2996](https://doi.org/10.1002/ece3.2996).
15. Andrew, A.L., B.W. Perry, **D.C. Card**, D.R. Schield, R.P. Ruggiero, S.E. McGaugh, A. Choudhary, 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. doi:[10.1186/s12864-017-3743-1](https://doi.org/10.1186/s12864-017-3743-1).
14. Schott, R.K., B. Panesar, **D.C. Card**, M. Preston, T.A. Castoe, & B. Chang. **2017**. Targeted hybrid enrichment of complete coding regions across divergent species. *Genome Biology & Evolution* 9(2): 398-414. doi:[10.1093/gbe/evx005](https://doi.org/10.1093/gbe/evx005).
13. Cox, R.M., C.L. Cox, J.W. McGlothlin, **D.C. Card**, A.L. Andrew, & T.A. Castoe. **2017**. Genetic disintegration: Ontogenetic increases in sex-biased gene expression underlie the breakdown of between-sex genetic correlations. *American Naturalist* 189(3): 315-332. doi:[10.1086/690105](https://doi.org/10.1086/690105).
12. Shortt, J.A., **D.C. Card**, D.R. Schield, Y. Liu, B. Zhong, T.A. Castoe, E.J. Carlton, & D.D. Pollock. **2017**. Whole genome amplification and targeted genome sequencing of *Schistosoma japonicum* miridia. *PLOS Neglected Tropical Diseases* 11(1): e0005292. doi:[10.1371/journal.pntd.0005292](https://doi.org/10.1371/journal.pntd.0005292).
11. Verity, R., C. Collins, **D.C. Card**, S.M. Schaal, L. Wang, & K.E. Lotterhos. **2017**. MINOTAUR: A platform for the analysis and visualization of multivariate results from genome scans with R Shiny. *Molecular Ecology Resources* 17(1): 33-43. doi:[10.1111/1755-0998.12579](https://doi.org/10.1111/1755-0998.12579).
10. Adams, R.H., D.R. Schield, **D.C. Card**, H. Blackmon, & T.A. Castoe. **2016**. GppFst: Genomic posterior predictive simulations of F_{ST} and d_{xy} for identifying outlier loci from population genomic data. *Bioinformatics*. doi:[10.1093/bioinformatics/btw795](https://doi.org/10.1093/bioinformatics/btw795).
9. Streicher, J.W., J.P. McEntee, L.C. Drzich*, **D.C. Card**, D.R. Schield, U. Smart, C.L. Parkinson, T. Jezkova, E.N. Smith, & T.A. Castoe. **2016**. Genetic surfing, not allopatric divergence, explains spatial sorting of mitochondrial haplotypes in venomous coral snakes. *Evolution*. doi:[10.1111/evo.12967](https://doi.org/10.1111/evo.12967). (Featured cover article.)
8. Adams, R.H., H. Blackmon, J. Reyes-Velasco, **D.C. Card**, D.R. Schield, N. Waynewood*, A.L. Andrew, & T.A. Castoe. **2016**. Microsatellite landscape evolutionary dynamics across 450 million years of vertebrate genome evolution. *Genome* 59(5): 295-310. doi:[10.1139/gen-2015-0124](https://doi.org/10.1139/gen-2015-0124).
7. Schield, D.R., M.R. Walsh, **D.C. Card**, A.L. Andrew, R.A. Adams, & T.A. Castoe. **2016**. EpiRADseq: scalable analysis of genome-wide patterns of methylation using next-generation sequencing. *Methods in Ecology & Evolution* 7(1): 60-69. doi:[10.1111/2041-210X.12435](https://doi.org/10.1111/2041-210X.12435). (Featured cover article.)
6. Andrew, A.L., **D.C. Card**, R.P. Ruggiero, D.R. Schield, R.H. Adams, D.D. Pollock, S.M. Secor, & 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. doi:[10.1152/physiolgenomics.00131.2014](https://doi.org/10.1152/physiolgenomics.00131.2014).

5. 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. **2015**. Incipient speciation with biased gene flow between two lineages of the Western Diamondback Rattlesnake (*Crotalus atrox*). *Molecular Phylogenetics & Evolution* 83: 213-223. doi:[10.1016/j.ympev.2014.12.006](https://doi.org/10.1016/j.ympev.2014.12.006).
4. Reyes-Velasco, J., **D.C. Card**, A.L. Andrew, K.J. Shaney, R.H. Adams, D.R. Schield, N.R. Casewell, S.P. Mackessy, & T.A. Castoe. **2015**. Expression of venom gene homologs in diverse python tissues suggests a new model for the evolution of snake venom. *Molecular Biology & Evolution* 32(1): 173-183. doi:[10.1093/molbev/msu294](https://doi.org/10.1093/molbev/msu294). (Cover article.)
3. Jezkova, T., B.R. Riddle, **D.C. Card**, D.R. Schield, M.E. Eckstut, & T.A. Castoe. **2014**. Genetic consequences of a post-glacial range expansion in two co-distributed rodents (genus *Dipodomys*) depends on ecology and genetic marker choice. *Molecular Ecology* 24(1): 83-97. doi:[10.1111/mec.13012](https://doi.org/10.1111/mec.13012).
2. Gilbert, C., J.M. Meik, D. Dashevsky, **D.C. Card**, T.A. Castoe, & S. Schaack. **2014**. Endogenous hepadnaviruses, bornaviruses, and circoviruses in snakes. *Proceedings of the Royal Society B* 281(1791): 20141122. doi:[10.1098/rspb.2014.1122](https://doi.org/10.1098/rspb.2014.1122).
1. 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. Vandeweghe, 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(51): 20645-20650. doi:[10.1073/pnas.1314475110](https://doi.org/10.1073/pnas.1314475110). (Analyzed RNAseq data to infer differential gene expression.)

Book Sections & Perspective Articles

3. **Card, D.C.**, D.R. Schield, & T.A. Castoe. **2018**. Plasticity and local adaptation explain lizard cold tolerance. *Molecular Ecology* 27(9): 2173-2175. doi: [10.1111/mec.14575](https://doi.org/10.1111/mec.14575).
2. Schield, D.R., **D.C. Card**, J. Reyes-Velasco, A.L. Andrew, S.P. Mackessy, D.D. Pollock, T.A. Castoe. **2016**. A role for genomics in rattlesnake research - current knowledge and future potential. In: Schuett, G.W., L.W. Porras, & R.S. Reiserer (Eds.). *Rattlesnakes of Arizona*. ECO Wear & Publishing, Rodeo, NM, USA.
1. Shaney, K.J., D.R. Schield, **D.C. Card**, R.P. Ruggiero, D.D. Pollock, S.P. Mackessy, T.A. Castoe. **2014**. Squamate reptile genomics and evolution. In: Gopalakrishnakone (Ed.). *Handbook of Toxinology: Venom Genomics and Proteomics*. Springer Reference Press, New York, NY, USA.

Manuscripts in Review

Farleigh, K., A. Ascanio, M. Farleigh, D.R. Schield, **D.C. Card**, M. Leal, T.A. Castoe, T. Jezkova, & Rodriguez, J. **In Review**. Signals of differential introgression in the genome of natural hybrids of Caribbean anoles. *Molecular Ecology*.

MEDIA COVERAGE

- 2022 **Knowable Magazine** (published by Annual Reviews) highlighted our review article in *Annual Reviews Genetics* with a [Q&A on Museum Genomics](#).
- 2021 The **Harvard Gazette** [featured](#) a selection of favorite or essential tools used by Harvard scientists where I highlighted the utility of modern sequencing machines.

- 2019 Coverage of our paper on venom evolution in *Solenodon* has appeared in the [New York Times](#).
- 2018 **UTA College of Science** [highlighted](#) my NSF Postdoctoral Fellowship award and project.
- 2018 Interviewed for **Inverse** [article](#) on a high profile publication on independent dwarfism in humans from the island of Flores that includes a solicited comment from me about the impact of the research.
- 2017 **Particle**, a new science news website based in Western Australia, ran an [article](#) on island dwarfism, which featured some of my work on island dwarf boas.
- 2017 The **National Science Foundation** was nice enough to advertise our research on their [Twitter feed](#), and included a couple pictures of the dwarf *Boa* I researched during my Ph.D.
- 2017 **Texas Advanced Computing Center** wrote an [article](#) featuring our work, which has utilized the high-performance computing environment at TACC extensively. Article was also picked up by EurekAlert, Science Daily, Motherboard/Vice, and other news outlets.
- 2015 **UTA College of Science Maverick Science Magazine** featured [cover article](#) on work conducted in our laboratory, focusing on understanding regenerative organ growth in Burmese pythons.
- 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 congratulating me on receiving a NSF Doctoral Dissertation Improvement Grant.
- 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, Science Daily, Nature World News, Science Codex, Science World Report, French Tribune, Planet Earth, Design and Trend, and Phys.Org**.
- 2013 [Five-page in-print](#) editorial coverage of our work on snake genomics in: **Science** 342:1159-1167.
- 2013 Radio interview with Todd Castoe discussing our research on the Burmese python on: **National Public Radio – Dallas KERA**.
- 2013 Extensive news coverage of our 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, GenomeWeb, University Herald, Science Recorder, Nature World News, Mother Nature Network, ScienceDaily, and LiveScience**.

PRESENTATIONS

Invited Presentations

- 2023 Comparative genomics of the skink genomes supports multiple mechanisms of limb reduction in squamate reptiles. Session on Genomics of Non-Classical Model Animals. International Plant & Animal Genomes XXX. San Diego, CA.
- 2022 Comparative genomics of the first skink genomes supports multiple mechanisms of limb reduction in squamate reptiles. Session on Genomics of Non-Classical Model Animals. International Plant & Animal Genomes XXIX. San Diego, CA. [cancelled]

- 2021 Investigating adaptation and convergent evolution in squamate reptiles – a clade of evolutionary transitions. [Early Career Scientist Seminar](#). J.F. Crow Institute for the Study of Evolution. University of Wisconsin – Madison. Madison, WI.
- 2021 Evolutionary genomics in squamate reptiles: Mechanisms of adaptation and convergence. Department of Biology Seminar. University of Nebraska Omaha. Omaha, NE.
- 2019 Evolutionary genomics in squamate reptiles: Mechanisms of adaptation and convergence. Department of Biology Seminar. Clark University. Worcester, MA.
- 2019 An enduring frontier: early results and future directions of comparative genomics in squamate reptiles. Genome10K-Vertebrate Genome Project Meeting. New York, NY.
- 2017 Genomic basis of convergent phenotypic evolution in island populations of *Boa constrictor*. Scott Edwards' lab group. Harvard University. Cambridge, MA.
- 2017 Genome-wide evidence of evolution and adaptation in the invasive Florida python population. Andy Clark's lab group. Cornell University. Ithaca, NY.
- 2016 Adaptation in snakes. UT-Arlington Genome Biology Group. Arlington, TX.
- 2013 Using evolutionary genomics to gain insight into vertebrate diversity and adaptation. UT-Arlington Genome Biology Group. Arlington, TX.

Contributed Abstracts (contributor to 80 abstracts total since 2013)

- 2022 Comparative genomics of skink genomes supports multiple mechanisms of limb reduction in squamate reptiles. Joint Evolution Meetings. Cleveland, OH.
- 2021 Comparative genomics of the first skink genomes supports multiple mechanisms of limb reduction in squamate reptiles. Joint Evolution Meetings. Virtual.
- 2019 Genomic basis of convergent island phenotypes in boa constrictors. Gordon Research Seminar – Ecological & Evolutionary Genomics. Manchester, NH.
- 2019 Genomic basis of convergent island phenotypes in boa constrictors. Joint Evolution Meetings. Providence, RI.
- 2018 Genomic basis of adaptive island dwarfism in *Boa constrictor* snakes. GSA – Population, Evolutionary, and Quantitative Genetics Meeting. Madison, WI.
- 2017 Genome-wide evidence of evolution and adaptation in the invasive Florida python population. Joint Evolution Meetings. Portland, OR.
- 2016 Genome-wide evidence of evolution and adaptation in the invasive Florida python population. Joint Evolution Meetings. Austin, TX.
- 2015 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 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.
- 2014 Genome-wide evidence of evolution and adaptation in the invasive Florida python population. Joint Evolution Meetings. Raleigh, NC.
- 2014 The genome of the Prairie Rattlesnake (*Crotalus viridis viridis*). Biology of the Pitvipers 2. Tulsa, OK.

- 2014 Evolution and putative adaptation in the Florida python population inferred using genome-wide RADseq data. Ecological Genomics Symposium. Kansas City, MO.
- 2013 Evolution and population genomics of *Boa constrictor*, and comparisons between island and mainland population pairs. Joint Evolution Meetings. Snowbird, UT.
- 2013 Evolutionary dynamics of protein domains across snake and lizard genomes. Mechanisms of Protein Evolution II. Denver, CO.

SUMMARY OF TECHNICAL SKILLS

Programming Languages: Bash, R/RStudio, Python, Markdown, HTML, Git/GitHub

Statistics: Parametric and non-parametric statistics, linear regression, PCA, maximum likelihood & Bayesian statistics, machine learning

Computer Systems: Unix/Linux, MacOS, high performance computing, cloud computing, tape storage, SLURM

Genomics Software: BLAST+, BWA, SAMtools, BEDtools, BCFtools, GATK, Picard, Trinity, MAKER, RepeatMasker/Modeler, CD-HIT, Cactus, HALtools, UCSC utils, PHAST, PhyloAcc, IQTREE

Data Curation: Genomics data & metadata, project management, natural history specimens & metadata

Molecular Lab Work: DNA & RNA extraction, cell isolation, PCR, primer design, gel electrophoresis, Sanger sequencing, BioAnalyzer/TapeStation, Qubit, Nanodrop, sonication, qPCR, magnetic bead purification, lab safety, dry ice shipping

Sequencing: Illumina library prep & data processing (WGS, RNA-seq, ATAC-seq, Hi-C, RAD-seq)

Writing/Administration: Technical writing, grant writing, report writing, maintaining animal ethics protocols, securing collecting permits, transferring specimens internationally, laboratory safety

Productivity Software: Microsoft Office Suite, Google Workspace, Adobe Illustrator/Photoshop

Museum Science: Collection/preparation of genetic specimens & metadata, curation of cryogenic collections, preparation/curation of herpetological specimens & metadata, use of collections databases

TEACHING & ADVISING EXPERIENCE

Graduate Teaching Assistant

University of Texas at Arlington, Arlington, TX

Zoology Laboratory (BIOL 3454; UG; ~60 students/semester) 15 semesters 2012–18

Human Anatomy Laboratory (BIOL 3446; UG; ~60 students) Fall 2013

- Approximately 750 students taught in total
- Engaged students in hands-on laboratory activities designed around course curriculum
- Managed classroom of 30 students and 1-2 undergraduate teaching assistants
- Prepared and graded all quizzes and examinations
- Served as lead TA for 4 years, helping to manage fellow TAs and ordering supplies

Instructor

Software Carpentry/Data Carpentry

Experience Teaching: SWC Unix Shell, Git/GitHub, R, & Python; DC Genomics

8 Workshops Taught: UTA – Jan./Apr./Oct. 2016; Feb./Nov. 2017; Feb. 2018

UC San Francisco – Dec. 2016

SUNY Upstate – May 2017

- Approximately 250 students taught in total
- Co-founder of [UTA Carpentries](#). Submitted successful proposal for instructor training with group of 10 instructors at UTA, which was 1 of 2 funded in the United States (out of 25 applications).
- Funding to facilitate these workshops has been generously provided by the UTA Library and there is also ongoing work to build a broader data science training program at UTA, with our group and the SWC/DC curriculum serving as a foundation.

Undergraduate Mentoring

2 high school students in biological research and computational data analysis.

3 Harvard undergraduates in computational data analysis.

5 UTA undergraduates in research tasks, including lab work, computational data analysis, and manuscript writing.

Note: 4 former research assistants have pursued research-based graduate degrees.

Other Experiences

Harvard University: OEB 190 – Biology and Diversity of Birds

- Assisted Professor Scott Edwards on 2022 spring break field trip to coastal/south Texas
- 9-day trip; 20 undergraduate students; 26 checklists/locations; ~120 bird species
- Helped guide daily field trips to observe, identify, and discuss the natural history of birds
- Assisted with transporting students, chaperoning, and other logistical needs

PROFESSIONAL SERVICE

Ad hoc Reviewer

Ad hoc grant proposal reviewer for:

- National Science Foundation (2021)
- Society for the Study of Evolution Graduate Research Excellence Grants (2017-2020)
- Harvard College Research Program (2022-2023)

Journal Reviewing

35 reviews for 25 journals

Journal of Biogeography (1); Biological Journal of the Linnean Society (3); Biology Letters (1); Biology Methods & Protocols (1); Chromosoma (1); Ecology & Evolution (1); Genetica (1); Genetics & Molecular Biology (1); Genome Biology & Evolution (2); G3: Genes | Genomes | Genetics (3); Integrative & Comparative Biology (1); Journal of Molecular Evolution (1); Journal of Heredity (2); Molecular Biology & Evolution (1); Molecular Ecology (2); Molecular Ecology Resources (2); Molecular Phylogenetics & Evolution (1); Nature Ecology & Evolution (1); PeerJ (1); PLOS ONE (2); Proceedings of the National Academy of Sciences USA (2); Proceedings of the Royal Society B (1); Science Advances (1); Systematic Biology (1); Zoological Journal of the Linnean Society (1)

Leadership Experience

[Faculty of Arts & Sciences Postdoctoral Association](#), Harvard University

Present: Careers Committee Chair

Past: Careers Committee Member

[Graduate Student Advisory Council](#), Society for the Study of Evolution

Past: 2-year term (2017-2018)

Biology Graduate Student Phi Sigma Society, UTA

Present: Member

Past: President, Secretary, Manual Sales Coordinator

Workshop, Meeting, or Symposia Organization

2022–23 Co-organizer of Harvard University FAS Postdoctoral Association Career Fair

- Identified and secured location, food service, parking, and other logistical details for 2 on-campus career fair (>100 postdocs).
- Recruited relevant businesses and organizations from the broader community to attend the fair.

2021–23 Organizer of biweekly Museum of Comparative Zoology Lunchtime Seminars at Harvard University

- Selected and invited speakers (largely postdocs) from inside and outside the museum community.

2019–23 Co-organizer of Department of Organismic & Evolutionary Biology Postdoc-Invited Speaker at Harvard University

- Polled fellow postdocs for speaker suggestions and preferences for 2 speakers per year.
- Worked with department administration to invite and host selected speakers.

2020 Organizer of a workshop on evolutionary simulations using [SLiM](#) at Harvard University.

- Fully organized but cancelled due to COVID-19.
- Co-organized with Tim Sackton (Harvard Informatics) and Ben Haller (SLiM developer).
- Sponsored by Harvard FAS Informatics and Department of Organismic & Evolutionary Biology.

2015 Organizer of Software Carpentry workshop at UT-Arlington.

- Sponsored by Phi Sigma Biology Graduate Honor Society, Department of Biology, College of Science, & Office of Graduate Studies.
- Organized a two-day Software Carpentry workshop for 80 graduate level participants from UTA and other Dallas-Fort Worth universities.
- This workshop provided introductory, hands-on instruction in valuable data analysis software, including manipulating data with the Unix shell, version control with Git/GitHub, and statistical analysis and figure generation with R.

Working Group Participation

2015 Population Genetics in R Hackathon. Sponsored and hosted by the National Evolutionary Synthesis Center (NESCent).

Professional Societies

American Association for the Advancement of Science
Society for the Study of Evolution
Society for Molecular Biology and Evolution

Genetics Society of America
American Genetics Association
Consortium for Snake Genomics