
CONTACT INFORMATION

Department of Evolution, Ecology, & Organismal Biology
The Ohio State University
318 W. 12th Avenue
Columbus, OH 43210-1293

Museum of Biological Diversity
Tetrapod Division
1315 Kinnear Road
Columbus, OH 43212

phone: (734) 474-8527 e-mail: carstens.12@osu.edu twitter: [@bryanccarstens](https://twitter.com/bryanccarstens) web: <http://carstenslab.osu.edu/>

EDUCATION & PROFESSIONAL PREPARATION

B.A. in Literature (1993), Department of English, Michigan State University
B.S. in Zoology (1998), Department of Zoology, Michigan State University
M.S. in Zoology (2001), Department of Zoology, Michigan State University, under Barb Lundrigan
Ph.D. in Zoology (2004), Department of Biological Sciences, University of Idaho, under Jack Sullivan

RESEARCH INTERESTS

Research in the Carstens lab seeks to identify the factors that promote the formation of biodiversity. It incorporates data science, biogeography, species delimitation, and phylogeography to make inferences about the evolutionary history of species ranging from slugs to salamanders to bats.

APPOINTMENTS

July 2022 – present: **Chairperson**, Department of Evolution, Ecology, and Organismal Biology, The Ohio State University
August 2018 – present: **Professor**, Department of Evolution, Ecology, and Organismal Biology, The Ohio State University
August 2018 – present: **Head of the Tetrapod Division**, Museum of Biological Diversity, The Ohio State University
January 2020 – December 2020: **Faculty Fellow** in Publishing, The Ohio State University Libraries.
August 2017 – July 2021: **Vice Chair of Administration and Research**, Department of Evolution, Ecology, and Organismal Biology, The Ohio State University
August 2014—July 2018: **Associate Professor**, Department of Evolution, Ecology, and Organismal Biology, The Ohio State University
August 2012—July 2014: **Assistant Professor**, Department of Evolution, Ecology, and Organismal Biology, The Ohio State University
May 2012—August 2012: **Associate Professor**, Department of Biological Sciences, Louisiana State University.
August 2007 — May 2012: **Assistant Professor**, Department of Biological Sciences, Louisiana State University.
January 2005 — May 2007: **Postdoctoral Researcher**, Department of Ecology and Evolutionary Biology, University of Michigan.

HONORS & AWARDS

2022 – Awarded the *Harlan Hatcher Arts & Sciences Distinguished Professor Award* by The Ohio State University.
2019 – Elected as a Fellow in the *American Association for the Advancement of Science*.
2010 – Awarded the *Rainmakers Emerging Scholar Award in Engineering, Science, and Technology* by Louisiana State University.

CURRENT FUNDING

2021. Senior Personnel on ¹³HDR Institute: *Imageomics: A new frontier of biological information powered by knowledge-guided machine learning*. ¹³Tanya Berger-Wolfe is PI. (NSF-2118240). \$10,969,077.
2018. PI on *Dimensions US-BIOTA-Sao Paulo: Traits as predictors of adaptive diversification along the Brazilian Dry Diagonal*. (DEB-1831319), \$383,071.

PREVIOUS FUNDING

2020. PI on *SG: Leveraging massive song databases and deep learning to examine the mechanisms causing diversification of bird vocalizations*. (NSF DEB-2016189). \$199,833 + \$72,813 Covid-19 extension.
2020. Co-PI on ¹²*BII-design: Defining the point of no return in microbe mediated symbioses*. (DBI-2021932). \$192,258. ¹²Alison Bennett is PI.
2019. PI on ¹⁰*Collaborative Research: Aggregating and Repurposing Phylogeographic Data*. (DBI-1910623). \$503,343. ¹⁰Tara Pelletier is coPI.
2019. Co-PI on ¹¹*EAGER: Bridging the Last Mile; Towards an Assistive Cyberinfrastructure for Accelerating Computationally Driven Science*. (NSF DBI-1945347). \$299,687. ¹¹Rajiv Ramnath is PI.
2017. PI on *ABI Innovation: Posterior Predictive Checks of Evolutionary Models* (DBI 1661029). \$403,649.
2016. PI on ⁹*Dissertation Research: Does phenotypic evidence support ecological speciation in western long-eared Myotis bats?* (DEB-1701810), \$20,020. ⁹Ariadna Morales is coPI.
2016. Co-PI on ⁸*REU site: Next generation Evolutionary Biology*. (NSF DBI-1560116), \$425,000. ⁸Meg Daly is the PI.
2014. PI on ⁷*Dissertation Research. Inferring the evolutionary history of arthropods associated with pitcher plants using phylogeographic concordance factors*. (DEB 1501474), \$20,020. ⁷Jordan Satler is coPI.
2014. Co-PI on ⁶*Collaborative Research: Comparative Phylogeographic Approach to Predicting Cryptic Diversity – the Inland Temperate Rainforest as a Model System*. (DEB-1457519), \$960,796. ⁶Jack Sullivan is the PI; Dave Tank is coPI; OSU budget is \$284,182.
2014. PI on ⁵*Dissertation Research. Spatial Sorting and Postglacial Population Dynamics in *Plethodon dunni* and *P. vehiculum** (DEB 1403034), \$20,016. ⁵Tara Pelletier is coPI
2014. Co-PI on ⁴*Connecting new Systematic Biologists across borders: A workshop in model-based phylogenetics at Evolution 2015*. (DEB 1500774), \$47,608. ⁴Stacey Smith was the PI.
2012. Co-PI on ³*Phylogeographic Inference using Approximate Likelihoods*. National Science Foundation (DEB 1257784), \$540,828. ³Brian O’Meara was the PI; OSU budget is \$226,828.
2011. Co-PI on ²*US-Mexico workshop on evolutionary genomics of non-model species: next-gen sequencing, data management, hypothesis testing*. Irapuato, Mexico. (OISE 1118408), \$49,841. ²Stacey Lance was PI.
2009. PI on *A novel approach to the identification of independent evolutionary lineages*. National Science Foundation (DEB 0918212), \$237,643.
2009. Co-PI on on ¹*EAGER: Developing bioinformatics tools for the application of next-generation sequencing technologies to phylogeography*. National Science Foundation (DEB 0956069), \$225,394. ¹Robb Brumfield was the PI.
2009. PI on *Evolution of the Louisiana pitcher plant and its commensal organisms*. Louisiana Board of Regents, \$102,500. July 2009 — June 2011.
2009. PI on *Community phylogeography of Louisiana pitcher plants, their inquiline insects, and commensal bacteria*. Louisiana State University Faculty Research Program, LSU Office of Research and Economic Development, \$9992.
2008. PI on *Genetics of the microbial fauna in the Louisiana Pitcher Plant (*Sarracenia alata*), and identification of the source of *Sarracenia* bacteria*. Louisiana EPSCoR - Pfund, \$10,000.
2004. Assessing abundance and genetic diversity in *Dicamptodon aterrimus*. Idaho Department of Fish and Game, \$13,150.
2001. University of Idaho Presidential Fellowship, \$75,000.

PUBLICATION METRICS

[ORCID](#) 0000-0002-1552-227X

[Goggle Scholar](#) Citations (11,016); h-index (47); i10-index (84)

[Web of Science](#) Citations (7805); h-index (40); Average citations per item (67)

PUBLICATIONS

Manuscripts in preparation

123. Romeiro-Brito M, Telhe MC, Lanna FM, Carstens BC, Kohler M, Digjampietri LA, Zappi DC, Taylor NP, Franco FF, Moraes EM. South American Cacti shed light on plant diversification of arid and semiarid regions in the Neotropics.
122. Fonseca EM, Carstens BC. Artificial intelligence enables unified analysis of historical and landscape influences on genetic diversity. *Molecular Phylogenetics & Evolution*

Manuscripts currently in review

121. Yang J, Provost KL, Carstens BC. Dialect differences correlate with environment in migratory coastal White-crowned Sparrows. <https://www.biorxiv.org/content/10.1101/2023.03.08.531720v1.abstract>
121. Nagel J., et al. Range-wide population genetic structure and effective sizes of three migratory tree bat species in North America.
120. Parsons DJ, Green AE, Carstens BC, Pelletier TA. Predicting genetic biodiversity in salamanders using geographic, climatic, and life history traits.
119. Wieringa JG, Nagel J, Campbell CJ, Nelson DM, Carstens BC, Gibbs HL. Geographic source of bats killed at multiple wind power facilities in the United States.
118. Fonseca EM, Pope NS, Peterman WE, Werneck FP, Colli GR, Carstens BC. Genetic structure and landscape effects on gene flow in the Neotropical lizard *Norops brasiliensis* (Squamata: Dactyloidae).

Manuscripts with revisions in review

117. Duckett DJ, Calder K, Sullivan J, Tank D, Carstens BC. Reduced representation approaches produce similar result to whole genome sequencing for some common phylogeographic analyses. *PLoS One*, revision in review.
116. Fonseca EM, Pope N, Peterman W, Werneck FR, Colli G, Carstens BC. Inferring landscape effects on gene flow in a Neotropical lizard using machine learning. *Heredity*, revision in review.

Manuscripts in press

115. Fonseca EM, Pelletier TA, Decker SK, Parsons DJ, Carstens BC. Pleistocene glaciations contributed to the latitudinal gradient of within-species genetic diversity. *Evolution Letters*, *in press*.
114. Smith ML, C Lang, D Sneddon, J Wallace, AM Rankin, A Espíndola, DC Tank, J Sullivan, BC Carstens. Comparative Phylogeography of Leaf-litter dwelling invertebrates from the Pacific Northwest. *Journal of Northwest Science* 96(2), *in press*. <https://www.northwestscience.org/page-1844575>

2023 publications

113. Wieringa JG, Nagel J, Campbell CJ, Nelson DM, Carstens BC, Gibbs HL. Combining stable isotope, trace element, and species distribution models to assess the geographic origins of migratory bats. *Ecosphere* 14: e4588. <https://doi.org/10.1002/ecs2.4588>
112. Rao A, Baken L, Lubertozzi A, Jahan I, Tedeschi F, Jankowsky E, Carstens BC, Poss KD, Basking KK, Goldman JA. The Translation Initiation Factor Homolog, eif4e1c, Regulates Cardiomyocyte Metabolism and Proliferation During Heart Regeneration. *Development* 150: dev 2011376. <https://doi.org/10.1242/dev.201376>
111. Pérez-Alquicira J, Wehncke EV, García-Loza GA, Carstens BC, Domínguez CA, Pérez-Ishiwara R, Molina-Freaner F. Geographic isolation and long-distance gene flow influence the genetic structure of the blue fan palm *Brahea Armata* (Arecaceae). *Journal of Plant Research* 136,277-290. <https://doi.org/10.1007/s10265-023-01445-9>

110. Larkin I, Meyers EA, Carstens BC, Barrow LN. Predictors of genetic diversity in North American squamates. *Heredity* 114(2), 131-142. <https://doi.org/10.1093/jhered/esad001>

2022 publications

109. Provost KL, Yang J, Carstens BC. The impacts of transfer learning, phylogenetic distance, and sample size on big-data bioacoustics. *PLoS One* 17 (12) e02785222.
108. Pelletier TA, Parsons D, Decker SK, Crouch S, Franz E, Ohrstrom J, Carstens BC. phylogatR: Phylogeographic data aggregation and repurposing. *Molecular Ecology Resources* 22(8), 2830-2842. DOI:10.1111/1755-0998.13673.
107. Fonseca EM, Duckett DJ, Almeida FG, Smith ML, Thomé MCT, Carstens BC. Assessing model adequacy for Bayesian Skyline Plots using posterior predictive simulation. *PLoS ONE* 17(7): e0269438. DOI:10.1371/journal.pone.0269438
106. Smith ML, Wallace J, Tank DC, Sullivan J, Carstens BC. The role of multiple Pleistocene refugia in promoting diversification in the Pacific Northwest. *Molecular Ecology* 31, 4402-4416. DOI:10.1111/mec.16595
105. Carstens BC, Moshier SP. 2022. Giant tree frogs exemplify the promise of integrating multiple types of data in phylogeographic investigations. *Molecular Ecology* 31(10), 3971-3974. DOI:10.1111/mec.16593
104. Ruffley M, Smith ML, Espindola A, Turck D, Mitchel N, Carstens BC, Tank DC, Sullivan J. Genomic evidence of an ancient Inland Temperate Rainforest. *Molecular Ecology* 31(10), 2985-3001. DOI:10.1111/mec.16431
103. Parsons D, Duckett DJ, Wieringa J, Pelletier TA, Carstens BC. Analysis of biodiversity data suggest that mammal species are hidden in predictable places. *Proceedings of the National Academy of Sciences* 119(14), e2103400119. DOI:10.1073/pnas.2103400119
102. Carstens BC, Smith ML, Duckett DJ, Fonseca EM, Thomé MCT. Assessing model adequacy leads to more robust phylogeographic inference. *Trends in Ecology and Evolution* 37(5), 402-410. DOI:10.1016/j.tree.2021.12.007
101. Lanna FM, Colli GR, Burbrink FT, Carstens BC. Identifying traits that enable lizard adaptation to different environments. *Journal of Biogeography* 49(1), 104-116. DOI:10.1111/jbi.14285
100. Bonatelli IAS, Gehara M, Carstens BC, Colli GR, Moraes EM. Comparative and predictive phylogeography in the dry diagonal of South America: The role of Pleistocene climate change on multi-taxon phylogeography. *Molecular Ecology* 31(1) 331-342. DOI:10.1111/mec.16210

2021 publications

99. Duckett DJ, Sullivan J, Pirro S, Carstens BC. Genomic resources for the North American water vole (*Microtus richardsoni*) and the montane vole (*Microtus montanus*). *Gigabyte* 1, 1-13. DOI:10.46471/gigabyte.19
98. Barrow L, Fonseca EM, Thompson CE, Carstens BC. Identifying predictors of genetic diversity in amphibians with machine learning. *Molecular Ecology Resources* 21, 2818-2831. DOI:10.1111/1755-0998.13303
97. Fonseca EM, Colli G, Werneck F, Carstens BC. Phylogeographic model selection with convolutional neural networks. *Molecular Ecology Resources* 21, 2661-2675. DOI:10.1111/1755-0998.13427
96. Thomé MTC, Carstens BC, Rodrigues MT, Galetti Jr. PM, Haddad CFB. Asynchrony of seasons determines genetic differentiation in a Neotropical toad through neutral and selective mechanisms. *Heredity* 127, 363-372. DOI:10.1038/s41437-021-00460-7
95. Satler JD, Carstens BC, Garrick RC, Espíndola A. The phylogeographic shortfall in hexapods: A lot of legwork remaining. *Insect Systematics & Diversity* 5, 1-18. DOI:10.1093/isd/ixab015
94. Morales AE, Fenton MB, Carstens BC, Simmons NB. *Myotis evotis* and *Myotis keenii* are two different species. *Canadian Journal of Zoology* 99, 415-422. DOI:10.1139/cjz-2020-0048
93. Rankin AM, Anderson FE, Clutts SA, Espíndola A, Carstens BC, Lucid M, Sullivan J. 2021. Comparative phylogeography of two Northern Rocky Mountain endemics: the widespread *Anguispira kochi occidentalis* and the narrow-range *Anguispira nimapuna* (Gastropoda: Discidae). *Biological Journal of the Linnean Society* 133, 817-834. DOI:10.1093/biolinnean/blab030
92. Wieringa JG, Carstens BC, Gibbs HL. Seasonal distribution and migratory pathways for three species of tree bats: Implications for conservation. *PeerJ* 9: e11177. DOI:10.7717/peerj.11177
91. Thomé MTC, Carstens BC, Rodrigues MT, Alexandrino J, Haddad CFB. Rapid diversification patterns in a Neotropical frog supports opposite responses to Pleistocene climates at the Caatinga and Cerrado, regional

variation within the Caatinga, and uninterrupted gene flow across a geographic barrier. [Journal of Biogeography 21\(48\), 1112-1123](#). DOI:10.1111/jbi.14064

90. Fonseca EM, Duckett DJ, Carstens BC. P2C2M.GMYC: An R package for identifying model violations under the Generalized Mixed Yule Coalescent model. [Methods in Ecology & Evolution 12\(3\), 487-493](#). DOI:10.1111/2041-210X.13541
89. Thompson CE, Pelletier TA, Carstens BC. Genetic diversity in North American Vertebrates in protected areas. [Biological Journal of the Linnean Society 132, 388-389](#). DOI:10.1093/biolinnean/blaa195

2020 publications

88. Wieringa JG, Nagel J, Nelson DM, Carstens BC, Gibbs HL. Using trace elements to identify the geographic origin of migratory tree-roosting bats. [PeerJ 8: e10082](#). DOI:10.7717/peerj.10082
87. Lado P, Smith ML, Carstens BC, Klompen H. Population genetic structure and demographic history of the lone star tick, *Amblyomma americanum* (Ixodida: Ixodidae): New evidence supporting an old hypothesis. [Molecular Ecology 29, 2810-2823](#). DOI:10.1111/mec.15524
86. Wieringa J, M Boot, MD de Queiroz, DJ Duckett, EM Fonseca, H Glon, N Hamilton, S Kong, FM Lanna, KR Mattingly, D Parsons, ML Smith, B Stone, C Thompson, L Zou, BC Carstens. Does habitat instability structure intraspecific genetic diversity? It's complicated... [Frontiers in Biogeography 12, e45377](#). DOI:10.21425/F5FBG45377
85. Smith ML, Carstens BC. A machine learning approach to delimiting species with gene flow. [Evolution 74, 216-229](#). DOI:10.1111/evo.13878
84. Duckett DJ, Pelletier TA, Carstens BC. Posterior Predictive Simulation for SNAPP Species Tree Inference. [PeerJ 8: e8271](#). DOI:10.7717/peerj.8271

2019 publications

83. Morales AE, Ruedi M, Field K, Carstens BC. Diversification rates have no effect on the convergent evolution of foraging strategies in the most species-rich genus of bats, *Myotis*. [Evolution 73, 2263-3380](#). DOI:10.1111/evo.13849
82. Rankin AM, Wilke T, Lucid M, Leonard W, Espíndola A, Smith ML, Ruffley M, Tank DC, Carstens BC, Sullivan J. Complex interplay of ancient vicariance and in situ speciation in northwestern North American temperate rainforests. [Biological Journal of the Linnean Society 127, 876-889](#). DOI:10.1093/biolinnean/blz040
81. Sullivan J, Smith ML, Espíndola AE, Ruffley MR, Rankin AM, Tank DC, Carstens BC. Integrating life history traits in predictive phylogeography. [Molecular Ecology 28, 2062-2073](#). DOI:10.1111/mec.15029
80. Satler JD, Carstens BC. The *Sarracenia alata* pitcher plant system and obligate arthropod inquilines should be considered an evolutionary community. [Journal of Biogeography 46, 485-496](#). DOI:10.1111/jbi.13498

2018 publications

79. Pelletier TA, Carstens BC, Tank DC, Sullivan J, Espíndola A. Predicting plant conservation priorities on a global scale. [Proceedings of the National Academy of Sciences USA, 115, 13027-13032](#). DOI:10.1073/pnas.1804098115
78. Smith ML, Ruffley MR, Rankin A, Espíndola A, Tank DC, Sullivan J, Carstens BC. (2018) Testing for the presence of cryptic diversity in the tail-dropper slugs (Genus *Prophyaon*) using molecular data. [Biological Journal of the Linnean Society 124, 518-532](#). DOI:10.1093/biolinnean/bly067
77. Morales AE, Carstens BC. Evidence that *Myotis lucifugus* 'subspecies' are five non-sister species, despite gene flow. [Systematic Biology 67, 756-769](#). DOI:10.1093/sysbio/syy010
76. Wheeler GL, Carstens BC. (2018) Evaluating the adaptive evolutionary convergence of carnivorous plant taxa through functional genomics. [PeerJ 6:e4322](#). DOI 10.7717/peerj.4322
75. Ruffley MR, Smith ML, Espíndola AE, Carstens BC, Tank DC, Sullivan J. (2018) Model selection reveals complex phylogeography of Red Alder, *Alnus rubra*, in the Pacific Northwest temperate rainforest. [Molecular Ecology 27, 1012-1024](#). DOI:10.1111/mec.14491.
74. Carstens BC, Morales AE, Field KA, Pelletier TA. (2018) A global analysis of bats using automated comparative

phylogeography uncovers a surprising impact of Pleistocene glaciation. [Journal of Biogeography 45, 1795-1805](#). DOI:10.1111/jbi.13382

73. Pelletier TA, Carstens BC. (2018) Geographic range size and latitude predict population genetic structure in a global survey. [Biology Letters 14, 20170566](#). DOI:10.1098/rsbl.2017.0566

2017 publications

72. Carstens BC, Morales AE, Jackson ND, O'Meara BC. (2017) Objective Choice of Phylogeographic Models. [Molecular Phylogenetics and Evolution 116, 136-140](#). DOI: 10.1016/j.ympev.2017.08.018
71. Silva-Arias G, Reck-Kortmann M, Carstens BC, Hasenack H, Bonatto S, Freitas L. (2017) from inland to the coast: spatial and environmental signatures on the genetic diversity in the colonization of the South Atlantic Coastal Plain. [Perspectives in Plant Ecology, Evolution & Systematics 28, 47-57](#). DOI: 10.1016/j.ppees.2017.06.006
70. Smith ML, Ruffley MR, Espíndola AE, Tank DC, Sullivan J, Carstens BC. (2017) Demographic model selection using random forests and the site frequency spectrum. [Molecular Ecology 26, 4562-4573](#). DOI:10.1111/mec.14223.
69. Satler JD, Carstens BC. (2017) Do ecological communities disperse across biogeographic barriers as a unit? [Molecular Ecology 26, 3533-3545](#). DOI:10.1111/mec.14137
68. Jackson ND, Morales AE, Carstens BC, O'Meara BC. (2017) PHRAPL: Phylogeographic Inference using approximate likelihoods. [Systematic Biology 66, 1045-1053](#). DOI:10.1093/sysbio/syx001
67. Jackson ND, Morales A, Carstens BC, O'Meara BC. (2017) Species delimitation with gene flow. [Systematic Biology 66, 799-812](#). DOI:10.1093/sysbio/syw117
66. Gruenstaeudl M, Carstens BC, Santos-Guerra A, Jansen RK. (2017) Statistical hybrid detection and the inference of ancestral distribution areas in *Tolpis* (Asteraceae). [Biological Journal of the Linnean Society 121, 133-149](#).
65. Morales AE, Jackson ND, Dewey TA, O'Meara BC, Carstens BC. (2017) Speciation with gene flow in North American *Myotis* bats. [Systematic Biology 66, 440-452](#). DOI:10.1093/sysbio/syw100

2016 publications

64. Espíndola A, Ruffley M, Smith M, Carstens BC, Tank DC, Sullivan J. (2016) Predicting cryptic diversity from phylogeographic, climatic and taxonomic data. [Proceedings of the Royal Society B 283, 20161529](#). DOI:10.1098/rspb.2016.1529
63. Pelletier TA, Carstens BC. (2016) Comparing range evolution in two western *Plethodon* salamanders: Glacial refugia, competition, ecological niches, and spatial sorting. [Journal of Biogeography 43, 2237-2249](#). DOI:10.1111/jbi.12833
62. Thomé MTC, Carstens BC. (2016) Phylogeographic model selection leads to insight into the evolutionary history of Four-eyed frogs. [Proceedings of the National Academy of Sciences USA, 113, 8010-8017](#). DOI:10.1073/pnas.1601064113
61. Carstens BC, Gruenstaeudl M, Reid NM. (2016) Community Trees: Identifying co-diversification in the Páramo dipteran community. [Evolution 70, 1105-1119](#). DOI:10.1111/evo.12916
60. Perez MF, Carstens BC, Rodrigues GL, Moraes EM (2016) Anonymous nuclear markers reveal taxonomical incongruences and long-term disjunction in a cactus species complex with continental-island distribution in South America. [Molecular Phylogenetics and Evolution 95, 11-19](#). DOI:10.1016/j.ympev.2015.11.005
59. Thomé MCT, Brusquetti F, Sequeira F, Carstens BC, Haddad CFB, Rodrigues MT, Alexandrino J (2016) Recurrent connections between Amazon and Atlantic forests shaped diversity in Caatinga Four-Eyed frogs. [J. Biogeography 43, 1045-1056](#). DOI:10.1111/jbi.12685
58. Satler JD, Carstens BC. (2016) Phylogeographic concordance factors quantify phylogeographic congruence among co-distributed species. [Evolution 70, 1080-1093](#). DOI:10.1111/evo.12924
57. Perez MF, Bonatelli IAS, Moraes E, Carstens BC. (2016) Refining phylogeographic inference in two interglacial microrefuge-dwelling cactus species using model-based analysis. [Journal of Heredity 116, 550-557](#). DOI:10.1038/hdy.2016.17
56. Sovic MG, Carstens BC, Gibbs HL (2016) Genetic diversity in migratory bats: Results from RADseq data for three tree bat species at a wind farm in northwestern Ohio. [PeerJ 4:e1647](#); DOI:10.7717/peerj.1647

55. Gruenstaeudl M, Reid NM, Wheeler G, Carstens BC (2016) Posterior predictive checks of coalescent models: P2C2M, an R package. [Molecular Ecology Resources 16, 193–205](#). DOI:10.1111/1755-0998.12435
54. Satler JD, Zellmer AJ, Carstens BC (2016) Biogeographic barriers drive co-diversification within associated eukaryotes of the *Sarracenia alata* pitcher plant system. [PeerJ 4:e1576](#). DOI:10.7717/peerj.1576
53. Perez MF, Carstens BC, Rodrigues GL, Moraes EM (2016) Anonymous nuclear markers data supporting species tree phylogeny and divergence time estimates in a cactus species complex in South America. [Data in Brief 6, 456-460](#). DOI:10.1016/j.dib/2015.12.002

2015 Publications

52. Bonatelli IAS, Carstens BC, Moraes EM (2015) Using next generation RAD sequencing to isolate multispecies microsatellites for *Pilosocereus* (Cactaceae) genus. [PLoS ONE 10: e0142602](#). DOI:10.1371/journal.pone.0142602
51. Hird SM, Sanchez C, Carstens BC, Brumfield RT (2015) Comparative gut microbiota of 59 Neotropical bird species. [Frontiers in Microbiology 6, 1403](#). DOI:10.3389/fmicb.2015.01403
50. Pelletier TA, Crisafulli C, Wagner S, Zellmer AJ, Carstens BC. (2015) Historical species distributions predict species limits. [Systematic Biology 64, 909-925](#). DOI:10.1093/sysbio/syu090
49. McVay JD, Flores-Villela O, Carstens BC (2015) Diversification of North American Natricine snakes. [Biological Journal of the Linnean Society 116, 1-12](#). DOI:10.1111/bij.12558
48. Garrick RC, Bonatelli IAS, Morales AE, Pelletier TA, Perez MF, Rice E, Satler JD, Symula RE, Thomé MTC, Carstens BC (2015) The evolution of phylogeographic datasets. [Molecular Ecology 24, 1164-1171](#). DOI:10.1111/mec.13108

2014 Publications

47. Espindola A, Carstens BC, Alvarez N. (2014) Comparative phylogeography of mutualists and the effect of the host on the genetic structure of its partners. [Biological Journal of the Linnean Society 113, 1021-1035](#). DOI:10.1111/bij.12393
46. Gavin DG, Fitzpatrick MC, Gugger PF, Heath KS, Rodriguez-Sanches F, Dobrowski SZ, Hampe A, Hu FS, Ashcroft MB, Bartlein PJ, Blois JL, Carstens BC, Davis EB, de Lafontaine G, Edwards ME, Fernandez M, Henne PD, Herring RM, Holden ZA, Kong W-S, Liu J, Magri D, Matzke NJ, McGlone MS, Saitre F, Stigall AL, Tsai Y-H E, Williams JW. (2014) Climate refugia: Using fossils, genetics, and spatial modeling to explain the past and project the future of biodiversity. [New Phytologist 204, 37-54](#). DOI:10.1111/nph.12929
45. Pelletier TA, Carstens BC. (2014) Model choice in phylogeography using a large set of models. [Molecular Ecology 23, 3028-3043](#). DOI:10.1111/mec.12722
44. Hird SM, Carstens BC, Cardiff SW, Dittman DL, Brumfield RT. (2014) Sampling locality is more important than taxonomy or ecology in the gut microbiota of the brood-parasitic Brown-Headed Cowbird (*Molothrus ater*). [PeerJ 2; e21](#). DOI:10.7717/peerj.321
43. Reid NM, Brown JM, Satler JD, Pelletier TA, McVay JD, Hird SM, Carstens BC. (2014) Poor fit to the multi-species coalescent model is widely detectable in empirical data. [Systematic Biology 63, 322-333](#). DOI:10.1093/sysbio/syt057

2013 Publications

42. Carstens BC, Brennan RS, Chua V, Duffie CV, Harvey MG, Koch RA, McMahan CD, Nelson BJ, Newman CE, Satler JD, Seeholzer G, Prosbic K, Tank DC, Sullivan J (2013) Model selection as a tool for phylogeographic inference: An example from the willow *Salix melanopsis*. [Molecular Ecology 22, 4014-4028](#). DOI:10.1111/mec.12347
41. Carstens BC, Satler JD. (2013) The carnivorous plant described as *Sarracenia alata* contains two cryptic species. [Biological Journal of the Linnean Society 109, 737-746](#). DOI:10.1111/bij.12093
40. Carstens BC, Pelletier TA, Reid NM, Satler JD (2013) How to fail at species delimitation. [Molecular Ecology 22, 4369-4383](#). DOI:10.1111/mec.12413
39. Salter JD, Carstens BC, Hedin M (2013) Multilocus species delimitation in a complex of morphologically conserved trapdoor spiders (Mygalomorphae, Antrodiaetidae, *Aliatypus*). [Systematic Biology 62, 805-823](#).

38. McVay JD, Carstens BC (2013) Phylogenetic model choice: Justifying a species trees or concatenation analysis. [Phylogenetics and Evolutionary Biology 1, 1000114](#). DOI:10.4172/2329-9002.1000114
37. Andrew R, Bernatchez L, Bonin Z, Buerkle CA, Carstens BC, Emerson BC, Garant D, Giraud T, Kane NC, Rogers SM, Slate J, Smith H, Sork VL, Stone GN, Vines TH, Waits LS, Widmer A, Rieseberg LH (2013) A Roadmap for Molecular Ecology. [Molecular Ecology 22, 2605-2626](#). DOI:10.1111/mec.12319
36. McVay JD, Carstens BC. (2013) Testing monophyly without well-supported gene trees: Evidence from multi-locus nuclear data conflicts with existing taxonomy in the snake tribe Thamnophiini. [Molecular Phylogenetics & Evolution 68, 425-431](#). DOI:10.1016/j.ympev.2013.04.028
35. McCormack JE, Hird SM, Zellmer AJ, Carstens BC, Brumfield RT (2013). Applications of next-generation sequencing to phylogeography and phylogenetics. [Molecular Phylogenetics and Evolution 66, 526-538](#). DOI:10.1016/j.ympev.2011.12.007
34. Tsai Y-H E, Carstens BC (2013) Assessing model fit in phylogeographic investigations: An example from the North American willow *Salix melanopsis*. [Journal of Biogeography 40, 131-141](#). DOI:10.1111/j.1365-2699.2012.02775.x

2012 Publications

33. Reid NM, Carstens BC (2012). Phylogenetic estimation error can decrease the accuracy species delimitation: A Bayesian implementation of the General Mixed Yule Coalescent model. [BMC Evolutionary Biology 12, 196, 1-11](#). DOI:10.1186/1471-2148-12-196
32. Carstens BC, Lemmon AR, Moriarty-Lemmon E (2012). The promises and pitfalls of next-generation sequencing data in phylogeography. [Systematic Biology 61, 713-715](#). DOI:10.1093/sysbio/sys050
31. Zellmer AJ, Hanes MM, Hird S, Carstens BC. (2012). Deep phylogeographic structure and environmental differentiation in the carnivorous plant *Sarracenia alata*. [Systematic Biology 61, 763-777](#). DOI:10.1093/sysbio/sys048

2008-2011 Publications (research at Louisiana State University)

30. Hird SM, Brumfield RT, Carstens BC (2011). PRGMATIC: an efficient pipeline for collating genome-enriched second-generation sequencing data using a 'provisional reference genome'. [Molecular Ecology Resources 11, 743-748](#). DOI:10.1111/j.1755-0998.2011.03005.x
29. Ence DD, Carstens BC (2011). SpedeSTEM: A rapid and accurate method for species delimitation. [Molecular Ecology Resources 11, 473-480](#). DOI:10.1111/j.1755-0998.2010.02947.x
28. Koopman MM, Carstens BC (2011) Plant genetic divergence predicts microbial community structure: Molecular phylogeography of carnivorous pitcher plants. [Microbial Ecology 61, 750-758](#). DOI:10.1007/s00248-011-9832-9
27. Carstens BC, Dewey TA (2010) Species delimitation using a combined coalescent and information theoretic approach: An example from North American *Myotis* bats. [Systematic Biology 59, 400-414](#). DOI:10.1093/sysbio/syq024
26. Hird S, Kubatko L, Carstens BC (2010) Replicated subsampling enables accurate species tree estimation in empirical systems. [Molecular Phylogenetics & Evolution 57, 888-898](#). DOI:10.1016/j.ympev.2010.08.006
25. Koopman MM, Carstens BC (2010) Conservation genetic inferences in the carnivorous plant *Sarracenia alata* (Sarraceniaceae). [Conservation Genetics 11, 2027-2038](#). DOI:10.1007/s10592-010-0095-7
24. Koopman MM, Fuselier DM, Hird S, Carstens BC (2010) Bacterial characterization of the carnivorous Pale Pitcher Plant reveals diverse, distinct, and temporally dependent communities. [Applied and Environmental Microbiology 76, 1851-1860](#). DOI:10.1128/AEM.02440-09
23. Hickerson MJ, Carstens BC, Cavender-Bares J, Crandall KA, Graham CH, Johnson JB, Rissler L, Victoriano PF, Yoder AD (2010) Phylogeography's past, present, and future: 10 years after *Avis* 2000. [Molecular Phylogenetics & Evolution 54, 291-301](#). DOI:10.1016/j.ympev.2009.09.016
22. Carstens BC, Stoute HN, Reid NM (2009) An information theoretical approach to phylogeography. [Molecular Ecology 18, 4270-4282](#). DOI:10.1111/j.1365-294X.2009.04327.x
21. Koopman MM, Gallagher E, Carstens BC (2009) Isolation and characterization of nine microsatellite loci in the Pale Pitcher Plant *Sarracenia alata* (Sarraceniaceae). [Molecular Ecology Resources 9, 1460-1466](#). DOI:10.1111/j.1755-0998.2009.02759.x
20. Cantrell M, Carstens BC, Wichman HA (2009) X Chromosome Inactivation and XIST Evolution in a Rodent Lacking LINE-1 Activity. [PLoS One 4, e6252](#). DOI:10.1371/journal.pone.0006252
19. Kubatko L, Carstens BC, Knowles LL (2009) STEM: Species tree estimation using maximum likelihood for gene trees under coalescence. [J. Bioinformatics 25, 971-973](#). DOI:10.1093/bioinformatics/btp079
18. Eckert AJ, Carstens BC. (2008) Does gene flow destroy phylogenetic signal? The performance of three methods for estimating species phylogenies in the presence of gene flow. [Molecular Phylogenetics & Evolution 49, 832-842](#). DOI:10.1016/j.ympev.2008.09.008

2006-2007 Publications (postdoctoral research)

17. Carstens BC, Knowles LL (2007) Estimating phylogeny from gene tree probabilities in *Melanoplus* grasshoppers despite incomplete lineage sorting. [Systematic Biology 56, 400-411](#).
16. Carstens BC, Richards CL (2007) Integrating coalescent and ecological niche modeling in comparative phylogeography. [Evolution 61, 1439-1454](#).

15. Carstens BC, Knowles LL (2007) Shifting distributions and speciation: genomic resolution of species divergence during rapid climate change. [Molecular Ecology 16, 619-627.](#)
14. Knowles LL, Carstens BC (2007) Delimiting species without monophyletic gene trees. [Systematic Biology 56, 887-895.](#)
13. Richards CL, Carstens BC, Knowles LL (2007) Distribution modeling and statistical phylogeography: an integrative framework for generating and testing alternate biogeographical hypotheses. [J. Biogeography 34, 1833-1845.](#)
12. Knowles LL, Carstens BC, Keat ML (2007) Coupling genetic and ecological-niche models to examine how past population distributions contribute to divergence. [Current Biology 17, 1-7.](#)
11. Brunsfeld SJ, Miller TR, Carstens BC (2007) Insights into the biogeography of the Pacific Northwest of North America: Evidence from the phylogeography of *Salix melanopsis* (Salicaceae). [Systematic Botany 32, 129-139.](#)
10. Knowles LL, Carstens BC (2007) Estimating a population-divergence model for statistical phylogeographic tests in montane grasshoppers. [Evolution 61, 477-493.](#)
9. Carstens BC, Knowles LL (2006) Variable nuclear markers for *Melanoplus oregonensis* identified from the screening of a genomic library. [Molecular Ecology Notes 6, 683-685.](#)

2000-2005 Publications (graduate school)

8. Carstens BC, Brunsfeld SJ, Demboski JR, Good JD, Sullivan J (2005) Investigating the evolutionary history of the Pacific Northwest mesic forest ecosystem: Hypothesis testing within a comparative phylogeographic framework. [Evolution 59, 1639-1652.](#)
7. Carstens BC, Degenhardt JD, Stevenson AL, Sullivan J (2005) Accounting for coalescent stochasticity in testing phylogeographic hypotheses: Modeling Pleistocene population structure in the Idaho Giant Salamander *Dicamptodon aterrimus*. [Molecular Ecology 14, 255-265.](#)
6. Carstens BC, Bankhead III A, Joyce P, Sullivan J (2005) Testing population genetic structure using parametric bootstrapping. [Genetica 124, 71-75.](#)
5. Steele CA, Carstens BC, Storfer A, Sullivan J (2005) Testing hypotheses of speciation timing in *Dicamptodon copei* and *Dicamptodon aterrimus* (Caudata: Dicamptodontidae). [Molecular Phylogenetics & Evolution 36, 90-100.](#)
4. Johnson DG, Carstens BC, Sheppard WS, Zack RS (2005) Phylogeny of the leafhopper subgenus *Errhomus* (*Erronus*) (Hemiptera: Homoptera: Cicadellidae) based on mitochondrial DNA sequences. [Annals of the Entomological Society of America 98, 165-172.](#)
3. Carstens BC, Stevenson AL, Degenhardt JD, Sullivan J (2004) Testing nested phylogenetic and phylogeographic hypotheses in the *Plethodon vandykei* species group. [Systematic Biology 53, 781-792.](#)
2. Carstens BC, Sullivan J, Davalos LM, Larsen PA, Pedersen SC (2004) Exploring population genetic structure in three species of Lesser Antillean bats. [Molecular Ecology 13, 2557-2566.](#)
1. Carstens BC, Lundrigan BL, Myers P (2002) A phylogeny of the Neotropical nectar-feeding bats (Chiroptera: Phyllostomidae) based on morphological and molecular data. [Journal of Mammalian Evolution 9, 23-53.](#)

Book Chapters, Invited Commentaries, and other works

10. Parsons DJ, Carstens BC. 2022. Thousands of undiscovered mammal species may be hidden in plain sight, new research finds. The Conversation. <https://theconversation.com/thousands-of-undiscovered-mammal-species-may-be-hidden-in-plain-sight-new-research-finds-179988>
9. Carstens BC. 2022. DNA In *PhylogatR* by BC Carstens, SK Decker, A Espindola, S Foltz, A Green, DJ Parsons, TA Pelletier, JD Satler. <https://phylogatr.org/book/index.html>
8. Provost KL, Yang J, Carstens BC. The impacts of transfer learning, phylogenetic distance, and sample size on big-data bioacoustics. *bioRxiv*: <https://www.biorxiv.org/content/10.1101/2022.02.24.481827v2.abstract>
7. Smith ML, Carstens BC. Species delimitation using molecular data. In *Species and Beyond*, Contemporary Philosophy and Practice. eds. Frank Zachos, John Wilkins, Igor Pavlinov. *Appearing soon* in CAT#: 337948 ISBN: 9780367425371.
6. Smith ML, Carstens BC. Disentangling the process of speciation using machine learning. *bioRxiv*: <https://doi.org/10.1101/356345>.
5. Carstens BC. (2018) Review of Species Concepts in Biology: Historical Development, Theoretical Foundations and Practical Relevance by Frank E. Zachos. *Quarterly Review of Biology* 93, 36.

4. O'Meara BC, Jackson ND, Morales AE, Carstens BC (2015). Phylogeographic Inference using approximate likelihoods. *bioRxiv*: <http://biorxiv.org/content/early/2015/08/24/025353>
3. Carstens BC (2013) *Phylogeography*. Oxford Bibliographies, invited contribution.
2. Carstens BC, Knowles LL (2010) Navigating the Unknown: Model selection in phylogeography. *Molecular Ecology* 19, 4581–4582.
1. Fleming TH, Murray KL, Carstens BC (2010) Phylogeography and Genetic Structure of Three Evolutionary Lineages of West Indian Phyllostomid Bats. Chapter 5 in *Evolution, Ecology, and Conservation of Island Bats*, T.H. Fleming and P.A. Racey, eds. Univ. Chicago Press.

 INVITED TALKS

- 2022 'Predictive Biodiversity Science' Departmental Seminar presented to Miami (OH) Department of Biology. September 21, 2022.
- 2022 'Building an effective time machine from genomic data' Symposium presentation at the 19th International Bat Research Conference in Austin, TX.
- 2021 'How to delimit species with one weird trick!' August 16, 2021. Online presentation to the *Species Delimitation* symposium organized by Andrea Quattrini sponsored by NSF and the SMNH.
- 2021 'Scientific Societies and the Publishing Ecosystem'. July 15, 2021. Online seminar to the SSB DEIC Symposium at the 2021 Evolution Annual Meeting.
- 2020 'Is there any point to the (re)analysis of old phylogeographic data?' August 3, 2020. Online presentation to the *Biodiversity and Bioinformatics* talk series organized by NYU & AMNH.
- 2019 'Bats: Hidden species and imperiled populations.' Columbus Science Pub. October 10, 2019.
- 2018 'Manipulation, deceit, and symbiosis by a terrifyingly carnivorous plant.' University of Maryland, Department of Entomology. October 24, 2018.
- 2017 'Big data for global inferences in biodiversity science.' Ohio Supercomputer Center, State Users Group Meeting. September 18, 2017.
- 2017 'Big data for global inferences in biodiversity science.' Department of Biological Sciences, University of Idaho.
- 2017 'Big data for global inferences in biodiversity science.' Pymatuning Lab of Ecology, University of Pittsburgh.
- 2017 'Evolution of (and in) the carnivorous plant *Sarracenia alata*.' Center for Applied Plant Sciences, The Ohio State University.
- 2016 'Evolution of (and in) the carnivorous plant *Sarracenia alata*.' Department of Horticulture and Crop Sciences, The Ohio State University.
- 2016 'Phylogeographic model selection leads to insight into the evolutionary history of four-eyed frogs.' In the Light of Evolution X: Comparative Phylogeography. Arthur M. Sackler Colloquia of the National Academy of Sciences.
- 2015 'Phylogeography and biodiversity', 5th Biological Evolution Workshop (PABEW) in Porto Alegre, Brazil.
- 2015 'Speciation with gene flow in *Myotis* bats', Department of Biology, University of Texas-Arlington.
- 2015 'Gene flow should be explicitly modeled (rather than ignored) in species delimitation investigations that utilize genetic Data.' Species Delimitation in the Age of Genomics, Center for Biodiversity Analysis, Australian National University.
- 2015 'Introduction to Phrapl and P2C2M: R modules for assessing phylogeographic model fit.' Species Delimitation in the Age of Genomics, Center for Biodiversity Analysis, Australian National University.
- 2015 'What can we learn from genetic data.' Ohio Bat Working Group, Annual Meeting.
- 2014 'Evolution of the carnivorous plant *Sarracenia alata*.' Center for Applied Plant Science, The Ohio State University.
- 2014 'Model selection as a tool for inference in phylogeographic research.' IX Coloquio Estudiantil "Filogeografía y Biogeografía: retos para el siglo XXI" INECOL, Xalapa, Mexico.
- 2014 'The stories that we tell ourselves about our phylogeographic data.' Texas Tech University, Department of Biological Sciences.
- 2013 'Model selection as a tool for inference in Evolutionary Genetics.' University of Alaska-Fairbanks, Department of Biology and Wildlife.

- 2012 Community Phylogeography in the carnivorous plant *Sarracenia alata*.¹ University of Georgia, Department of Genetics.
- 2012 'Model selection as a tool for inference.'¹ First Joint Congress on Evolutionary Biology, Molecular Ecology Symposium.
- 2012 'Species delimitation using Species Trees.'¹ Estimating Species Trees Workshop, The Ohio State University.
- 2011 'Community Phylogeography in the carnivorous plant *Sarracenia alata*.¹ University of Vermont, Department of Biology.
- 2011 'The Promises and Pitfalls of Next-generation Sequencing in Phylogeography.'¹ Evolution Annual Meeting, Society for Systematic Biology symposium.
2011. 'Next generation sequencing allows identification of the timing and causes of diversification in the carnivorous plant *Sarracenia alata*.¹ American Genetics Association Annual Meeting, invited symposium.
- 2011 'Generating (and Testing) Hypotheses in Comparative Phylogeography.'¹ Trinity University, Department of Biology.
- 2011 'Generating (and Testing) Hypotheses in Comparative Phylogeography.'¹ University of Texas-Austin, Integrative Biology Department.
- 2010 'Species delimitation using Species Trees.'¹ NIMBios Working Group, Knoxville, TN.
- 2010 'Community Phylogeography in the carnivorous plant *Sarracenia alata*.¹ BIOTA-FAPESP International Symposium on Phylogeography, São Paulo, Brazil.
- 2010 'Community Phylogeography in the carnivorous plant *Sarracenia alata*.¹ University of Mississippi, Department of Biology.
- 2010 'Community Phylogeography in the carnivorous plant *Sarracenia alata*.¹ Southeastern Louisiana University, Department of Biology.
- 2009 'Generating (and Testing) Hypotheses in Comparative Phylogeography.'¹ Florida State University, Department of Biological Sciences.
- 2009 'Community Phylogeography in the carnivorous plant *Sarracenia alata*.¹ University of Minnesota, Department of Ecology and Evolutionary Biology.
- 2009 'Community Phylogeography in the carnivorous plant *Sarracenia alata*.¹ University of South Alabama, Department of Biology.
- 2008 'Generating (and Testing) Hypotheses in Comparative Phylogeography.'¹ University of New Mexico, Department of Biology.
- 2008 Generating (and Testing) Hypotheses in Comparative Phylogeography, Virginia Commonwealth University, Department of Biology.
- 2008 'Species limits in Myotis bats.'¹ Merging Phylogenetic Biology and Spatial Ecology Symposium, Evolution Annual Meeting, Minneapolis, MN.
- 2008 'Phylogeography of Western North America.'¹ Comparative Phylogeography Symposium, Botany Annual Meeting.
- 2008 'Generating (and Testing) Hypotheses in Comparative Phylogeography.'¹ Nescent-PIRE, Durham, NC.
- 2007 'Generating (and Testing) Hypotheses in Comparative Phylogeography.'¹ University of New Orleans, Department of Biological Sciences.

CONTRIBUTED TALKS

*student presenter, + postdoc presenter

2023 Contributions

Moraes EM, Romeiro-Brito M, Telhe MC, Lanna FM, Carstens BC, Köhler M, Digiampietri LA, Franco FF, Taylor NP, Zappi DC. 'Diversification of South American *cacM*: insights of diversification of arid and semiarid regions in Neotropics'. Evolution Annual Meeting, Albuquerque NM.

2022 Contributions

Moshier SP*, Carstens BC. 'Bats on the move: Modeling seasonal changes in species distributions on a global scale.'¹ Contributed to the 19th International Bat Research Conference in Austin, TX.

Decker SK*, Carstens BC. 'Identifying the factors influencing phylogeographic breaks in bats and other taxa.'¹ Contributed to the 19th International Bat Research Conference in Austin, TX.

DA Parsons*, TA Pelletier, J Wieringa, DD Duckett, BC Carstens 'Analysis of biodiversity data suggests that mammal species are hidden in predictable places.' Contributed to the 101st meeting of the American Society of Mammalogists.

2021 Contributions

Decker SK*, Carstens BC. Quality control and data processing for analysis of phylogeographic breaks. Talk. 2021 *phylogatR* beta-tester workshop. Mountain Lake Biological Station, Pembroke, VA.

Provost K*, Yang J, Carstens BC. Big-data bioacoustics, biogeography, and biases in birds. Talk presented at: 2021 Joint Virtual Meeting of the AOS and SCO-SOC; Aug. 9 2021; Virtual.

Duckett DJ*, Calder KC, Sullivan J, Tank DC, Carstens BC. Cost-benefit analysis of genomic sequencing for phylogeography. 2021 Evolution Annual Meeting, Virtual.

2020 Contributions

Duckett DJ*, Pirro S, Sullivan J, Tank DC, Carstens BC. Detecting model violations of the pairwise sequentially Markovian coalescent. 2020 Society of Systematic Biologists Standalone Meeting: University of Florida, Gainesville, FL.

2019 Contributions

Morales AE*, Carstens BC. Local adaptation and convergence evolution of foraging strategies in the most species-rich genus of bats, *Myotis*. Evolution Annual Meeting, Providence, RI.

Duckett DJ*, Calder K, Sullivan J, Tank D, Carstens BC. From RADseq to whole genomes: Phylogeographic history of the North American water vole (*Microtus richardsoni*). Evolution Annual Meeting, Providence, RI.

Smith ML*, Carstens BC. Considering the process of speciation while investigating species limits leads to more accurate and biologically relevant species delimitations. Evolution Annual Meeting, Providence, RI.

Lanna FM*, Burbrink F, Colli G, Carstens BC. Squamate diversification in the South American Dry Diagonal. Evolution Annual Meeting, Providence, RI.

2018 Contributions

Duckett DJ*, Sullivan, J, Carstens BC. Genomic signatures of convergent adaptation in semiaquatic mammals. Ohio Supercomputer Statewide Users Group Conference: Ohio Supercomputer Center, Columbus, OH.

Morales AM*, Ruedi M, Field KE, Carstens BC. Ecomorphological convergence of *Myotis* bats 2018 Society of Systematic Biologists meeting. Columbus, OH.

Smith ML*, Carstens BC. Species Delimitation Using Random Forests and the Site Frequency Spectrum. 2018 Society of Systematic Biologists meeting. Columbus, OH.

Thompson C*, Carstens BC, Pelletier TA. Understanding the genetic diversity of Mammals in Protected Areas: A big data approach. 2018 Society of Systematic Biologists meeting. Columbus, OH.

Thompson C*, Pelletier TA, Carstens BC. Understanding the Genetic Diversity of Vertebrates in North American Protected Areas: A Big Data Approach. 2018 Three Rivers Evolution Event (TREE), Pittsburg, PA

2017 Contributions

Pelletier TA[†], Carstens BC. Barcoding Genes Reveal High Numbers of Cryptic Species in Bats. 2017 North American Society for Bat Research Meeting; Knoxville, TN.

Wieringa, JG*, Gibbs, HL, and Carstens BC. Trace elements as a method for sourcing migratory Tree Bats. Presentation, North American Society for Bat Research, Knoxville, TN, October 2017.

Wieringa JG*, Gibbs HL, and Carstens BC. Trace elements as a method for sourcing migratory Tree Bats. Rapid talk. Student Conference on Conservation Science, AMNH, New York, NY, October 2017.

Carstens BC, Morales AE, Pelletier TA. Do Organismal Traits or Species Range Attributes Offer the Best Predictions of How Species Respond to Climate Change? 2017 North American Society for Bat Research Meeting; Knoxville, TN.

Morales AE*, Carstens BC. Genomic Evidence That *Myotis lucifugus* 'Subspecies' Are Five Non-sister Species, Despite Gene Flow. 2017 North American Society for Bat Research Meeting; Knoxville, TN.

Morales AE*, Carstens BC. Gene flow interferes with phylogenetic signal: *Myotis lucifugus* subspecies are five non-sister species. 2017 SSB Meeting, Baton Rouge, LA

Carstens BC, Pelletier TA. Big Data for Phylogeography. 2017 SSB Meeting, Baton Rouge, LA
 Smith ML*, Carstens BC, Tank DC, Sullivan J, Ruffley MA, Espíndola A. Species limits and relationships within tail-dropper slugs (genus *Prophyaon*) from the Pacific Northwest.
 Espíndola A⁺, Pelletier TA, Carstens BC, Sullivan J, Tank DC. Predictive methods for conservation prioritization.
 Morales AE*, Jackson N, O'Meara BC, Carstens BC. Unraveling the effects of gene flow on species limits and phylogenetic signal in *Myotis* bats. 2017 Evolution Meeting, Portland, OR.

2016 Contributions

Carstens BC*, Morales AE, Pelletier TA. Phylogeographic meta-analysis into global patterns of genetic variation. 2016 Evolution meeting, Austin, TX.
 Espíndola A⁺, Ruffley M, Smith ML, Tank DC, Carstens BC, Sullivan J. Predicting cryptic diversity from phylogeographic, climatic and taxonomic data. 2016 Evolution meeting, Austin, TX.
 Morales AE*, Jackson N, O'Meara BC, Carstens BC. Speciation with gene flow in North American *Myotis* bats. 2016 Evolution meeting, Austin, TX.
 Satler JD*, Carstens BC. Testing for co-diversification in an ecological community: an example from the *Sarracenia alata* pitcher plant system. 2016 Evolution, Austin, TX.
 Smith ML*, Ruffley M, Espíndola A, Tank DC, Sullivan J, Carstens BC. Testing models of colonization in the robust lancetooth snail (*Haplotrema vancouverense*) from the Pacific Northwest using Approximate Bayesian Computation and the Site Frequency Spectrum. 2016 Evolution, Austin, TX.
 Ruffley M*, Espíndola A, Smith ML, Carstens BC, Tank DC, Sullivan J. Phylogeography of *Alnus rubra* in the Pacific Northwest temperate rainforest. 2016 Evolution meeting, Austin, TX.

2015 Contributions

Carstens BC. Evolutionary models and the OSC. 2015 Statewide Users Group Meeting of the Ohio Supercomputer Center.
 Morales-García AE*, ND Jackson, BC O'Meara, BC Carstens. *Myotis* divergence with migration. 2015 North American Society for Bat Research, Monterey, CA.
 Carstens BC, Morales-García AE, Jackson ND, O'Meara BC. 2015. Gene flow should be explicitly modeled (rather than ignored) in species delimitation investigations that utilize genetic Data. Evolution Annual Meeting.
 Morales-García AE*, Carstens BC. Species delimitation of western long-eared *Myotis* bats using approximated likelihood. Society of Systematic Biologists Annual Meeting.

2014 Contributions

Satler JD*, Carstens BC. Do ecological communities co-diversify? An investigation into the *Sarracenia alata* pitcher plant system. Evolution Annual Meeting, Raleigh, NC.
 Gruenstaeudl M⁺, Carstens BC, Jansen R, Santos-Guerra A. Hybrid taxa can mislead phylogeographic analyses in *Tolpis* (Asteraceae). Evolution Annual Meeting, Raleigh, NC.
 Jackson ND⁺, Morales-García AE, Carstens BC, O'Meara BC. Phylogeographic model selection using approximated likelihoods. Evolution Annual Meeting, Raleigh, NC.

2013 Contributions

Pelletier TA*, Zellmer AJ, Carstens BC. Using ecological niche models to predict species boundaries. Evolution Annual Meeting, Snowbird, Utah.
 O'Meara BC, Carstens BC. Simulated likelihood for species delimitation and phylogeography. Evolution Annual Meeting, Snowbird, Utah.
 Carstens BC*. SpedeSTEM 2.0: New, improved & more fun than ever. Evolution Annual Meeting, Snowbird, Utah.
 Reid NM*, Carstens BC. What can we learn from sequence-based species discovery? An example using sky island fly communities. Evolution Annual Meeting, Snowbird, Utah.
 Hird SM*, Carstens BC, Brumfield RT. Nature, nurture and the gut microbiota in the brood parasitic Brown-headed Cowbird. Evolution Annual Meeting, Snowbird, Utah.

2012 Contributions

Hird SM*, Carstens BC, Brumfield RT. Using gut microbiota to explore ecology and evolution in Neotropical birds; Evolution Annual Meeting, Ottawa, Ontario, Canada.

Hird SM*, Carstens BC and RT Brumfield. Gut microbiota of an avian brood parasite (*Molothrus ater*) and nine potential host species; Ecology and Evolution of Host-associated Microbiota Workshop, Basel, Switzerland.

Pelletier TA*, Carstens BC. Piecing together demographic models: an example from *Plethodon idahoensis*. Evolution Annual Meeting, Ottawa, Ontario, Canada.

Satler JD*, Carstens BC. Species delimitation in the carnivorous plant species *Sarracenia alata*. Evolution Annual Meeting, Ottawa, Ontario, Canada.

Reid NM*, Hird SM, Satler J, Pelletier TA, McVay JD, Brown J, and BC Carstens. Do multispecies coalescent models fit empirical data? Society of Systematic Biology Symposium. Evolution Annual Meeting, Ottawa, Ontario, Canada.

2011 Contributions

Reid NM*, BC Carstens. A Bayesian implementation of the mixed Yule-coalescent model for species delimitation. Talk. Evolution Annual Meeting. Norman, OK, USA.

Reid NM*, Koopman MM, Zellmer AJ, and BC Carstens. Integrating over taxonomic and phylogenetic uncertainty in analyses of phylogenetic community structure in the fluid of the pale pitcher plant (*Sarracenia alata*). Talk. Ecological Society of America Annual Meeting. Austin, TX, USA.

Hird SM*, Brumfield RT and BC Carstens. Creating and using a provisional-reference genome from anonymous next-gen fragments using PRGmatic; Society for the Study of Evolution, Norman, OK, USA.

Zellmer AJ*, Carstens BC. Testing for local adaptation in carnivorous plant populations using global climate data and next-generation sequencing. Evolution Annual Meeting, Norman, Oklahoma, USA.

2010 Contributions

Hird SM*, Koopman MM, Ence DD, Brumfield RT and BC Carstens. An Efficient Pipeline for the Preparation of Phylogeographic Data Collected Via Next-Generation Sequencing; Society for the Study of Evolution, Portland, OR, USA.

Zellmer AJ*, Koopman M, Carstens BC. Community phylogeography in a carnivorous plant. Evolution Annual Meeting, Portland, OR.

Pelletier TA*, Carstens BC. Demographic model selection in a terrestrial salamander. Evolution Annual Meeting, Portland, OR.

Carstens BC*, Koopman M, Hird SM. Analysis of phylogeographic data collected via next-generation sequencing in the carnivorous plant *Sarracenia alata*. Evolution Annual Meeting, Portland, OR.

2009 Contributions

McVay JD*, Carstens BC. A comparison of methods for estimating species phylogenies from gene trees: An example from *Thamnophis*. Evolution Annual Meeting, Moscow, ID.

Koopman M+, Carstens BC. Genetics of the Louisiana pitcher plant community. Evolution Annual Meeting, Moscow, ID.

EDITORIAL SERVICE

Editor-in-Chief: Systematic Biology (January 2019 – present)

Founding Editor: Bulletin of the Society of Systematic Biologists (January 2020 – present)

Associate Editor: Molecular Ecology (2010-2018), Molecular Ecology Resources (2014-2018), Systematic Biology (2017-2018).

Editorial Review Board: Systematic Biology (2010-2018).

Reviews provided for: American Midland Naturalist, American Museum Novitates, American Naturalist, Bioinformatics, Biological Conservation, Biological Journal of the Linnean Society, BMC Evolutionary Biology, Evolution, Gene, Genetica, Genome Biology, Journal of Biogeography, Journal of Heredity, Journal of Mammalogy, Journal of Mammalian Evolution, Journal of Molecular Evolution, Molecular Ecology, Molecular Biology & Evolution, Molecular Phylogenetics & Evolution, Occasional Papers of the Museum of Texas Tech

University, PeerJ, Proceedings of the National Academy of Sciences USA, Proceedings of the Royal Society of London (B), PLoS Biology, PLoS One, Science, Systematic Biology.

SERVICE TO PROFESSIONAL SOCIETIES

Program Chair (2010-2013), Society of Systematic Biologists
Executive Vice President (2014-2016), Society of Systematic Biologists.
 Joint Meeting Committee (2013-2015), Society of Systematic Biologists + Society for the Study of Evolution.
Memberships: American Association for the Advancement of Science, Society of Systematic Biologists, Society for the Study of Evolution, North American Society for Bat Research.

TEACHING

2022.EEOB 4220: Evolution and Ecology of Mammals (40 students in 4 sections)
 2022. EEOB 5330: Population Genetics and Phylogeography (17 students in 1 section)
 2021. EEOB 4220: Evolution and Ecology of Mammals (50 students in 4 sections)
 2020. EEOB 4220: Evolution and Ecology of Mammals (47 students in 3 sections)
 2019. ASC 1137: Biodiversity and Bioinformatics (14 students in 1 section)
 2019. EEOB 5330: Population Genetics and Phylogeography (15 students in 1 section, class published manuscript <https://doi.org/10.21425/F5FBG45377>)
 2019. EEOB 4220: Evolution and Ecology of Mammals (42 students in 3 sections)
 2019. EEOB 3310: Evolution (48 students in 1 section)
 2018. EEOB 3310: Evolution (48 students in 1 section)
 2018. EEOB 4220: Evolution and Ecology of Mammals (73 students in 4 sections)
 2018. EEOB 3310: Evolution (50 students in 1 section)
 2017. EEOB 4220: Evolution and Ecology of Mammals (67 students in 4 sections)
 2017. EEOB 3310: Evolution. (232 students in 8 sections)
 2016. ARTSSCI 1137: Biology of Sex Freshman Seminar (15 students in 1 section)
 2016. EEOB 3310H: Evolution (Honors Section) (26 students in 1 section)
 2016. EEOB 4220: Evolution and Ecology of Mammals (68 students in 4 sections)
 2015. EEOB 3310: Evolution (240 students in 16 sections)
 2015. EEOB 4220: Evolution and Ecology of Mammals (78 students in 4 sections)
 2014. EEOB 3310H: Evolution, Honors Section (27 students in 1 section)
 2014. EEOB 4220: Evolution and Ecology of Mammals (62 students in 3 sections)
 2014. Organized and led a 10-day course at the Universidade Estadual de Campinas in Campinas, Brasil titled "Model-based Phylogeography".
 2013. Organized and led a week-long course at the Universidad Nacional del Comahue in Bariloche, Argentina titled "Next-Generation Sequencing: State-of-the-art applications for population genetics and phylogeography" (with Brant Faircloth).
 2010, 2012. BS 7800: Computational Phylogeography, LSU. (Class project resulted in a published manuscript <https://doi.org/10.1111/mec.12347>)
 2011-2008. BS 3040: Evolution, Communications Intensive Section, LSU.
 2009. BS 7046: Current topics in Molecular Evolution Seminar, LSU.
 2009. BS 4299: Genetics of the Evolutionary Process, LSU.
 2009, 2010. Statistical Phylogeography Workshop, American Museum of Natural History Southwestern Field Station (with Mike Hickerson and Naoki Takebayashi).
 2008. BS 7901: Ecological Niche Modeling Seminar, LSU.
 2007. BS 3040: Evolution, LSU.
 2003. Teaching Assistant. Principles of Systematic Biology, UI.
 2001. Teaching Assistant. Center for Integrated Biological Sciences, MSU.
 2000-1998. Teaching Assistant. Biological Sciences, MSU.
 1996-1998. Education & Outreach Specialist. Organization for Bat Conservation.

 Other Service
Committee Member on Graduate Committees

LSU: Andres Cuervo; Melissa Debiasse; Haw-Chaun Lim; Carlos Prada; Eric Rittmeyer.

OSU: James Feller; Yuan Tian; Matt Holding; Robb Denton; Ben Titus; Ann Gregory; Rosa Rodriguez-Pena; Naava Honer; Paula Lado; Paul Blishak; Natalie Hamiton; Michele Taal; Ben Stone; Sungsik Kevin Kong; Heather Glon; Alonso Delgado, Charlotte Benedict; Matt Wolcuff; Jeremy Naredo.

Other: Evan Wong (U Cincinnati); Jenna Hamlin (UGA); Rafael Leite (BYU); Dan Gates (UNL).

Departmental Service

EEOB Graduate Studies Committee, August 2017 – 2020.

EEOB Search Committee Chair, Integrative Vertebrate Biologist search, August 2016-February 2017.

EEOB Advisory Committee. August 2014 – May 2016.

Graduate Admissions Committee Chair, The Ohio State University EEOB. August 2014 – May 2016 and August 2021 - *present*.

Integrative Vertebrate Biologist Search Committee Chair, The Ohio State University EEOB. October 2016–February 2017.

Moser Chair Search Committee Member, The Ohio State University EEOB. October 2014 – February 2015.

Phylogenetic Biology Search Committee Member, Louisiana State University Biology. October 2010-January 2011.

Arts and Sciences College Service

Arts & Sciences Honors Committee, The Ohio State University EEOB. August 2015-December 2018.

University Service

Ohio Supercomputer Center, Allocations Committee. April 2016 to December 2018.

Genomics Oversight Committee, January 2017 to May 2018.

MSBC Oversight Committee, January 2017 to June 2018.

Research Security Working Group, February 2017 to May 2018.

 MENTORING
Post-doctoral researchers supervised:

Kaiya L. Provost, Avian bioacoustics and big data (November 2020 – *present*).

Jordan D. Satler, Community Phylogeography (May 2022 – *present*).

Flavia M. Lanna, Data Science for Biodiversity Analysis in the Brazil Diagonal of Open Forests (August 2022 – *present*).

Lisa N. Barrow, amphibian conservation genetics (November 2018—December 2020). Currently an Assistant Professor at the University of New Mexico.

Tara A. Pelletier, big data phylogeography (January 2016—June 2018). Currently an Assistant Professor at Radford University.

Michael Gruenstaeudl, methods for posterior predictive simulation (February 2014—April 2015). Currently a post-doctoral researcher at the Freie Universität Berlin.

Tereza Thomé, phylogeography of Brazilian frogs (September 2013—February 2015 and July 2020 – August 2021). Currently a Managing Editor in the Netherlands.

Amanda Zellmer, genetics of *Sarracenia alata* (February 2010—May 2011). Currently an Associate Professor at Occidental College.

Erica Tsai, phylogeographic methods (February 2010—June 2012). Currently a Data Scientist in Denver.

Margaret M. Koopman (Hanes), microbiome and genetics of *S. alata* (August 2008—May 2010). Currently an Associate Professor at Eastern Michigan University.

Former Graduate Students, Dissertation Title, Current position:

- Sarah Hird**, Ph D (co-advised). Novel Computational Tools and Utilization of the Gut Microbiota for Phylogeographic Inference. (July 2009—May 2013). Currently an Assistant Professor in the Department of Molecular and Cell Biology / Microbiology at the University of Connecticut.
- John D. McVay**, Ph D. Molecular Phylogenetics of the North American Snake Tribe *Thamnophiini*. (August 2008—July 2013). Currently the Director of the Plant Pathogens lab at the Florida Department of Agriculture and Consumer Services.
- Noah M. Reid**, Ph D. Model-based Approaches to Discovering Diversity: New Implementations, Tests of Adequacy and an Empirical Application to Central American Diptera. (August 2008—July 2013). Currently a Research Professor in the Department of Molecular and Cell Biology / Microbiology at the University of Connecticut.
- Tara A. Pelletier**, Ph D. Species Delimitation in Western *Plethodon* salamanders. (June 2009—May 2015). Currently an Assistant Professor at Radford University.
- Jordan D. Satler**, Ph D. Community Phylogeography of *Sarracenia*-associated Arthropods. (August 2011—July 2016). Currently a Postdoctoral Researcher at The Ohio State University.
- Ariadna E. Morales**, Ph D. The evolutionary history of the bat genus *Myotis*, with emphasis on North American species. (August 2013—July 2018). Currently a Postdoctoral Researcher at the Max Planck Institute.
- Gregory L. Wheeler**, Ph D. Plant carnivory and the evolution of novelty in *Sarracenia alata*. (August 2014—July 2018). Currently a Bioinformatician at the Nationwide Children’s Hospital Cancer Genomics Center.
- Colleen E. Thompson**, M.S. Genetic diversity of North American vertebrates in protected areas. (August 2017 – May 2019). Currently working for the Ohio Department of Natural Resources.
- Megan L. Smith**, Ph D. Comparative phylogeography methods. (August 2015—May 2020). Currently a Postdoctoral Researcher in Matt Hahn’s lab at Indiana University. Assistant Professor at Mississippi State University starting fall of 2023.
- Jamin G. Wieringa**, Ph D. (co-advised with HL Gibbs), Bat conservation genetics. (August 2016—May 2022). Currently a Geneticist at the Southwestern Native Aquatic Resources and Recovery Center of the USFWS.
- Drew J. Duckett**, Incorporating whole genome sequencing into phylogeographic analysis: A case study of the Water Vole, *Microtus richardsoni* (August 2018—present). Currently a Bioinformatics Specialist at Northwestern University Hospital.
- Emanuel M. da Fonseca**, Investigating the drivers of genetic variation in neotropical lizards. (August 2018—May 2022π). Currently a postdoctoral scientist at the University of Arizona with Ryan Gutenkunst.
- Flavia M. Lanna**, Big data in Brazil’s Dry Diagonal (August 2018—August 2022). Currently a postdoctoral researcher in my lab.

Current Graduate Students:

- Danielle J. Parsons**, Phylogeography and Species delimitation of the Water Shrew, *Sorex palustris* (August 2018—present).
- Sydney K. Decker**, Big data, bat diversity, and species limits in yellow bats (August 2019 – present).
- Shelby P. Moshier**, *Topic to be determined* (August 2020 – present).
- Jessica Wallace**, *Topic to be determined* (August 2022 – present).

Publications with undergraduate students:

Jeremiah Degenhardt, Angela Stevenson, Peter Larsen, Marcia Keat, Elizabeth Gallagher, Holly Stoute, Danielle Fuselier, Edwin Rice, Katy Field, Connor Lang, Jessica Wallace, David Sneddon, Ivy Larkin.

FIELD EXPERIENCE

Collecting plant and environmental microbe samples, basic ecological field methods, surveying amphibians in the Pacific Northwest, behavioral ecology of ground squirrel populations in the Sierra Nevada Mountains, handling and preparing a variety of amphibians, reptiles and small mammals, mist-netting bats.

OUTREACH

2019. 'Bats: Hidden species and imperiled populations.' Columbus Science Pub. October 10, 2019.
2019. Museum of Biological Diversity WestFest. Participated in WestFest, a campus outreach event that drew over 1000 people. Discussed museum collections, showed specimens, answered questions.
- 2017-2019. Museum of Biological Diversity Open House. Over 3000 people toured the MBD in each year. Hosted ~350 people for tour of our wet lab, with hands-on demonstrations of DNA extraction, PCR, and alignment.
2016. Provided tours of lab and greenhouse space for Amy Miller's 5th grade class from Wickcliffe Progressive School. Guest presentations on the Biology of Sex to Experience ASC Day
2016. Guest presentation on Carnivorous Plants to Wickcliffe Progressive School.
2014. Guest presentation to the Westland Area Library on Bug Eating Plants.
2013. Guest presentation to OSU Camp Recky Environmental Camp on Carnivorous Plants.
2013. Guest presentation to Science Café at the Worthington Public Library on Carnivorous Plants.
- 2010-2011. Guest presentations to Westdale Heights Academic Magnet School on Carnivorous Plants.
- 2010-2011. Guest presentations on Carnivorous Plants to Zachary, LA, Elementary School.
2010. Testimony before the Louisiana Board of Education regarding high school biology textbooks in October of 2010.
2008. Testimony before the Louisiana Senate and House Education Committees regarding SB 733 in the spring of 2008. In addition to this testimony, I conducted print interviews and radio interviews regarding the 'Academic Freedom' bill in Louisiana.

DEI ACTIVITIES

2021. Presenter and Panelist at SSB DEIC Symposium at the 2021 Evolution Annual Meeting. Presented a talk arguing how changes to scientific publishing could broaden participation and improve equity among scientists.
2020. Participant in college reading / learning community about the need for proactive DEI actions in STEM disciplines.
2016. Co-PI on REU site: Next generation Evolutionary Biology. (NSF DBI-1560116). Co-leader of a REU program that focused on attracting students from underrepresented groups to the discipline of genomics and computational biology. Seven of these students are currently enrolled in Ph D programs.
2014. Co-PI on Connecting new Systematic Biologists across borders: A workshop in model-based phylogenetics at Evolution 2015. (DEB 1500774). Participated in panel discussion and learned from Brazilian students and researchers.
2009. As part of a project funded by the Louisiana Board of Regents, I led a field trip consisting of 3 school busses from urban schools in Baton Rouge to a nature preserve containing Longleaf Pine Savannah. We spent the day catching bugs, investigating carnivorous pitcher plants, talking about ecology, having a picnic lunch and playing kickball in the parking lot.

POPULAR (AND NOT SO POPULAR) PRESS

2022 press

- USA Today: [There are hundreds of undiscovered mammals – and you've probably seen one, new study says](#)
- New Scientist: [Why masses of new species have been staring us in the face all along](#)
- Science Daily: [Hundreds of new mammal species waiting to be found, study says](#)
- Monga bay: [Of rats and bats: Hundreds of mammal species still unidentified, study says](#)
- Science Alert: [100s of Undiscovered Mammal Species Could Still Be Out There in The Wild : ScienceAlert](#)
- The Guardian: [Hundreds of mammal species still to be identified, predict researchers | Wildlife | The Guardian](#)
- Phys.org: [Analysis of biodiversity data suggests hundreds of mammals are as-yet unidentified](#)
- Daily Mail: [Hiding in plain sight: HUNDREDS of new species of mammals are yet to be discovered | Daily Mail Online](#)
- OSU News: [Hundreds of new mammal species waiting to be found, study says](#)
- Scitech Daily: [Hundreds of "Hidden" New Mammal Species Waiting to Be Found](#)
- WIONews: [Hundreds of mammal species still waiting to be discovered, says study - Science News](#)
- Lab Manager: [Hundreds of New Mammal Species Waiting to Be Found, Study Says | Lab Manager](#)

Courthouse News: [Hundreds of mammal species await discovery | Courthouse News Service](#)

OSC Research Report: [Data Consolidation | Ohio Supercomputer Center](#)

Donku: [Hundreds of new mammal species waiting to be found, study says - doniku](#)

2020 press

[Carstens centralizes diffuse species data](#). OSC 2019-2020 Research Report.