
Curriculum Vitae

Mark J. Margres

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Education and Experience

- 2020– Assistant Professor, Department of Integrative Biology, University of South Florida.
- 2019–2020 Sarah and Daniel Hrdy Visiting Fellow in Conservation Biology, Department of Organismic and Evolutionary Biology, Harvard University. Sponsor: Michael Desai.
- 2018–2019 Postdoctoral associate with Chris Parkinson, Clemson University.
- 2017–2018 Postdoctoral associate with Andrew Storfer, Washington State University.
- 2011–2016 Ph.D., Biology, Florida State University. Summa cum laude. Advisor: Darin R. Rokytka.
- 2007–2011 B.A., Biology, Bethany College, Lindsborg, Kansas. Summa cum laude.

Funding

- 2020– National Science Foundation: Bridging Ecology and Evolution grant (NSF DEB-2027446) entitled “Eco-evolutionary dynamics of disease-induced apex predator decline” in the amount of \$207,738 (\$1,500,000 total across all CoPIs; other CoPIs: Andrew Storfer at Washington State University, Menna Jones at University of Tasmania, Hamish McCallum at Griffith University).
- 2019– National Geographic Exploration Grant (NGS-61140R-19) entitled “Venomous archipelagos: Integrating adaptability and island biogeography theory to assess persistence in the Anthropocene” in the amount of \$29,360.
- 2019–2020 Sarah and Daniel Hrdy Visiting Fellowship in Conservation Biology, Department of Organismic and Evolutionary Biology, Harvard University entitled “The genetic basis of transmission and virulence in an infectious cancer” in the amount of \$90,000.
- 2019 Theodore Roosevelt Memorial Grant, American Museum of Natural History entitled “Does island biogeography theory predict venom complexity in island rattlesnakes?” in the amount of \$3,500.
- 2014 The Graduate Student Research and Creativity Award at Florida State University entitled “The genetics of adaptation of island rattlesnakes” in the amount of \$675.
- 2013 The J. Larry Landers Student Research Award from the Gopher Tortoise Council entitled “Conservation genetics of the eastern diamondback rattlesnake” in the amount of \$500.
- 2013 The Robert B. Short Zoology Scholarship from the Department of Biological Science at Florida State University entitled “Local adaptation in rattlesnake venoms” in the amount of \$1,000.

- 2013 Dissertation Research Grant from Florida State University entitled “The genetics of adaptation of insular rattlesnake populations” in the amount of \$750.

Publications (Contributed equally[§], corresponding author[†], undergraduate*)

Calculated by Google Scholar (<https://scholar.google.com/citations?hl=en&user=HyuvK6AAAAAJ>) on 8/11/2020: 916 citations, h-index=16, i10-index=20

29. **Margres MJ[†]**, Ruiz-Aravena M, Hamede R, Chawla K, Patton A, Lawrance MF, Fraik AK, Stahlke A, Davis BW, Ostrander EA, Jones ME, McCallum H, Paddison PJ, Hohenlohe PA, Hockenbery, Storfer A. Spontaneous tumor regression in Tasmanian devils associated with *RASL11A* activation. *Genetics*. **215**:4, 1143–1152. Highlighted article.
28. Kozakiewicz C^{§†}, Ricci R[§], Patton A, Stahlke A, Hendricks S, **Margres MJ**, Ruiz-Aravena M, Hamilton D, Hamede R, McCallum H, Jones M, Hohenlohe PA, Storfer A[†]. Comparative landscape genetics reveals differential effects of environment on host and pathogen genetic structure in Tasmanian devils (*Sarcophilus harrisii*) and their transmissible tumor. *Molecular Ecology*. Accepted.
27. Fraik A, **Margres MJ**, Epstein B, Jones M, Hendricks S, Schonfeld B, Stahlke A, Hamede R, McCallum H, Lopez-Contreas E*, Kallinen SJ*, Lazenby B, Hawkins C, Fox S, Lachish S, Huxtable S, Kelley JL, Hohenlohe P, and Storfer A[†]. Disease-driven selection swamps local adaptation to abiotic factors in Tasmanian devil (*Sarcophilus harrisii*) populations. *Evolution*. **74**:7, 1392–1408. Cover Article.
26. Patton A[†], **Margres MJ**, Epstein E, Eastman J, Harmon L, and Storfer A. 2020. Hybridizing salamanders experience accelerated diversification. *Scientific Reports*. **10**, 6566. <https://doi.org/10.1038/s41598-020-63378-w>.
25. Mason AJ, **Margres MJ**, Strickland JL, Rokyta DR, Sasa M, and Parkinson, CL[†]. 2020. Trait differentiation and modular toxin expression in Palm-Pitvipers. *BMC Genomics*. **21**:1, 1–20.
24. **Margres MJ[†]**, Patton A, Wray KP, Hassinger ATB, Ward MJ, Lemmon EM, Lemmon AR, Rokyta DR. 2019. Tipping the scales: the migration-selection balance leans toward selection in snake venoms. *Molecular Biology and Evolution*. **36**:2, 271–282; <https://doi.org/10.1093/molbev/msy207>.
23. Patton A, **Margres MJ**, Stahlke A, Lewallen K, Hamede R, McCallum H, Jones M, Hohenlohe P, and Storfer A[†]. 2019. Contemporary demographic reconstruction methods are robust to genome assembly quality: a case study in Tasmanian devils. *Molecular Biology and Evolution*. msz191, <https://doi.org/10.1093/molbev/msz191>.
22. Fraik A, Quackenbush C, **Margres MJ**, Comte S, Hamilton D, Kozakiewicz C, Jones M, Hamede R, Hohenlohe PA, Storfer A, Kelley JL. Transcriptomics of Tasmanian devil (*Sarcophilus harrisii*) ear tissue reveals homogeneous gene expression patterns across a heterogeneous landscape. *Genes*. **10**:801, <https://doi.org/10.3390/genes10100801>.
21. Rautsaw R, Hofmann E, **Margres MJ**, Holding M, Strickland J, Mason A, Rokyta DR, and Parkinson, C[†]. 2019. Intraspecific sequence and gene expression variation contribute little to venom diversity in Sidewinder Rattlesnakes (*Crotalus cerastes*). *Proceedings of the Royal Society B: Biological Sciences*. **286**, 20190810. <https://doi.org/10.1098/rspb.2019.0810>; Cover Article.
20. **Margres MJ**, Ruiz-Aravena M, Hamede R, Jones ME, Lawrance MF, Hendricks SA, Patton A, Davis BW, Ostrander EA, McCallum H, Hohenlohe PA, Storfer A[†]. 2018. The genomic basis of tumor regression in Tasmanian devils (*Sarcophilus harrisii*). *Genome Biology and Evolution*. **10**:11, 3012–3025.
19. **Margres MJ[§]**, Jones M[§], Epstein B[§], Comte S, Fox S, Fraik AK, Hendricks SA, Huxtable S, Lachish S, Lazenby B, O’Rourke SM, Stahlke AR, Wiench CG*, Hamede R, Schonfeld B, McCallum H, Miller MR, Hohenlohe PA[†], Storfer A[†]. 2018. Large-effect loci affect survival in Tasmanian devils infected with a transmissible cancer. *Molecular Ecology*. **27**:4189–4199; doi:10.1111/mec.14853.

18. Holding M[†], **Margres MJ**, Rokyta DR, Gibbs HL. 2018. Local community composition and genetic distance predict venom divergence among populations of the Northern Pacific rattlesnake (*Crotalus oreganus*). *BMC Evolutionary Biology*. doi:10.1111/jeb.13347.
17. Holding M, **Margres MJ**, Mason A, Parkinson CL, Rokyta DR[†]. 2018. Evaluating the performance of *de novo* assembly methods for venom-gland transcriptomics. *Toxins* **10**:6, 249; doi:10.3390/toxins10060249. Invited article.
16. Storfer A[†], Hohenlohe PA, **Margres MJ**, McCallum H, Patton AH, Fraik AK, Lawrance M, Stahlke A, Jones ME, Ricci L. 2018. The devil is in the details: genomics of transmissible cancers in Tasmanian Devils. *PLOS Pathogens*. **14**:8, e1007098. Invited article.
15. **Margres MJ**[†], Wray KP, Hassinger ATB*, Ward MJ, McGivern JJ, Lemmon EM, Lemmon AR, Rokyta DR. 2017. Quantity, not quality: rapid adaptation in a polygenic trait proceeded exclusively through expression differentiation. *Molecular Biology and Evolution* **34**:12, 3099–3110.
14. **Margres MJ**, Bigelow AB*, Lemmon EM, Lemmon AR, Rokyta DR[†]. 2017. Selection to increase expression, not sequence diversity, precedes gene family origin and expansion in rattlesnake venom. *Genetics* **206**:3, 1569–1580.
13. Rokyta DR[†], **Margres MJ**, Ward MJ, Sanchez EE. 2017. The genetics of venom ontogeny in the eastern diamondback rattlesnake (*Crotalus adamanteus*). *PeerJ* **5**:e3249.
12. **Margres MJ**, Wray KP, Seavy M, McGivern JJ, Herrera NH, Rokyta DR[†]. 2016. Expression differentiation is constrained to low-expression proteins over ecological timescales. *Genetics* **202**:1, 273–283.
11. **Margres MJ**, Walls R, Suntravat M, Lucena S, Sanchez EE, Rokyta DR[†]. 2016. Functional characterizations of venom phenotypes in the eastern diamondback rattlesnake (*Crotalus adamanteus*) and evidence for expression-driven divergence in toxic activities among populations. *Toxicon* **119**:28–38.
10. **Margres MJ**, McGivern JJ, Seavy M, Wray KP, Facente J, Rokyta DR[†]. 2015. Contrasting modes and tempos of venom expression evolution in two snake species. *Genetics* **199**:1, 165–176. Highlighted article.
9. **Margres MJ**, Wray KP, McGivern JJ, Seavy M, Sanader D*, Rokyta DR[†]. 2015. Phenotypic integration in the feeding system of the eastern diamondback rattlesnake (*Crotalus adamanteus*). *Molecular Ecology* **24**:13, 3405–3420.
8. Rokyta DR[†], **Margres MJ**, Calvin, K. 2015. Post-transcriptional mechanisms contribute little to phenotypic variation in snake venoms. *G3: Genes, Genomes, Genetics* g3-115.
7. Wray KP, **Margres MJ**, Seavy M, Rokyta DR[†]. 2015. Early significant ontogenetic changes in snake venoms. *Toxicon* **96**:74–81.
6. Rokyta DR[†], Wray KP, McGivern JJ, **Margres MJ**. 2015. The transcriptomic and proteomic basis for the evolution of a novel venom phenotype within the Timber Rattlesnake (*Crotalus horridus*). *Toxicon* **98**:34–48.
5. **Margres MJ**, McGivern JJ, Wray KP, Seavy M, Calvin K, Rokyta DR[†]. 2014. Linking the transcriptome and proteome to characterize the venom of the eastern diamondback rattlesnake (*Crotalus adamanteus*). *Journal of Proteomics* **96**:145–158.
4. McGivern JJ, Wray KP, **Margres MJ**, Couch ME*, Mackessy SP, Rokyta DR[†]. 2014. RNA-seq and high-definition mass spectrometry reveal the complex and divergent venoms of two rear-fanged colubrid snakes. *BMC Genomics* **15**:1061.

3. **Margres MJ**, Aronow K*, Loyacano J*, Rokyta DR[†]. 2013. The venom-gland transcriptome of the eastern coral snake (*Micrurus fulvius*) reveals high venom complexity in the intragenomic evolution of venoms. *BMC Genomics* **14**:531. Highly accessed.
2. Rokyta DR[†], Wray KP, **Margres, MJ**. 2013. The genesis of an exceptionally deadly venom in the timber rattlesnake (*Crotalus horridus*) revealed through comparative venom-gland transcriptomics. *BMC Genomics* **14**:394. Highly accessed.
1. Rokyta DR[†], Lemmon AR, **Margres MJ**, Aronow K*. 2012. The venom-gland transcriptome of the eastern diamondback rattlesnake (*Crotalus adamanteus*). *BMC Genomics* **13**:312.

Submitted Manuscripts (Contributed equally[§], corresponding author[†], undergraduate*)

1. **Margres MJ**[†], Rautsaw RM, Strickland JL, Mason AJ, Schramer TD, Hofmann EP, Stiers E, Ellsworth SA, Nystrom GS, Hogan MP, Bartlett DA, Colston TJ, Gilbert DM, Rokyta DR, Parkinson C[†]. The Tiger Rattlesnake genome reveals how a complex genotype produces the simplest venom phenotype. *PNAS*. In review.
2. Patton A, Lawrance M, **Margres MJ**, Kozakiewicz C, Hamede R, Ruiz-Aravena M, Hamilton DG, Comte S, Ricci L, Taylor R, Stadler T, Leachè, McCallum H, Jones M, Hohenlohe P, Storfer A[†]. Phylodynamics of Tasmanian devil transmissible cancer reveals a shift from emergence to endemism. *Science*. In revision.
3. Huff E*, Schonour R*, Holding M, Claunch N, Ellsworth S, Hogan M, Wray K, McGivern J, **Margres MJ**, Colston T, Rokyta DR[†]. Gradual and discrete ontogenetic changes in venom composition in two rattlesnake species associate with shifts in dietary ecology. *Toxins*. Submitted.
4. Rautsaw R, Schramer T, Acuna R, Arick L, DiMeo M, Hickson J, Mercier K, Schrum M, Mason A, **Margres MJ**, Strickland J, Parkinson C[†]. Genomic adaptations to salinity resist gene flow in the evolution of Floridian Watersnakes. *Molecular Biology and Evolution*. In revision.
5. Holding ML, Strickland JL, Rautsaw RM, Hofmann EP, Mason AJ, Hogan MP, Nystrom GS, Ellsworth SA, Colston TJ, Borja M, Castaneda-Gaytan G, Grunwald CI, Jones JM, Freitas-de-Sousa L, Viala VL, **Margres MJ**, Graziotin FG, Junqueira-da-Azevedo ILM, Moura-da-Silva AM, Hingst-Zaher E, Gibbs HL, Rokyta, DR, Parkinson C[†]. Phylogenetically diverse diets favor more complex venoms in North American pitvipers. *PNAS*. Submitted.

Invited talks

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| 2020 | Harvard Museum of Natural History Public Lecture (Cambridge, Massachusetts): Infectious cancer in Tasmanian devils |
| 2020 | University of South Florida (Tampa, Florida): Complex disruptions: genetic mechanisms underlying coevolutionary dynamics |
| 2020 | Arkansas State University (Jonesboro, Arkansas): Patterns, processes, and mechanisms of adaptive evolution |
| 2020 | Oklahoma State University (Stillwater, Oklahoma): Patterns, processes, and mechanisms of adaptive evolution |
| 2019 | Auburn University (Auburn, Alabama): Devil cancer, viper venom, and adaptive coevolution |
| 2018 | University of South Carolina (Columbia, South Carolina): Genetics of adaptation in complex traits |
| 2018 | Fred Hutchinson Cancer Research Center (Seattle, Washington): Comparative genomics of tumor regression in Tasmanian devils |
| 2018 | University of Memphis (Memphis, Tennessee): Genetics of adaptation in complex traits |
| 2017 | University of Tulsa (Tulsa, Oklahoma): Genetics of adaptation in complex traits |
| 2016 | International Symposium on Coral Snakes (Goiania, GO, Brazil): The relationship between complexity, variability, and toxicity in North American coralsnakes |
| 2016 | University of Utah (Salt Lake City, Utah): Quantity, not quality: rapid adaptation to local prey proceeds through venom-gene expression changes in rattlesnakes |

- 2015 Apalachicola National Estuarine Research Reserve (Eastpoint, Florida): Population venomics of the eastern diamondback rattlesnake (*Crotalus adamanteus*) identifies selection-driven incipient speciation
- 2014 Catalysis meeting at the National Evolutionary Synthesis Center (Durham, North Carolina): Integrating Organismal and Applied Perspectives on Animal Venom Diversity
- 2013 36th Annual Herpetology Conference (Gainesville, Florida): Genotype-phenotype mapping in the eastern diamondback rattlesnake (*Crotalus adamanteus*): quantifying differential gene expression in toxin genes
- 2013 Tall Timbers Research Station and Land Conservancy (Tallahassee, Florida): Venoms: Ties to Ecology, Evolution, and Conservation

Presentations

- 2019 Harvard Museum of Comparative Zoology Seminar Series (Cambridge, Massachusetts): Population venomics in island rattlesnakes (Talk)
- 2018 Genetics Symposium, Clemson University (Clemson, South Carolina): Genetics of adaptation in complex traits (Talk)
- 2018 Department of Biological Sciences Seminar Series, Clemson University (Clemson, South Carolina): A mechanism for tumor regression in a transmissible cancer (Talk)
- 2018 Washington State University Alumni Association Research Presentation (Pullman, Washington): The devil's cancer (Talk)
- 2018 EVO-WIBO (Port Townsend, Washington): A mechanism for tumor regression in a transmissible cancer (Talk)
- 2017 Evolution (Portland, Oregon): Variants of large-effect underlie sex-specific resistance to a transmissible cancer (Talk)
- 2017 Palouse Ecology, Evolution and Systematics Seminar (Pullman, Washington): Quantity, not quality: rapid adaptation in a complex, polygenic trait proceeded exclusively through expression differentiation (Talk)
- 2016 Evolution (Austin, Texas): Quantity, not quality: rapid adaptation to local prey proceeds through venom-gene expression changes in rattlesnakes (Talk)
- 2016 Ecology and Evolution Seminar Series, Florida State University (Tallahassee, Florida): Quantity, not quality: rapid adaptation to local prey proceeds through venom-gene expression changes in rattlesnakes (Talk)
- 2014 Evolution (Raleigh, North Carolina): Expression evolution in island snake venoms (Talk)
- 2014 Biology of the Pitvipers 2 (Tulsa, Oklahoma): The evolution of island venoms (Talk)
- 2013 35th Annual Gopher Tortoise Council Meeting (Ponte Vedra, Florida): Protein expression variation contributes to the evolution of the venom of the eastern diamondback rattlesnake (Talk)
- 2013 Southeast Partners in Amphibian and Reptile Conservation (SEPARC) Annual Meeting (Hickory Knob State Park, South Carolina): Population genomics and ecological diversification in North American venomous snakes (Talk)
- 2012 34th Annual Gopher Tortoise Council Meeting (Bainbridge, Georgia): Population and ecological diversification in North American venomous snakes (Talk)
- 2012 17th World Congress of the International Society on Toxinology and Venom Week (Honolulu, Hawaii): The venom-gland transcriptome of the eastern coral snake (*Micrurus fulvius*) reveals cryptic venom complexity in the intragenomic evolution of venoms (Poster)

Awards

- 2014 Three-Minute Thesis Competition Finalist at Florida State University.
- 2013 Best student presentation at the 36th Annual Herpetology Conference.
- 2012 Best young investigator poster at the 17th World Congress of the International Society on Toxinology.
- 2012 Best student presentation at the 34th Annual Gopher Tortoise Council Meeting.

Teaching

2020	Spring	ESPP90e: Conservation Biology, Harvard University
2016	Fall	ZOO4343C: Herpetology (Co-instructor of record), Florida State University

Graduate Advisory Committees

2020-present Jeanette Calarco, Ph.D. Department of Integrative Biology, USF.

General Service

2020–	Guest Editor for Special Issue on “Using genomics to understand venom evolution” in <i>Toxins</i> . https://www.mdpi.com/journal/toxins/special_issues/genomics_venom
2019–	Participant in National Geographic’s Explorer Classroom outreach program that connects classrooms around the world with National Geographic Explorers.
2019	BIOSCIence Expo, Clemson University: “Snakes of South Carolina.” Educational exhibit following the Annual Biology Merit Exam for middle and high school students in SC.
2018	“Ask Dr. Universe”: What is venom? https://askdruniverse.wsu.edu/2018/10/26/what-is-venom/
2015	Guest speaker at the Venom Adventures Summer Camp at the Tallahassee Museum.
2014–2015	Instructor for Saturday-at-the-Sea, an outreach program for middle school students through the Office of Science Teaching Activities and the Florida State University Coastal and Marine Laboratory. Through this program, students gain hands-on experience in the lab and field in an attempt to stimulate a strong interest in science.
2014–2015	Guide for Boy Scouts of America Troop 115 for the Reptile Amphibian Merit Badge. I led a group of young scouts into the field to catch, identify, and describe ten species of reptile and amphibian, discuss the ecology of these animals, and explain how these organisms are critical components of the ecosystems they inhabit.

Manuscript Review

- BMC Evolutionary Biology
- BMC Genomics
- Cellular & Molecular Life Sciences
- Chemical Research in Toxicology
- Conservation Genetics
- Current Biology
- Current Medicinal Chemistry
- eLife
- Genes
- Genome Biology & Evolution
- GigaScience
- International Journal of Environmental Research & Public Health
- Journal of Molecular Evolution
- Journal of Proteomics
- Marine Drugs
- Molecular Biology & Evolution
- Molecular Ecology
- Molecular Phylogenetics & Evolution
- Molecules
- PeerJ
- PLOS One
- Scientific Reports
- Toxicology in Vitro
- Toxins