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# MELANIE LACAVA

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## EDUCATION

**Ph.D. in Ecology**, University of Wyoming 2021
Dissertation: "Genetic connectivity and infectious disease ecology in two Wyoming ungulates" (Dr. Holly Ernest, Advisor)
Minor in Environment and Natural Resources

**B.Sc. in Wildlife, Fish and Conservation Biology**, University of California, Davis 2013
Honors thesis: "Genetics of Delta smelt spawning behavior" (Dr. Bernie May, Advisor)

## PUBLICATIONS

Gustafson, K.D., R.B. Gagne, M.R. Buchalski, T.W. Vickers, S.P.D. Riley, J. Sikich, J.L. Rudd, J.A. Dellinger, **M.E.F. LaCava**, H.B. Ernest. 2022. Multi-population puma connectivity could restore genomic diversity to at-risk coastal populations in California. *Evolutionary Applications* doi: 10.1111/eva.13341

**LaCava, M.E.F.**, J.L. Malmberg, W.H. Edwards, L.N.L. Johnson, S.E. Allen, H.B. Ernest. 2021. Spatiotemporal analyses reveal infectious disease-driven selection in a free-ranging ungulate. *Royal Society Open Science* 8(8):210802. doi:10.1098/rsos.210802

**LaCava, M.E.F.**, R.B. Gagne, K.D. Gustafson, S.J. Oyler-McCance, K.L. Monteith, H. Sawyer, M.J. Kauffman, D.J. Thiele, H.B. Ernest. 2021. Functional connectivity in a continuously distributed, migratory species as revealed by landscape genomics. *Ecography* 44(7):987–999. doi:10.1111/ecog.05600

**LaCava, M.E.F.**, R.B. Gagne, S.M. Love Stowell, K.D. Gustafson, C.A. Buerkle, L. Knox, H.B. Ernest. 2020. Pronghorn population genomics show connectivity at the core of their range. *Journal of Mammalogy* 101(4):1061–1071. doi:10.1093/jmammal/gyaa054

Godwin, B.L., **M.E.F. LaCava**, B. Mendelsohn, R.B. Gagne, K.D. Gustafson, S.M. Love Stowell, A. Engilis, Jr., L.A. Tell, H.B. Ernest. 2020. Novel hybrid finds a peri-urban niche: Allen's hummingbirds in southern California. *Conservation Genetics* 21:989–998. doi:10.1007/s10592-020-01303-4

Mendelsohn, B., B. Bedrosian, S.M. Love Stowell, R.B. Gagne, **M.E.F. LaCava**, B.L. Godwin, J.M. Hull, H.B. Ernest. 2020. Population genomic diversity and structure at the discontinuous southern range of the Great Gray Owl in North America. *Conservation Genetics* 21:693–706. doi:10.1007/s10592-020-01280-8

**LaCava, M.E.F.**, E.O. Aikens, L.C. Megna, G. Randolph, C. Hubbard, C.A. Buerkle. 2019. Accuracy of *de novo* assembly of DNA sequences from double-digest libraries varies substantially among software. *Molecular Ecology Resources* 20(2):360–370. doi:10.1111/1755-0998.13108

**LaCava, M.**, K. Fisch, M. Nagel, J.C. Lindberg, B. May, A.J. Finger. 2015. Spawning behavior of cultured Delta Smelt (*Hypomesus transpacificus*) in a conservation hatchery. *North American Journal of Aquaculture* 77:255-266. doi:10.1080/15222055.2015.1007192

Long, J.Z., **M. LaCava**, X. Jin, B.F. Cravatt. 2011. An anatomical and temporal portrait of physiological substrates for fatty acid amide hydrolase. *Journal of Lipid Research* 52(2):337–344. doi:10.1194/jlr.M012153

## RESEARCH EXPERIENCE

**Postdoctoral scholar**, University of California, Davis 2021–present

Using a combination of experiments, simulations and empirical data, I am evaluating the genetic consequences of spawning strategy in a conservation hatchery of endangered Delta smelt (*Hypomesus transpacificus*) to inform production for supplementing wild populations. I am also using 10+ years of hatchery pedigree data to assess evidence of adaptation to captivity in relation to reproductive timing in Delta smelt. I am also investigating evolutionary relationships among Relict dace (*Relictus solitarius*) populations in the Great Basin.

**PhD candidate**, University of Wyoming 2015–2021

I used population genomics to study genetic connectivity and disease ecology in Wyoming pronghorn (*Antilocapra americana*) and mule deer (*Odocoileus hemionus*). For pronghorn, I performed a population genomic assessment using both microsatellites and a large SNP dataset generated by ddRAD sequencing. For mule deer, I generated a large SNP dataset for landscape genomics to relate spatial patterns of genomic variation to natural and anthropogenic environmental variables. I also Sanger sequenced the prion protein gene in mule deer to investigate chronic wasting disease-driven natural selection in mule deer.

**Laboratory manager**, University of Wyoming Aug–Nov 2018

I managed three undergraduate technicians, lab purchasing, and equipment maintenance for Dr. Holly Ernest's Wildlife Genomics and Disease Ecology laboratory.

**Research associate**, San Diego Zoo Global 2014–2015

I maintained the captive population of endangered Pacific Pocket mice (*Perognathus longimembris pacificus*) under the Pacific Pocket Mouse Conservation Breeding and Reintroduction Program. I monitored health and reproductive status of animals, managed captive breeding, and performed behavioral experiments. I also assisted in trapping wild Los Angeles pocket mice (*Perognathus longimembris brevinasus*) and Stephen's kangaroo rats (*Dipodomys stephensi*) for population monitoring.

**Field research assistant**, Barbary Macaque Project, Morocco 2013–2014

I used an ethogram-encoded handheld device to record focal and scan behavioral data and performed behavioral experiments on wild, endangered Barbary macaques (*Macaca sylvanus*) in the Atlas Mountains of Morocco.

**Laboratory technician**, Genomic Variation Lab, University of California, Davis 2011–2013

I performed DNA extraction and PCR for microsatellite genotyping of the endangered Delta smelt (*Hypomesus transpacificus*) to aid in the selection of breeding pairs for a captive refuge population. For my undergraduate honors thesis, I used genetic parentage analysis to assess natural spawning strategies of the captive Delta smelt population.

**Laboratory technician**, Grosholz Lab, University of California, Davis 2010–2013

I identified aquatic macroinvertebrates, tested water and soil samples, and assisted in field experiments for an NSF Coupled Natural and Human Systems project on ecosystem recovery following eradication of the invasive cordgrass (*Spartina alterniflora*) in the San Francisco Estuary.

**Summer fellowship**, San Diego Zoo Global Institute for Conservation Research 2012

I performed targeted cDNA sequencing to compare coding regions of genes related to heat tolerance in bovids. I compared polymorphisms between desert-dwelling bovids and non-desert-dwelling bovids to investigate the genetic basis of desert adaptation.

**Laboratory technician**, Cravatt Lab, The Scripps Research Institute 2010

I assisted on a chemical physiological project characterizing the metabolomic activity of the neurological enzyme fatty acid amide hydrolase (FAAH). I performed liquid chromatography-mass spectrometry, protein assays, gel electrophoresis, and lipid quantification.

## FUNDING AND AWARDS

**Carlton R. Barkhurst Dissertation Fellowship**, Univ. Wyoming (2020)

**Mary Mead Scholarship for Women in Agriculture**, Univ. Wyoming (2018)

**Y Cross Ranch Tuition and Fee Award**, Univ. Wyoming (2018)

**Program in Ecology Travel Grant**, Univ. Wyoming (2018)

**Student travel grant**, the Wildlife Society, Wyoming chapter annual meeting (2017)

**INBRE Sequencing and Bioinformatics Analysis Award** Univ. Wyoming (2016)
Pronghorn population genomics sequencing supported by NIH Institutional Development Award #2P20GM103432

**Best PhD Student Poster**, the Wildlife Society's annual conference (2016)

**Workshop Travel Grant**, Genomics of Adaptation to Human Contexts (2016)

**Program in Ecology Travel Grant**, Univ. Wyoming (2016)

**Program in Ecology Recruitment Initiative Award**, Univ. Wyoming (2015)

*Co-authored with P.I. Holly Ernest*

**U.S. Geological Survey** (2020)
Collaborative work with Co-P.I.s Matthew J. Kauffman, Kevin L. Monteith, Patricia Deibert, and Sara Oyler-McCance entitled, "Using genetic analyses to inform on-the-ground conservation for multiple sagebrush-associated wildlife species"

**Wyoming Governor's Big Game Grant** (2019)

**Wyoming Governor's Big Game Grant** (2018)

**INBRE Sequencing and Bioinformatic Analysis Award** Univ. Wyoming (2018)
Mule deer population genomics sequencing supported by NIH Institutional Development Award #2P20GM103432

**Wyoming Governor's Big Game Grant** (2017)

## TEACHING EXPERIENCE

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| *Invited lecture*: "Conservation and Genetics" in Introduction to Natural History, Oklahoma State Univ. | Spring 2021 |
| *Invited lecture*: "Behavioral Genetics" in Animal Behavior, Univ. Wyoming | Spring 2020 |
| *Teaching assistantships* | |
| Biology for Elementary Education, Univ. Wyoming | Fall 2017, Spring 2018, Spring 2019 |
| Conservation Genomics Seminar, Univ. Wyoming | Fall 2016, Fall 2018 |
| Disease Ecology, Univ. Wyoming | Spring 2016, Spring 2017 |

## CERTIFICATIONS AND TRAININGS

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| Certified Associate Ecologist, *Ecological Society of America* | 2019 |
| ConGen Population Genomic Data Analysis Workshop, *Univ. Montana* | September 2020 |
| Green Dot Strategy, *Univ.Wyoming*<br>Training to combat sexual harassment and violence on college campuses | July 2020 |

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| Science Communication Techniques for Advancing Justice, Diversity, Equity, and Inclusion, *RBR Ltd.* | July 2020 |
| Inclusive Leadership Workshop, *Univ. Wyoming* | Spring 2020 |
| Communicating Science and Management with the Media Workshop, *Wyoming Wildlife Society Meeting* | November 2018 |
| Safe Zone Workshop Series, *Univ. Wyoming*<br>Training in support and inclusivity for the LGBTQIA+ community | November 2018 |
| Genomics of Disease in Wildlife Workshop, *Colorado State University* | June 2018 |
| Introductory Wildlife Handling and Chemical Immobilization, *Wyoming Game and Fish Department* | May 2017 |
| Data Carpentry, *Colorado State University*<br>*Version* control with Git, Unix shell, Programming in R | July 2016 |
| Grant Writers' Workshop, *Univ. Wyoming* | June 2016 |
| Spatial Data Analysis in R Workshop, *Univ. Wyoming* | October 2015 |

## PROFESSIONAL SERVICE AND OUTREACH

*Leadership positions*

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| Finance committee, Univ. Wyoming Program in Ecology | 2019–2020 |
| Co-president, Univ. Wyoming Program in Ecology | 2018–2019 |
| Treasurer, Univ. Wyoming Graduate Student Network | 2017–2018 |
| Research Symposium committee, Univ. Wyoming Program in Ecology | 2016–2018 |
| Outreach committee, Univ. Wyoming Program in Ecology | 2015–2018 |

*Hiring committees*

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| Program coordinator, Univ. Wyoming Transdisciplinary Graduate Program | Sept. 2019 |
| Accountant, Univ. Wyoming Transdisciplinary Graduate Program | Sept. 2019 |

*Educational outreach* 2016–present

Elementary school: 15+ hours, reached 250+ students
Middle school: 12+ hours, reached 130+ students
High school: 20+ hours, reached 150+ students
*Including*: Women in STEM Day, STEM Saturday, Wyoming State Science Fair, Wyoming State Science Olympiad Tournament, Laramie Middle School STEAM Club

## PRESENTATIONS

*Discussion panels*

GBS/RADseq Genotyping, NSF Evolving Seas Research Coordinated Network MarineOmics working group. May 2021.

*Talks*

**LaCava, M.E.F.** "Chronic wasting disease drives natural selection in a free-ranging ungulate." Invited seminar, Department of Animal Science, University of California, Davis, November 2021.

**LaCava, M.E.F.**, J.L. Malmberg, W.H. Edwards, L.N.L. Johnson, S.E. Allen, H.B. Ernest. "Disease-driven selection in a free-ranging wildlife population as revealed by spatiotemporal analyses." Evolution, June 2021.

**LaCava, M.E.F.**, S.M. Love Stowell, R.B. Gagne, K.D. Gustafson, C.A. Buerkle, L. Knox, D. McWhirter, W.H. Edwards, H.B. Ernest. "Genetic structure reflects habitat requirements and social structure in three Wyoming ungulates." The Ecological Society of America Annual Meeting, August 2020.

**LaCava, M.E.F.,** R.B. Gagne, S.M. Love Stowell, K.D. Gustafson, C.A. Buerkle, L. Knox, H.B. Ernest. "Pronghorn population genomics show connectivity at the core of their range." University of Wyoming Program in Ecology Symposium, February 2020.

**LaCava, M.**, S.M. Love Stowell, R.B. Gagne, and H.B. Ernest. "Implications of marker type and species ecology on forensic use of genetic data: STRs and SNPs in wild ungulates." Oral presentation. Society for Wildlife Forensic Science Meeting, Denver, CO, USA, June 2019.

**LaCava, M.**, R.B. Gagne, S.M. Love Stowell, and H. B. Ernest. "Landscape genomic analysis of Wyoming pronghorn informs population biology and nomadic behavior." Oral presentation. 28th Biennial Western States and Provinces Pronghorn Workshop, Reno, NV, USA, August 2018.

**LaCava, M.**, R.B. Gagne, S.M. Love Stowell, and H. B. Ernest. "Development of population genomic tools for Wyoming pronghorn." Oral presentation. The Wildlife Society Wyoming State Annual Conference, Cody, WY, USA, November 2016.

**LaCava, M.** "Genetic analysis of Delta smelt spawning behavior" Oral presentation. Undergraduate Research, Scholarship and Creative Activities Conference, Davis, CA, April 2013.

**LaCava, M.** "Genetic variation of genes associated with heat response in desert-dwelling mammals," Oral presentation. San Diego Zoo Institute for Conservation Research Summer Fellowship Symposium, San Diego, CA, September 2012.

*Posters*

**LaCava, M.**, S.M. Love Stowell, M. Wood, and H. B. Ernest. "Landscape genomics and population health in Wyoming mule deer." Poster presentation. The Wildlife Society Wyoming State Annual Conference, Jackson, WY, USA, December 2017.

**LaCava, M.**, R.B. Gagne, S.M. Love Stowell, and H. B. Ernest. "Development and application of population genomic tools for conservation and management of Wyoming pronghorn." Poster presentation. The Wildlife Society's Annual Conference, Raleigh, NC, USA, October 2016.

**LaCava, M.**, R.B. Gagne, S.M. Love Stowell, and H. B. Ernest. "Development and application of population genomic tools for conservation and management of Wyoming pronghorn." Poster presentation. 27th Biennial Western States and Provinces Pronghorn Workshop, Anaconda, MT, USA, August 2016.

**LaCava, M.**, J. Halbert, and A. Kelley. "The influence of mammalian predation on potential avian nesting habitat in wetlands of Cache Creek Nature Preserve" Poster presentation. Habitat Restoration Ecology Undergraduate Project, Davis, CA, March 2013.